

Table 42: Comparative Sequences relating to SAG 0764

## SEQ ID NO. 4201: 2603 V/R STRAIN

ATGGTAAATAGTATTCGCACGCCACGGTGAATCTGAGTGGAAATAAGCTAACCTTTTC  
 ACTGGATGGGCTGACGTAGATCTTTTCAGAAAAAGGTACACAACAAGCTATTGATGCTGGG  
 AAATTAATTTCAAGCAGCAGGTATTGAGTTTCGACCTTGCTTTTACATCAGTTCTTTAAACGT  
 GCCATCAAAACAACCTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAA  
 AAATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAAAAATAAGCAGAA  
 GCAGCTGAACAATTTGGTGATGAGCAAGTTCATATTTGGCGTCGTTTATATGATGATTG  
 CTTCCAGATATGGCTAAAGATGATGAACATTTCAGCACATACTGATCGTCGCTATGCTTCA  
 CTAGATGATTCTGTTATTCAGATGCAGAAAACTTAAAGTTACTTTAGAGCGTGCTCTT  
 CCTTTCTGGGAAGATAAAATTTGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTGTTGGT  
 GCACACGGTAACCTCAATCCGTGCTCTTGTAAAAACATATCAACAATTTGTCAGATGATGAA  
 ATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTTTTCGAATTGATGAAAAATTA  
 AACCTTGTTTCAGAAATATTACTTAGGTAAA

## SEQ ID NO. 4202: 090 STRAIN

GTAAAAATTAGTATTCGCACGCCACGGTGAATCTGAGTG  
 GAATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTTCAGAAA  
 AAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAAGCAGCAGGT  
 ATTGAGTTTCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAAAC  
 AACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAAA  
 AATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAAAAAT  
 AAAGCAGAGCAGCTGAACAATTTGGTGATGAGCAAGTTTCATATTTGGCG  
 TCGTTTCATATGATGATTGCTCCAGATATGGCTAAAGATGATGAACATT  
 CAGCACATACTGATCGTCGCTATGCTTCACTAGATGATTCTGTTATTCCA  
 GATGCAGAAAACTTAAAGTTACTTTAGAGCGTGCTCTTCTTTCTGGGA  
 AGATAAAATTTGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTGTTGGTG  
 CACACGGTAACCTCAATCCGTGCTCTTGTAAAAACATATCAACAATTTGTC  
 GATGATGAAATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTTTT  
 CGAATTGATGAAAAATTAACCTTGTTTCAGAAATATTACTTAGGTAAA

## SEQ ID NO. 4203: A909 STRAIN

GTAAAAATTAGTATTCGCACGCCACGGTGAATCTGAGTGG  
 AATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTTCAGAAA  
 AAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAAGCAGCAGGT  
 TTGAGTTTCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAAACA  
 ACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAAAA  
 ATCATGGCGCTTAAACGAACGTCATTACGGTGGATTGACAGGAAAAATA  
 AAGCAGAGCAGCTGAACAATTTGGTGATGAGCAAGTTTCATATTTGGCGT  
 CGTTTCATATGATGATTGCTCCAGATATGGCTAAAGATGATGAACATT  
 AGCACATACTGATCGTCGCTATGCTTCACTAGATGATTCTGTTATTCCAG  
 ATGCAGAAAACTTAAAGTTACTTTAGAGCGTGCTCTTCTTTCTGGGA  
 GATAAAATTTGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTGTTGGTG  
 ACACGGTAACCTCAATCCGTGCTCTTGTAAAAACATATCAACAATTTGTC  
 ATGATGAAATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTTTT  
 GAATTTGATGAAAAATTAACCTTGTTTCAGAAATATTACTTAGGTAAA

## SEQ ID NO. 4204: H36B STRAIN

GTAAAAATTAGTATTCGCACGCCACGGTGAATCTGAG  
 TGGAATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTTCAGAA  
 AAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAAGCAGCAG  
 GTATTGAGTTTCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAA  
 ACAACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAA  
 AAATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAAAAATA  
 ATAAAGCAGAGCAGCTGAACAATTTGGTGATGAGCAAGTTTCATATTTGG  
 CGTCTTCATATGATGATTGCTCCAGATATGGCTAAAGATGATGAACA  
 TTCAGCACATACTGATCGTCGCTATGCTTCACTAGATGATTCTGTTATTTC  
 CAGATGCAGAAAACTTAAAGTTACTTTAGAGCGTGCTCTTCTTTCTGG  
 GAAGATAAAATTTGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTGTTGG  
 TGCACACGGTAACCTCAATCCGTGCTCTTGTAAAAACATATCAACAATTTG  
 CAGATGATGAAATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTT  
 TTCGAATTTGATGAAAAATTAACCTTGTTTCAGAAATATTACTTAGGTAA  
 A

## SEQ ID NO. 4205: 18RS21 STRAIN

GTAAAAATTAGTATTCGCACGCCACGGTGAATCTGAGTGG  
 AATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTTCAGAAA  
 AAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAAGCAGCAGGT  
 TTGAGTTTCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAAACA  
 ACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAAAA  
 ATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAAAAATA  
 AAGCAGAGCAGCTGAACAATTTGGTGATGAGCAAGTTTCATATTTGGCGT  
 CGTTTCATATGATGATTGCTCCAGATATGGCTAAAGATGATGAACATT  
 AGCACATACTGATCGTCGCTATGCTTCACTAGATGATTCTGTTATTCCAG  
 ATGCAGAAAACTTAAAGTTACTTTAGAGCGTGCTCTTCTTTCTGGGA  
 GATAAAATTTGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTGTTGGTG  
 ACACGGTAACCTCAATCCGTGCTCTTGTAAAAACATATCAACAATTTGTC  
 ATGATGAAATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTTTT  
 GAATTTGATGAAAAATTAACCTTGTTTCAGAAATATTACTTAGGTAAA

## SEQ ID NO. 4206: M732 STRAIN

GTAAAAATTAGTATTCGCACGCCACGGTGAATCTGAGTGG  
 AATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTTCAGAAA  
 AAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAAGCAGCAGGT

Table 42: Comparative Sequences relating to SAG 0764

TTGAGTTCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAAACA  
 ACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACAGTTGAAAA  
 ATCATGGCGCTTGAACGACGTCATTACGGTGGATTGACAGGAAAAATA  
 AAGCAGAGCAGCTGAACCAATTGGTGATGAGCAAGTTCATATTTGGCGT  
 CGTTTCATATGATGATTGCTCCAGATATGGCTAAAGATGATGAACATTC  
 AGCACATACTGATCGTTCGCTATGCTTCACTAGATGATTCTGTTATTCCAG  
 ATGCAGAAAACTTAAAGTTACTTTAGAGCGTGCTCTTCCCTTCTGGGAA  
 GATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTTGTGGTGC  
 ACACGGTAACTCAATCCGTGCTCTTGTAAACATATCAACCAATTGTGAG  
 ATGATGAAATCATGGACGTTGAATTCCTAACCTCCACCACTTGTTTTC  
 GAATTTGATGAAAAATTAAACCTTGTTTTCAGAAATATTACTTAGGTAAA

**SEQ ID NO. 4207: COH1 STRAIN**

GTAAAAATTAGTATTCGCACGCCACGG  
 TGAATCTGAGTGGAAATAAGCTAACCTTTTCACTGGATGGGCTGACGTAG  
 ATCTTTTCAGAAAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAATT  
 CAAGCAGCAGGTATTGAGTTTCGACCTTGCTTTTACATCAGTTCTTAAACG  
 TGCCATCAAAACAATAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGG  
 TACCAGTTGAAAAATCATGGCGCTTGAACGAACTCATTACGGTGGATTG  
 ACAGGAAAAAATAAGCAGAGCAGCTGAACAATTGGTGATGAGCAAGT  
 TCATATTTGGCGTCGTTTCATATGATGATTGCTCCAGATATGGCTAAAG  
 ATGATGAACATTGAGCACAATACTGATCGTCGCTATGCTTCACTAGATGAT  
 TCTGTTATTCCAGATGCAGAAAACTTAAAGTTACTTTAGAGCGTGCTCT  
 TCCCTTCTGGGAAGATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATG  
 TGTGTTGTTGGTGACACGGTAACTCAATCCGTGCTCTTGTAAAAACATATC  
 AAACAATTGTCAGATGATGAAATCATGGACGTTGAAATTCTTAACCTCCC  
 ACCACTTGTTTTCGAATTTGATGAAAAATTAAACCTTGTTTTCAGAAATATT  
 ACTTAGGTAAA

**SEQ ID NO. 4208: CJB110 STRAIN**

GTAAAAATTAGTATTCGCACGCCACGG  
 TGAATCTGAGTGGAAATAAGCTAACCTTTTCACTGGATGGGCTGACGTAG  
 ATCTTTTCAGAAAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAATT  
 CAAGCAGCAGGTATTGAGTTTCGACCTTGCTTTTACATCAGTTCTTAAACG  
 TGCCATCAAAACAATAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGG  
 TACCAGTTGAAAAATCATGGCGCTTGAACGAACTCATTACGGTGGATTG  
 ACAGGAAAAAATAAGCAGAGCAGCTGAACAATTGGTGATGAGCAAGT  
 TCATATTTGGCGTCGTTTCATATGATGATTGCTCCAGATATGGCTAAAG  
 ATGATGAACATTGAGCACAATACTGATCGTCGCTATGCTTCACTAGATGAT  
 TCTGTTATTCCAGATGCAGAAAACTTAAAGTTACTTTAGAGCGTGCTCT  
 TCCCTTCTGGGAAGATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATG  
 TGTGTTGTTGGTGACACGGTAACTCAATCCGTGCTCTTGTAAAAACATATC  
 AAACAATTGTCAGATGATGAAATCATGGACGTTGAAATTCTTAACCTCCC  
 ACCACTTGTTTTCGAATTTGATGAAAAATTAAACCTTGTTTTCAGAAATATT  
 ACTTAGGTAAA

**SEQ ID NO. 4209: 1169NT STRAIN**

AGTATTCGCACGCCACGGTGAATCTGAGTGGAAATAAGCTAACCTTTTCA  
 CTGGATGGGCTGACGTAGATCTTTCAGAAAAAGGTACACAACAAGCTATT  
 GATGCTGGGAAATTAATTCAAGCAGCAGGTATTGAGTTTCGACCTTGCTTT  
 TACATCAGTTCTTAAACGTGCCATCAAAACAATAACCTTGCCCTTGAAG  
 CAGCTGATCAACTTTGGGTACAGTTGAAAAATCATGGCGCTTGAACGAA  
 CGTCAATTCGGTGGATTGACAGGAAAAATAAGCAGAGCAGCTGAACA  
 ATTTGGTGATGAGCAAGTTTCATATTTGGCGTCGTTTCATATGATGATTGCT  
 CTCAGATATGGCTAAAGATGATGAACATTGAGCACAATACTGATCGTCGC  
 TATGCTTCACTAGATGATTCTGTTATTCCAGATGCAGAAAACTTAAAGT  
 TACTTTAGAGCGTGCTCTTCCCTTCTGGGAAGATAAAATTGCTCCTGCTC  
 TTAAGATGCTTAAATGTGTTGTTGTTGTCACACGGTAACTCAATCCGT  
 GCTCTTGTAAAAACATATCAACAATTGTCAGATGATGAAATCATGGACGCT  
 TGAAATTCCTAACCTCCACCACTTGTTTTCGAATTTGATGAAAAATTAA  
 ACCTTGTTTTCAGAAATATTACTTAGGTAAA

**SEQ ID NO. 4210: M781 STRAIN**

GTAAAAATTAGTATTCGCACGCCACGGT  
 GAATCTGAGTGGAAATAAGCTAACCTTTTCACTGGATGGGCTGACGTAGA  
 TCTTTTCAGAAAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAATT  
 AAGCAGCAGGTATTGAGTTTCGACCTTGCTTTTACATCAGTTCTTAAACG  
 GCCATCAAAACAATAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGT  
 ACCAGTTGAAAAATCATGGCGCTTGAACGAACTCATTACGGTGGATTGA  
 CAGGAAAAATAAGCAGAGCAGCTGAACAATTGGTGATGAGCAAGTT  
 CATATTTGGCGTCGTTTCATATGATGATTGCTCCAGATATGGCTAAAGA  
 TGATGAACATTGAGCACAATACTGATCGTCGCTATGCTTCACTAGATGATT  
 GTGTTATTCCAGATGCAGAAAACTTAAAGTTACTTTAGAGCGTGCTCTT  
 CCTTCTGGGAAGATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATG  
 GTTGTGTTGGTGACACGGTAACTCAATCCGTGCTCTTGTAAAAACATATCA  
 AACAAATTGTCAGATGATGAAATCATGGACGTTGAAATTCCTAACCTCCA  
 CCCTTGTTTTCGAATTTGATGAAAAATTAAACCTTGTTTTCAGAAATATT  
 CTTAGGTAAA

**SEQ ID NO. 4211: JM930013 STRAIN**

GTAAAAATTAGTATTCGCACGCCACGGTGAATCT  
 GAGTGGAAATAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTC  
 AGAAAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAAGCAG

Table 42: Comparative Sequences relating to SAG 0764

CAGGTATTGAGTTGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATC  
 AAAACAACCTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCACT  
 TGAATAATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAA  
 AAAATAAAGCAGAAGCAGCTGAACAAATTTGGTGATGAGCAAGTTTCATATT  
 TGGCGTGGTTTCATATGATGATTTGCTCCAGATATGGCTAAAGATGATGA  
 ACATTGAGCAGCATACTGATCGTCTGCTATGCTTCACTAGATGATTCTGTTA  
 TTCCAGATGCAGAAAACCTAAAGATTACTTTAGAGCGTGCTCTTCCITTC  
 TGGGAAGATAAAATTTGCTCTGCTCTTAAAGATGGTAAATAATGTGTTGT  
 TGGTGACACCGGTAACCTCAATCCGTGCTCTTGTAAACATATCAAACAAT  
 TGTGATGATGAAATCATGGACGTTGAAATTCCTAACCTTCCACCACCTT  
 GTTTTCGAATTTGATGAAAAATTAACCTTGTTCAGAAATATTACTTAGG  
 TAAA

PRETTY of: /biotmp/msa63264.2{\*} March 10, 2003 09:30 ..

msa63264.2{110_090}	1	---	gtaaaat	tAGTATTGCG	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC	50
msa63264.2{110_1169NT}	-----	-	AGTATTGCG	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC		
msa63264.2{110_18RS21}	---	gtaaaat	tAGTATTGCG	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC		
msa63264.2{110_2603}	---	atggtaaaat	tAGTATTGCG	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC		
msa63264.2{110_CJB110}	---	gtaaaat	tAGTATTGCG	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC		
msa63264.2{110_COH1}	---	gtaaaat	tAGTATTGCG	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC		
msa63264.2{110_H36B}	---	gtaaaat	tAGTATTGCG	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC		
msa63264.2{110_JM9130013}	---	gtaaaat	tAGTATTGCG	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC		
msa63264.2{110_M732}	---	gtaaaat	tAGTATTGCG	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC		
msa63264.2{110_M781}	---	gtaaaat	tAGTATTGCG	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC		
msa63264.2{110_A909}	---	gtaaaat	tAGTATTGCG	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC		
Consensus	*****	-----	-----	-----	-----	-----	*****	

  

msa63264.2{110_090}	51	TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCITTCAGAA	AAAGGTACAC	100
msa63264.2{110_1169NT}	-----	TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCITTCAGAA	AAAGGTACAC	
msa63264.2{110_18RS21}	---	TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCITTCAGAA	AAAGGTACAC	
msa63264.2{110_2603}	---	TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCITTCAGAA	AAAGGTACAC	
msa63264.2{110_CJB110}	---	TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCITTCAGAA	AAAGGTACAC	
msa63264.2{110_COH1}	---	TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCITTCAGAA	AAAGGTACAC	
msa63264.2{110_H36B}	---	TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCITTCAGAA	AAAGGTACAC	
msa63264.2{110_JM9130013}	---	TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCITTCAGAA	AAAGGTACAC	
msa63264.2{110_M732}	---	TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCITTCAGAA	AAAGGTACAC	
msa63264.2{110_M781}	---	TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCITTCAGAA	AAAGGTACAC	
msa63264.2{110_A909}	---	TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCITTCAGAA	AAAGGTACAC	
Consensus	*****	*****	*****	*****	*****	*****	

  

msa63264.2{110_090}	101	AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC	150
msa63264.2{110_1169NT}	---	AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC	
msa63264.2{110_18RS21}	---	AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC	
msa63264.2{110_2603}	---	AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC	
msa63264.2{110_CJB110}	---	AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC	
msa63264.2{110_COH1}	---	AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC	
msa63264.2{110_H36B}	---	AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC	
msa63264.2{110_JM9130013}	---	AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC	
msa63264.2{110_M732}	---	AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC	
msa63264.2{110_M781}	---	AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC	
msa63264.2{110_A909}	---	AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC	
Consensus	*****	*****	*****	*****	*****	*****	

  

msa63264.2{110_090}	151	GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT	200
msa63264.2{110_1169NT}	---	GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT	
msa63264.2{110_18RS21}	---	GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT	
msa63264.2{110_2603}	---	GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT	
msa63264.2{110_CJB110}	---	GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT	
msa63264.2{110_COH1}	---	GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT	
msa63264.2{110_H36B}	---	GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT	
msa63264.2{110_JM9130013}	---	GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT	
msa63264.2{110_M732}	---	GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT	
msa63264.2{110_M781}	---	GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT	
msa63264.2{110_A909}	---	GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT	
Consensus	*****	*****	*****	*****	*****	*****	

  

msa63264.2{110_090}	201	TGCCCTTGAA	GCAGCTGATC	AACCTTGGGT	ACCAGTTGAA	AAATCATGGC	250
msa63264.2{110_1169NT}	---	TGCCCTTGAA	GCAGCTGATC	AACCTTGGGT	ACCAGTTGAA	AAATCATGGC	
msa63264.2{110_18RS21}	---	TGCCCTTGAA	GCAGCTGATC	AACCTTGGGT	ACCAGTTGAA	AAATCATGGC	
msa63264.2{110_2603}	---	TGCCCTTGAA	GCAGCTGATC	AACCTTGGGT	ACCAGTTGAA	AAATCATGGC	
msa63264.2{110_CJB110}	---	TGCCCTTGAA	GCAGCTGATC	AACCTTGGGT	ACCAGTTGAA	AAATCATGGC	
msa63264.2{110_COH1}	---	TGCCCTTGAA	GCAGCTGATC	AACCTTGGGT	ACCAGTTGAA	AAATCATGGC	
msa63264.2{110_H36B}	---	TGCCCTTGAA	GCAGCTGATC	AACCTTGGGT	ACCAGTTGAA	AAATCATGGC	
msa63264.2{110_JM9130013}	---	TGCCCTTGAA	GCAGCTGATC	AACCTTGGGT	ACCAGTTGAA	AAATCATGGC	
msa63264.2{110_M732}	---	TGCCCTTGAA	GCAGCTGATC	AACCTTGGGT	ACCAGTTGAA	AAATCATGGC	
msa63264.2{110_M781}	---	TGCCCTTGAA	GCAGCTGATC	AACCTTGGGT	ACCAGTTGAA	AAATCATGGC	
Consensus	*****	*****	*****	*****	*****	*****	

Table 42: Comparative Sequences relating to SAG 0764

msa63264.2{110_A909}	TGCCCCITGAA	GCAGCTGATC	AACITTTGGGT	ACCAGTTGAA	AAATCATGGC
Consensus	*****	*****	*****	*****	*****
251					
msa63264.2{110_090}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_1169NT}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_18RS21}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_2603}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_CJB110}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_COH1}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_H36B}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_JM9130013}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_M732}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_M781}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_A909}	GCTTaAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
Consensus	*****	*****	*****	*****	*****
301					
msa63264.2{110_090}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_1169NT}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_18RS21}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_2603}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_CJB110}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_COH1}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_H36B}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_JM9130013}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_M732}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_M781}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_A909}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
Consensus	*****	*****	*****	*****	*****
351					
msa63264.2{110_090}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_1169NT}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_18RS21}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_2603}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_CJB110}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_COH1}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_H36B}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_JM9130013}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_M732}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_M781}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_A909}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
Consensus	*****	*****	*****	*****	*****
401					
msa63264.2{110_090}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_1169NT}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_18RS21}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_2603}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_CJB110}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_COH1}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_H36B}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_JM9130013}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_M732}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_M781}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_A909}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
Consensus	*****	*****	*****	*****	*****
451					
msa63264.2{110_090}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_1169NT}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_18RS21}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_2603}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_CJB110}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_COH1}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_H36B}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_JM9130013}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_M732}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_M781}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_A909}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
Consensus	*****	*****	*****	*****	*****
501					
msa63264.2{110_090}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_1169NT}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_18RS21}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_2603}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_CJB110}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_COH1}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_H36B}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_JM9130013}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_M732}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA



Table 42: Comparative Sequences relating to SAG 0764

msa63264.2{110_M781}	TGCTCCTGCT	CTTAAAGATG	GTAAAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_A909}	TGCTCCTGCT	CTTAAAGATG	GTAAAAATGT	GTTTGTGGT	GCACACGGTA
Consensus	*****	*****	*****	*****	*****
msa63264.2{110_090}	551				600
msa63264.2{110_1169NT}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
msa63264.2{110_18RS21}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
msa63264.2{110_2603}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
msa63264.2{110_CJB110}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
msa63264.2{110_COH1}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
msa63264.2{110_H36B}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
msa63264.2{110_JM9130013}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
msa63264.2{110_M732}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
msa63264.2{110_M781}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
msa63264.2{110_A909}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
Consensus	*****	*****	*****	*****	*****
msa63264.2{110_090}	601				650
msa63264.2{110_1169NT}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTIT	TCGAATTGTA
msa63264.2{110_18RS21}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTIT	TCGAATTGTA
msa63264.2{110_2603}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTIT	TCGAATTGTA
msa63264.2{110_CJB110}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTIT	TCGAATTGTA
msa63264.2{110_COH1}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTIT	TCGAATTGTA
msa63264.2{110_H36B}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTIT	TCGAATTGTA
msa63264.2{110_JM9130013}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTIT	TCGAATTGTA
msa63264.2{110_M732}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTIT	TCGAATTGTA
msa63264.2{110_M781}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTIT	TCGAATTGTA
msa63264.2{110_A909}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTIT	TCGAATTGTA
Consensus	*****	*****	*****	*****	*****
msa63264.2{110_090}	651				690
msa63264.2{110_1169NT}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_18RS21}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_2603}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_CJB110}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_COH1}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_H36B}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_JM9130013}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_M732}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_M781}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_A909}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
Consensus	*****	*****	*****	*****	

## SEQ ID NO. 4212: 2603 V/R STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA  
 IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV  
 PDMKDDHSAHTDRRYASLDDSVI PDAENLKVTLEALPFWEDKIAPALDKGKNVFGA  
 HGNSIRALVKHIKQLSDEIMDVEIPNFPPLVFEFDEKLNLVSEYLLGK

## SEQ ID NO. 4213: 090 STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA  
 IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV  
 PDMKDDHSAHTDRRYASLDDSVI PDAENLKVTLEALPFWEDKIAPALDKGKNVFGA  
 HGNSIRALVKHIKQLSDEIMDVEIPNFPPLVFEFDEKLNLVSEYLLGK

## SEQ ID NO. 4214: A909 STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA  
 IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV  
 PDMKDDHSAHTDRRYASLDDSVI PDAENLKVTLEALPFWEDKIAPALDKGKNVFGA  
 HGNSIRALVKHIKQLSDEIMDVEIPNFPPLVFEFDEKLNLVSEYLLGK

## SEQ ID NO. 4215: H36B STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA  
 IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV  
 PDMKDDHSAHTDRRYASLDDSVI PDAENLKVTLEALPFWEDKIAPALDKGKNVFGA  
 HGNSIRALVKHIKQLSDEIMDVEIPNFPPLVFEFDEKLNLVSEYLLGK

## SEQ ID NO. 4216: 18RS21 STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA  
 IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV  
 PDMKDDHSAHTDRRYASLDDSVI PDAENLKVTLEALPFWEDKIAPALDKGKNVFGA  
 HGNSIRALVKHIKQLSDEIMDVEIPNFPPLVFEFDEKLNLVSEYLLGK

## SEQ ID NO. 4217: M732 STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA  
 IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV  
 PDMKDDHSAHTDRRYASLDDSVI PDAENLKVTLEALPFWEDKIAPALDKGKNVFGA  
 HGNSIRALVKHIKQLSDEIMDVEIPNFPPLVFEFDEKLNLVSEYLLGK

## SEQ ID NO. 4218: COH1 STRAIN

Table 42: Comparative Sequences relating to SAG 0764

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA  
IKITNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLPPDM  
PDMADDEHSAHTDRRYASLDDSVIPDAENLKVTILERALPFWEDKIAPALKDGNVVFVGA  
HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

## SEQ ID NO. 4219: CJB110 STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA  
IKITNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLPPDM  
PDMADDEHSAHTDRRYASLDDSVIPDAENLKVTILERALPFWEDKIAPALKDGNVVFVGA  
HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

## SEQ ID NO. 4220: 1169NT STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA  
IKITNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLPPDM  
AKDDEHSAHTDRRYASLDDSVIPDAENLKVTILERALPFWEDKIAPALKDGNVVFVGA  
SIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

## SEQ ID NO. 4221: M781 STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA  
IKITNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLPPDM  
PDMADDEHSAHTDRRYASLDDSVIPDAENLKVTILERALPFWEDKIAPALKDGNVVFVGA  
HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

## SEQ ID NO. 4222: JM9130013 STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA  
IKITNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLPPDM  
PDMADDEHSAHTDRRYASLDDSVIPDAENLKVTILERALPFWEDKIAPALKDGNVVFVGA  
HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

PRETTY of: /biotmp/msa70722.2{\*} March 10, 2003 09:33 ..

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      msa70722.2{110_090}      1
msa70722.2{110_18RS21}      vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_2603}      vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_A909}      vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_CJB110}      vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_COH1}      vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_H36B}      vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_JM9130013} vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_M732}      vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_M781}      vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_1169NT}    ---VFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
      Consensus            - - - * * * * *
                                     50

      msa70722.2{110_090}      51
msa70722.2{110_18RS21}      LAFTSVLKRA IKTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE
msa70722.2{110_2603}      LAFTSVLKRA IKTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE
msa70722.2{110_A909}      LAFTSVLKRA IKTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE
msa70722.2{110_CJB110}      LAFTSVLKRA IKTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE
msa70722.2{110_COH1}      LAFTSVLKRA IKTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE
msa70722.2{110_H36B}      LAFTSVLKRA IKTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE
msa70722.2{110_JM9130013} LAFTSVLKRA IKTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE
msa70722.2{110_M732}      LAFTSVLKRA IKTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE
msa70722.2{110_M781}      LAFTSVLKRA IKTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE
msa70722.2{110_1169NT}    LAFTSVLKRA IKTNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE
      Consensus            * * * * *
                                     100

      msa70722.2{110_090}      101
msa70722.2{110_18RS21}      AEQFGDEQVH IWRRSYDVLPPDMADDEHSAHTDRRYASLDDSVIPDAEN
msa70722.2{110_2603}      AEQFGDEQVH IWRRSYDVLPPDMADDEHSAHTDRRYASLDDSVIPDAEN
msa70722.2{110_A909}      AEQFGDEQVH IWRRSYDVLPPDMADDEHSAHTDRRYASLDDSVIPDAEN
msa70722.2{110_CJB110}      AEQFGDEQVH IWRRSYDVLPPDMADDEHSAHTDRRYASLDDSVIPDAEN
msa70722.2{110_COH1}      AEQFGDEQVH IWRRSYDVLPPDMADDEHSAHTDRRYASLDDSVIPDAEN
msa70722.2{110_H36B}      AEQFGDEQVH IWRRSYDVLPPDMADDEHSAHTDRRYASLDDSVIPDAEN
msa70722.2{110_JM9130013} AEQFGDEQVH IWRRSYDVLPPDMADDEHSAHTDRRYASLDDSVIPDAEN
msa70722.2{110_M732}      AEQFGDEQVH IWRRSYDVLPPDMADDEHSAHTDRRYASLDDSVIPDAEN
msa70722.2{110_M781}      AEQFGDEQVH IWRRSYDVLPPDMADDEHSAHTDRRYASLDDSVIPDAEN
msa70722.2{110_1169NT}    AEQFGDEQVH IWRRSYDVLPPDMADDEHSAHTDRRYASLDDSVIPDAEN
      Consensus            * * * * *
                                     150

      msa70722.2{110_090}      151
msa70722.2{110_18RS21}      LKVTILERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI
msa70722.2{110_2603}      LKVTILERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI
msa70722.2{110_A909}      LKVTILERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI
msa70722.2{110_CJB110}      LKVTILERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI
msa70722.2{110_COH1}      LKVTILERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI
msa70722.2{110_H36B}      LKVTILERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI
msa70722.2{110_JM9130013} LKVTILERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI
msa70722.2{110_M732}      LKVTILERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI

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Table 42: Comparative Sequences relating to SAG 0764

msa70722.2{110_M781}	LKVTLERALP	FWEDKIAPAL	KDGKNVFGA	HGNSIRALVK	HIKQLSDDEI
msa70722.2{110_1169NT}	LKVTLERALP	FWEDKIAPAL	KDGKNVFGA	HGNSIRALVK	HIKQLSDDEI
Consensus	*****	*****	*****	*****	*****
	201		229		
msa70722.2{110_090}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_18RS21}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_2603}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_A909}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_CJB110}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_COH1}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_H36B}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_JM9130013}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_M732}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_M781}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_1169NT}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
Consensus	*****	*****	*****		

Table 43: Comparative Sequences relating to SAG0079

## SEQ ID NO. 4301: 2603 V/R STRAIN

ATGAATCTTTTAATTATGGGTTTGCCCTGGTGTGCTGGTAAAGGTACTCAAGCAGCTAAGATC  
 GTTGAAGAATTTGGTGTGCTCAGATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCT  
 AATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCT  
 GATGAAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAA  
 GGTTTTTTACTTTGATGGATATCCACGTACTATTGAACAAGCACACGCCCTTAGATGCTACG  
 CTTGAAGAACTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCATCATGT  
 CTTATAGAGCGTTTGGTGTGCTATATCAATCGTAAAACTGGTGAAACTTTCCACAAA  
 GTGTTCAACCCACAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAG  
 CCTGAAACTGTCAACCGTCGCTTGGACGTTAATATTGCTCAAGGAGAACCTATTCTTGAA  
 CACTATCGTAAGCTTGGTCTTGTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTT  
 TTTGCAGATGTTGAAAAAGCGTTGCTAGAACTCAA

## SEQ ID NO. 4302: 090 STRAIN (reverse complement)

AATCTTTTAATTATGGGTTTGCCCTGGTGTGCTGGTAAAGGTACTCA  
 AGCAGCTAAGATCGTTGAAGAATTTGGTGTGCTCAGATCTCAACAGGGGATATGTTCCG  
 CGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGG  
 TGAATTTGGTTCCTGATGAAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGA  
 TATCGCAGAAAAAGGTTTCTTACTTTGATGGATATCCACGTACTATTGAACAAGCACACGC  
 CTTAGATGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGT  
 GGATCCATCATGTCTTATAGAGCGTTTGGTGTGCTATTATCAATCGTAAAACTGGTGA  
 AACTTTCCACAAAGTGTTCACCCACAGTAGATTATAAAGAAGAAGATTACTATCAACG  
 TGAAGATGATAAGCTGAAACTGTCAAACGTGCTTGGACGTTAATATTGCTCAAGGAGA  
 ACCATTTCTTGAACTACTATCGTAAGCTTGGTCTTGTACAGATATTGAAGGTAATCAAGA  
 AATAACAGAAGTTTTTGCAGATGTTGAAAAAGCGTTG

## SEQ ID NO. 4303: 1169NT STRAIN (REVERSE COMPLEMENT)

TGGTAAAGGGACTCAAGCAGCTAAGATTGTTGAAGAATTTGGTGTGCGCACATCTCAAC  
 AGGGGATATGTTCCGCGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAG  
 TTATATTGATAAAGGTGAATTGGTTCCTGATCAAGTAACAAACGGGATTGTAAAAGAGCG  
 CTTAGCTGAGGATGATATCGCAGAAAAAGGTTTTTACTTTGATGGGTATCCACGTACTAT  
 TGAACAAGCACACGCGCTTAGATGCTACGCTTGAAGAAGTGAAGTACGCTTAGATGGTGT  
 TATTAAATATTAAAGTGGATCCATCATGTCTTATAGAGCGTTTGGTGGTGTATTATCAA  
 TCGTAAACTGGTGAAGCTTTCCACAAAGTGTCAAACCCACAGTAGATTATAAAGAAGA  
 AGATTACTATCAACGTGAAGATGATAAGCTGAAACTGTCAAACGTGCTTGGACGTTCA  
 TATTGCTCAAGGAGAACCTATTCTTGAACTACTATAGTAAGCTTGGCTTGTACAGATAT  
 TGAAGGTAATCAAGAAATAA

## SEQ ID NO. 4304: 18RS21 STRAIN (REVERSE COMPLEMENT)

AATCTTTTAACACCGGGTTGCGCTGGTGTGCTGGTAAAGGTACTCAAGCAGCTAAGATCG  
 TTGAAGAATTTGGTGTGCTCAGATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCTA  
 ATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCTG  
 ATGAAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAG  
 GTTTTTTACTTTGATGGATATCCACGTACTATTGAACAAGCACACGCTTAGATGCTACGC  
 TTGAAGAACTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCATCATGTG  
 TTTATAGAGCGTTTGGTGTGCTATTATCAATCGTAAAACTGGTGAAGCTTTCCACAAAG  
 TGTTCACCCACAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGC  
 CTGAAACTGTCAAACGTGCTTGGACGTTAATATTGCTCAAGGAGAACCTATTCTTGAAC  
 ACTATCGTAAGCTTGGTCTTGTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTT  
 TTTGCAGATGTTGAAAAAGCGTTG

## SEQ ID NO. 4305: A909 STRAIN (REVERSE COMPLEMENT)

AATCTTTTAATTATGGGTTTGCCCTGGTGTGCTGGTAAAGGTACTCAAGCAG  
 CTAAGATCGTTGAAGAATTTGGTGTGCTCAGATCTCAACAGGGGATATGTTCCGCGCCG  
 CAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAAT  
 TGGTTCCTGATGAAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCG  
 CAGAAAAAGGTTTTTACTTTGATGGATATCCACGTACTATTGAACAAGCACACGCTTAG  
 ATGCTACGCTTGAAGAAGTACGCTTAGATGGTGTATTAAATATTAAAGTGGATC  
 CATCATGTCTTATAGAGCGTTTGGTGTGCTATTATCAATCGTAAAACTGGTGAAGCTT  
 TCCACAAAGTGTTCACCCACAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAG  
 ATGATAAGCCTGAAACTGTCAAACGTGCTTGGACGTTAATATTGCTCAAGGAGAACCTA  
 TCTTGAACACTATCGAAAGCTTGGTCTTGTACAGATATTGAAGGTAA

## SEQ ID NO. 4306: CJB110 STRAIN (REVERSE COMPLEMENT)

AATCTTTTAACCAACGGGTTTGCTTGGTGTGCTGGTAAAGGTACTCAAGCAGCTAA  
 GATCGTTGAAGAATTTGGTGTGCTCAGATCTCAACAGGGGATATGTTCCGCGCCGCAAT  
 GGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGT  
 TCCTGATGAAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGA  
 AAAAGGTTTTTACTTTGATGGATATCCACGTACTATTGAACAAGCACACGCTTAGATGC  
 TACGCTTGAAGAAGTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCATC  
 ATGCTTATAGAGCGTTTGGTGTGCTATTATCAATCGTAAAACTGGTGAAGCTTTCCA  
 CAAAGTGTTCACCCACAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGA  
 TAAGCTGAAACTGTCAAACGTGCTTGGACGTTAATATTGCTCAAGGAGAACCTATTCT  
 TGAACACTATAG

## SEQ ID NO. 4307: COH1 STRAIN (REVERSE COMPLEMENT)

ATCTTTTAATTATGGGTTTGCCCTGGTGTGCTGGTAAAGGTACTCAAGCAGCTAAGATGTTG  
 AAGAATTTGGTGTGCTCAGATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCTAATC  
 AAACCAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCTGATG  
 AAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAGGTT  
 TTTTACTTTGATGGATATCCACGTACTATTGAGCAAGCACACGCTTAGATGCTACGCTTG  
 AAGAAGTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCACATGCTTTA  
 TAGAGCGTTTGGTGGCCGTATTATCAATCGTAAAACTGGTGAAGCTTTCCACAAAGTGT

Table 43: Comparative Sequences relating to SAG0079

TCAACCCACCCAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCTG  
AAACTGTCAAACGTCGCTTGGACGTTAAATATTGCTCAAGGAGAACCTATCTTTGAACACT  
ATCGTAAGCTTGGTCTTGTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTTTTG  
CAGATGTTGAAAAAGCGTTG

SEQ ID NO. 4308: H36B STRAIN (REVERSE COMPLEMENT)

CAGGGGATATGTTCCGCGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAA  
GTTATATTGATAAAGGTGAATGGTTCCTGATGAAGTAACAAACGGGATTTGTAAGAGAGC  
GCTTAGCTGAGGATGATATCGCAGAAAAAGGTTTTTACTTGTGATGGATATCCACGTACTA  
TTGAACAAGCACACGCCCTTAGATGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTG  
TTATTAATATTAAAGTGGATCCATCATGTCTTATAGAGCGTTTGGTGGTTCGATTATCA  
ATCGTAAAACTCGCAGAAAAAGCTTTCCACAAAGTGTCAACCCACCGTAGATTATAAAGAAG  
AAGATTACTATCAACGTGAAGATGATAAGCCTGAAACTGTCAAACGTGCGTTGGACGTTA  
ATATTGCTCAAGGAGAATCTATTTCTTGAACACTATCGTAAGCTTGGTCTTGTACAGATA  
TTAAGGTAATCAAGAAATAACAGAAGTTTTTGCAGATGTTGAAAAAGCGTTG

SEQ ID NO. 4309: JM9130013 STRAIN (REVERSE COMPLEMENT)

AATCTTTTAATTATGGGTTTGCTGGTGTGTTAAAGGT  
ACTCAAGCAGCTAAGATCGTTGAAGAATTTGGTGTGCTCACATCTCAACAGGGGATATG  
TTCCGCGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAAGTTATATTGAT  
AAAGGTGAATTTGGTTCCTGATGAAGTAACAAACGGGATTTGTAAGAGAGCGCTTAGCTGAG  
GATGATATCGCAGAAAAAGGTTTTTACTTGTGATGGATATCCACGTACTATTGAACAAGCA  
CACGCCCTTAGATGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTGTATTATTAATATT  
AAAGTGGATCCATCATGTCTTATAGAGCGTTTGGTGGTTCGATTATCAATCGTAAAACT  
GGTGAACCTTTCCACAAAGTGTTCACCCACCGTAGATTATAAAGAAGAAGATTACTAT  
CAACGTGAAGATGATAAGCCTGAAACTGTAAACGTGCGTTGGACGTTAATATTGCTCAA  
GGAGAACCTATTTCTTGAACACTATAAAAAAGCTTGGTCTTGTACAGATATTGAAGGTAAT  
CA

SEQ ID NO. 4310: M732 STRAIN (REVERSE COMPLEMENT)

CTTTAATTATGGGTTTGCTGGTGTGTTAAAGGTACTCAAGCAGCTAAGATTTGTGAA  
GAATTTGGTGTGTTGCTCACATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCTAATCAA  
ACCCAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTTGGTTCCTGATGAA  
GTAACAAACGGGATTTGTAAGAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAGGTTTTT  
TTACTTGTATGGATATCCACGTACTATTGAGCAAGCACACGCCCTTAGATGCTACGCTTGAA  
GAACTAGGACTACGCTTAGATGGTGTATTATTAATTTAAAGTGGATCCAACATGCCCTTATA  
GAGCGTTTGAAGTGGCGCTTATTATCAATCGTAAACTGGTGAACCTTTCCACAAAGTGTTC  
AACCCACCGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCTGAA  
ACTGTCAAACGTGCGTTGGACGTTAATATTGCTCAAGGAGAACCTATTCTTGAACACTAT  
CGTAAGCTTGGTCTTGTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTTTTGCA  
GATGTTGAAAAAGCGTTG

SEQ ID NO. 4311: M781 STRAIN (REVERSE COMPLEMENT)

AATCTTTTAATTACGGGTTTGCTGGTGTGTTAAAGGTACTCAA  
GCAGCTAAGATTGTTGAAGAATTTGGTGTGCTCACATCTCAACAGGGGATATGTTCCGCG  
GCCGCAATGGCTAATCAAACCCAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGT  
GAATTTGGTTCCTGATGAAGTAACAAACGGGATTTGTAAGAGAGCGCTTAGCTGAGGATGAT  
ATCGCAGAAAAAGGTTTTTACTTGTATGGATATCCACGTACTATTGAGCAAGCACACGCC  
TTAGATGCTACGCTTGAAGAAGTAGGACTACGCTTAGATGGTGTATTATTAATTTAAAGT  
GATCCACATGCCCTTATAGAGCGTTTGGTGGCGGTATTATCAATCGTAAAACTGGTGAA  
ACTTTCCACAAAGTGTTCACCCACCGTAGATTATAAAGAAGAAGATTACTATCAACGT  
GAAGATGATAAGCCTGAAACTGTCAAACGTGCGTTGGACGTTAATATTGCTCAA

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa25038.2{\*} April 17, 2002 08:53 ..  
PRETTY of: /biotmp/msa252229.2{\*} January 31, 2003 03:05 ..

	1		50
msa252229.2{114_COH1}	----atcttt taattatggg tttgcctggg gctggtaaag gtactcaagc		
msa252229.2{114_M732}	-----cttt taattatggg tttgcctggg gctggtaaag gtactcaagc		
msa252229.2{114_M781}	---Aatcttt taattacggg tttgcctggg gctggtaaag gtactcaagc		
msa252229.2{114_A909}	---Aatcttt taattatggg tttgcctggg gctggtaaag gtactcaagc		
msa252229.2{114_JM9130013}	---Aatcttt taattatggg tttgcctggg gctggtaaag gtactcaagc		
msa252229.2{114_CJB110}	---Aatcttt taaccacggg tttgcttggg gctggtaaag gtactcaagc		
msa252229.2{114_090}	---Aatcttt taattatggg tttgcctggg gctggtaaag gtactcaagc		
msa252229.2{114_2603}	atgAatcttt taattatggg tttgcctggg gctggtaaag gtactcaagc		
msa252229.2{114_H36B}	-----		
msa252229.2{114_18RS21}	---Aatcttt taaccacggg ttcgcctggg gctggtaaag gtactcaagc		
msa252229.2{114_1169NT}	-----		
Consensus	*****		
	51		100
msa252229.2{114_COH1}	agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA		
msa252229.2{114_M732}	agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA		
msa252229.2{114_M781}	agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA		
msa252229.2{114_A909}	agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA		
msa252229.2{114_JM9130013}	agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA		
msa252229.2{114_CJB110}	agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA		
msa252229.2{114_090}	agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA		
msa252229.2{114_2603}	agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA		
msa252229.2{114_H36B}	-----		
msa252229.2{114_18RS21}	agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA		
msa252229.2{114_1169NT}	agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA		

Table 43: Comparative Sequences relating to SAG0079

Consensus	-----	-----	-----	-----	-----	*****
	101					150
msa252229.2{114_COH1}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCc	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_M732}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCc	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_M781}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCc	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_A909}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCg	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_JM9130013}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCg	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_CJB110}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCg	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_090}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCg	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_2603}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCg	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_H36B}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCg	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_18RS21}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCg	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_1169NT}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCg	AAATGGGACG	TTTAGCTAAA	
Consensus	*****	*****	*****	*****	*****	*****
	151					200
msa252229.2{114_COH1}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_M732}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_M781}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_A909}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_JM9130013}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_CJB110}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_090}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_2603}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_H36B}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_18RS21}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_1169NT}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
Consensus	*****	*****	*****	*****	*****	*****
	201					250
msa252229.2{114_COH1}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC	
msa252229.2{114_M732}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC	
msa252229.2{114_M781}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC	
msa252229.2{114_A909}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC	
msa252229.2{114_JM9130013}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC	
msa252229.2{114_CJB110}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC	
msa252229.2{114_090}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC	
msa252229.2{114_2603}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC	
msa252229.2{114_H36B}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC	
msa252229.2{114_18RS21}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC	
msa252229.2{114_1169NT}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC	
Consensus	*****	*****	*****	*****	*****	*****
	251					300
msa252229.2{114_COH1}	TTGATGGaTA	TCCACGTACT	ATTGAGCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_M732}	TTGATGGaTA	TCCACGTACT	ATTGAGCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_M781}	TTGATGGaTA	TCCACGTACT	ATTGAGCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_A909}	TTGATGGaTA	TCCACGTACT	ATTGAaCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_JM9130013}	TTGATGGaTA	TCCACGTACT	ATTGAaCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_CJB110}	TTGATGGaTA	TCCACGTACT	ATTGAaCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_090}	TTGATGGaTA	TCCACGTACT	ATTGAaCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_2603}	TTGATGGaTA	TCCACGTACT	ATTGAaCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_H36B}	TTGATGGaTA	TCCACGTACT	ATTGAaCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_18RS21}	TTGATGGaTA	TCCACGTACT	ATTGAaCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_1169NT}	TTGATGGgTA	TCCACGTACT	ATTGAaCAAG	CACACGCCTT	AGATGCTACG	
Consensus	*****	*****	*****	*****	*****	*****
	301					350
msa252229.2{114_COH1}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_M732}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_M781}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_A909}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_JM9130013}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_CJB110}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_090}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_2603}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_H36B}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_18RS21}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_1169NT}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
Consensus	*****	*****	*****	*****	*****	*****
	351					400
msa252229.2{114_COH1}	TCCAaCATGc	CTTATAGAGC	GTTTGAGTGg	cCGTATTATC	AATCGTAAAA	
msa252229.2{114_M732}	TCCAaCATGc	CTTATAGAGC	GTTTGAGTGg	cCGTATTATC	AATCGTAAAA	
msa252229.2{114_M781}	TCCAaCATGc	CTTATAGAGC	GTTTGAGTGg	cCGTATTATC	AATCGTAAAA	
msa252229.2{114_A909}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGg	tCGTATTATC	AATCGTAAAA	
msa252229.2{114_JM9130013}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGg	tCGTATTATC	AATCGTAAAA	
msa252229.2{114_CJB110}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGg	tCGTATTATC	AATCGTAAAA	
msa252229.2{114_090}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGg	tCGTATTATC	AATCGTAAAA	
msa252229.2{114_2603}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGk	tCGTATTATC	AATCGTAAAA	
msa252229.2{114_H36B}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGg	tCGTATTATC	AATCGTAAAA	
msa252229.2{114_18RS21}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGg	tCGTATTATC	AATCGTAAAA	

Table 43: Comparative Sequences relating to SAG0079

msa252229.2{114_1169NT}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGG	tCGTATTATC	AATCGTAAAA
Consensus	****-****	*****	*****	-*****	*****
401					450
msa252229.2{114_COH1}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_M732}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_M781}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_A909}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_JM9130013}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_CJB110}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_090}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_2603}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_H36B}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_18RS21}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_1169NT}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
Consensus	*****	*****	*****	*****	*****
451					500
msa252229.2{114_COH1}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_M732}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_M781}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_A909}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_JM9130013}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_CJB110}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_090}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_2603}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_H36B}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_18RS21}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_1169NT}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
Consensus	*****	*****	*****	*****	*-*****
501					550
msa252229.2{114_COH1}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgta
msa252229.2{114_M732}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgta
msa252229.2{114_M781}	CTTGGACGTT	aATATTGCTC	AA-----	-----	-----
msa252229.2{114_A909}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgaa
msa252229.2{114_JM9130013}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactataaaa
msa252229.2{114_CJB110}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatag--
msa252229.2{114_090}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgta
msa252229.2{114_2603}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgta
msa252229.2{114_H36B}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgta
msa252229.2{114_18RS21}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgta
msa252229.2{114_1169NT}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatagta
Consensus	*****	*****	*****	-----	-----
551					600
msa252229.2{114_COH1}	agcttggtct	tggtacagat	attgaaggta	atcaagaaat	aacagaagtt
msa252229.2{114_M732}	agcttggtct	tggtacagat	attgaaggta	atcaagaaat	aacagaagtt
msa252229.2{114_M781}	-----	-----	-----	-----	-----
msa252229.2{114_A909}	agcttggtct	tggtacagat	attgaaggta	a-----	-----
msa252229.2{114_JM9130013}	agcttggtct	tggtacagat	attgaaggta	atca-----	-----
msa252229.2{114_CJB110}	-----	-----	-----	-----	-----
msa252229.2{114_090}	agcttggtct	tggtacagat	attgaaggta	atcaagaaat	aacagaagtt
msa252229.2{114_2603}	agcttggtct	tggtacagat	attgaaggta	atcaagaaat	aacagaagtt
msa252229.2{114_H36B}	agcttggtct	tggtacagat	attgaaggta	atcaagaaat	aacagaagtt
msa252229.2{114_18RS21}	agcttggtct	tggtacagat	attgaaggta	atcaagaaat	aacagaagtt
msa252229.2{114_1169NT}	agcttggtct	tggtacagat	attgaaggta	atcaagaaat	aa-----
Consensus	-----	-----	-----	-----	-----
601					636
msa252229.2{114_COH1}	tttgcagatg	ttgaaaaagc	gttg-----	-----	-----
msa252229.2{114_M732}	tttgcagatg	ttgaaaaagc	gttg-----	-----	-----
msa252229.2{114_M781}	-----	-----	-----	-----	-----
msa252229.2{114_A909}	-----	-----	-----	-----	-----
msa252229.2{114_JM9130013}	-----	-----	-----	-----	-----
msa252229.2{114_CJB110}	-----	-----	-----	-----	-----
msa252229.2{114_090}	tttgcagatg	ttgaaaaagc	gttg-----	-----	-----
msa252229.2{114_2603}	tttgcagatg	ttgaaaaagc	gttgctagaa	ctcaaa	-----
msa252229.2{114_H36B}	tttgcagatg	ttgaaaaagc	gttg-----	-----	-----
msa252229.2{114_18RS21}	tttgcagatg	ttgaaaaagc	gttg-----	-----	-----
msa252229.2{114_1169NT}	tttgcagatg	ttgaaaaagc	gttg-----	-----	-----
Consensus	-----	-----	-----	*****	*****
SEQ ID NO. 4312: 2603 V/R STRAIN					
MNLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRILAKSYIDKGELVP					
DEVINGIVKERLAEDDIAEKGFLLDGYPTIEQAHALDATALLEELGLRLDGVINIKVDPSC					
LIERLSKRIINRKTGETFHKVFNPFPVYKEDDYQREDDKPETVKRRLDVNIAQGEPILE					
HYRKLGLVTDIEGNQETIEVFADVEKALLELK					
SEQ ID NO. 4313: 090 STRAIN					
NLLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRILAKSYIDKGELVP					
EVINGIVKERLAEDDIAEKGFLLDGYPTIEQAHALDATALLEELGLRLDGVINIKVDPSC					
LIERLSGRIINRKTGETFHKVFNPFPVYKEDDYQREDDKPETVKRRLDVNIAQGEPILE					

Table 43: Comparative Sequences relating to SAG0079

YRKLGLVTDIEGNQEITEVFADVEKALLELK

SEQ ID NO. 4314: 1169NT STRAIN

GKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRLAQSYIDKGELVPDQVTNGIVKER  
LAEDDIAEKGFLLDGYPRTEQAHALDATLEELGLRLDGVINIKVDPSCLIERLSGRI IN  
RKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVHIAQGEPILEHYSKGLVTDI  
EGNQEI

SEQ ID NO. 4315: 18RS21 STRAIN

NLLITGSPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRLAQSYIDKGELVPD  
EVTNGIVKERLAEDDIAEKGFLLDGYPRTEQAHALDATLEELGLRLDGVINIKVDPSCLI  
ERLSGRI INRKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVHIAQGEPILEH  
YRKLGLVTDIEGNQEITEVFADVEKALLE

SEQ ID NO. 4316: A909 STRAIN

NLLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRLAQSYIDKGELVPD  
EVTNGIVKERLAEDDIAEKGFLLDGYPRTEQAHALDATLEELGLRLDGVINIKVDPSCLI  
ERLSGRI INRKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVHIAQGESILEH  
YRKLGLVTDIEG

SEQ ID NO. 4317: A909 STRAIN

NLLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRLAQSYIDKGELVPD  
EVTNGIVKERLAEDDIAEKGFLLDGYPRTEQAHALDATLEELGLRLDGVINIKVDPSCLI  
ERLSGRI INRKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVHIAQGESILEH  
YRKLGLVTDIEG

SEQ ID NO. 4318: CJB110 STRAIN

NLLITGGLGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRLAQSYIDKGELVPD  
EVTNGIVKERLAEDDIAEKGFLLDGYPRTEQAHALDATLEELGLRLDGVINIKVDPSCLI  
ERLSGRI INRKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVHIAQGEPILEH  
Y

SEQ ID NO. 4319: COH1 STRAIN

LLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRLAQSYIDKGELVPDE  
VTNGIVKERLAEDDIAEKGFLLDGYPRTEQAHALDATLEELGLRLDGVINIKVDPCLII  
ERLSGRI INRKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVHIAQGEPILEHY  
RKLGLVTDIEGNQEITEVFADVEKALL

SEQ ID NO. 4320: H36B STRAIN

GDMFRAAMANQTEMGRLAQSYIDKGELVPDEVNTNGIVKERLAEDDIAEKGFLLDGYPRTE  
QAHALDATLEELGLRLDGVINIKVDPSCLIERLSGRI INRKTGETFHKVFNPVDYKEE  
DYQREDDKPETVKRRLDVHIAQGESILEHYRKLGLVTDIEGNQEITEVFADVEKAL

SEQ ID NO. 4321: JM9130013 STRAIN

NLLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRLAQSYIDKGELVPD  
EVTNGIVKERLAEDDIAEKGFLLDGYPRTEQAHALDATLEELGLRLDGVINIKVDPSCLI  
ERLSGRI INRKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVHIAQGEPILEH  
YKGLGLVTDIEGN

SEQ ID NO. 4322: M732 STRAIN

LLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRLAQSYIDKGELVPDE  
VTNGIVKERLAEDDIAEKGFLLDGYPRTEQAHALDATLEELGLRLDGVINIKVDPCLII  
ERLSGRI INRKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVHIAQGEPILEHY  
RKLGLVTDIEGNQEITEVFADVEKALLELK

SEQ ID NO. 4323: M781 STRAIN

NLLITGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRLAQSYIDKGELVPD  
EVTNGIVKERLAEDDIAEKGFLLDGYPRTEQAHALDATLEELGLRLDGVINIKVDPCLII  
ERLSGRI INRKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVHIAQ

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa32357.2{\*} April 17, 2002 09:17 ..

	1				50
msa252352.2{114_18RS21}	-nllttgspg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTeMGRlak
msa252352.2{114_M781}	-nllitglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTqMGRlak
msa252352.2{114_CJB110}	-nllttgllg	agkgtqaaki	veefgvahis	tGDMFRAAMA	tGDMFRAAMA
msa252352.2{114_090}	-nllimglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTeMGRlak
msa252352.2{114_JM9130013}	-nllimglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	tGDMFRAAMA
msa252352.2{114_A909}	-nllimglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTeMGRlak
msa252352.2{114_1169NT}	-----	-gkgtqaaki	veefgvahis	tGDMFRAAMA	NQTeMGRlak
msa252352.2{114_2603}	mnllimglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	tGDMFRAAMA
msa252352.2{114_COH1}	--llimglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTqMGRlak
msa252352.2{114_M732}	--llimglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTeMGRlak
msa252352.2{114_H36B}	-----	-----	-----	-GDMFRAAMA	NQTeMGRlak
Consensus	*	-----	-----	*****	*****
	51				100
msa252352.2{114_18RS21}	SYIDKGELVP	DeVINGIVKE	RLAEDDIAEK	GFLLDGYPRT	IEQAHALDAT
msa252352.2{114_M781}	SYIDKGELVP	DeVINGIVKE	RLAEDDIAEK	GFLLDGYPRT	IEQAHALDAT
msa252352.2{114_CJB110}	SYIDKGELVP	DeVINGIVKE	RLAEDDIAEK	GFLLDGYPRT	IEQAHALDAT



Table 43: Comparative Sequences relating to SAG0079

msa252352.2{114_090}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
msa252352.2{114_JM9130013}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
msa252352.2{114_A909}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
msa252352.2{114_1169NT}	SYIDKGELVP	DqVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
msa252352.2{114_2603}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
msa252352.2{114_COH1}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
msa252352.2{114_M732}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
msa252352.2{114_H36B}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
Consensus	*****	*-*****	*****	*****	*****
101					
msa252352.2{114_18RS21}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_M781}	LEELGLRLDG	VINIKVDPtC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_CJB110}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_090}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_JM9130013}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_A909}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_1169NT}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_2603}	LEELGLRLDG	VINIKVDPsC	LIERLSxRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_COH1}	LEELGLRLDG	VINIKVDPtC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_M732}	LEELGLRLDG	VINIKVDPtC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_H36B}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
Consensus	*****	*****	*****	*****	*****
151					
msa252352.2{114_18RS21}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hyrklglvtd	iegnqeitev
msa252352.2{114_M781}	EDYYQREDDK	PETVKRRLDV	nIAQ-----	-----	-----
msa252352.2{114_CJB110}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hy-----	-----
msa252352.2{114_090}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hyrklglvtd	iegnqeitev
msa252352.2{114_JM9130013}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hykklglvtd	iegn-----
msa252352.2{114_A909}	EDYYQREDDK	PETVKRRLDV	nIAQgesile	hyrklglvtd	ieg-----
msa252352.2{114_1169NT}	EDYYQREDDK	PETVKRRLDV	hIAQgepile	hysklglvtd	iegnqe---
msa252352.2{114_2603}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hyrklglvtd	iegnqeitev
msa252352.2{114_COH1}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hyrklglvtd	iegnqeitev
msa252352.2{114_M732}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hyrklglvtd	iegnqeitev
msa252352.2{114_H36B}	EDYYQREDDK	PETVKRRLDV	nIAQgesile	hyrklglvtd	iegnqeitev
Consensus	*****	*****	-----	-----	-----
201					
msa252352.2{114_18RS21}	fadvekalle	--			
msa252352.2{114_M781}	-----	--			
msa252352.2{114_CJB110}	-----	--			
msa252352.2{114_090}	fadvekalle	LK			
msa252352.2{114_JM9130013}	-----	--			
msa252352.2{114_A909}	-----	--			
msa252352.2{114_1169NT}	-----	--			
msa252352.2{114_2603}	fadvekalle	LK			
msa252352.2{114_COH1}	fadvekal--	--			
msa252352.2{114_M732}	fadvekalle	LK			
msa252352.2{114_H36B}	fadvekal--	--			
Consensus	-----	**			
212					

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

SEQ ID NO. 4401  
**STRAIN 2603**  
 GTGGATAAACATCACTCAAAAAAGGCTATTTTAAAGTTAACA  
 CTTATAACAACCTAGTATTTTATTAATGTCATAGCAATCAAGTGAATGCAGAGGAGCAAGAA  
 TTAATAAACCAAGAGCAATCACCTGTAATTGCTAATGTTGCTCAACAGCCATCGCCATCG  
 GTAACCTACTAATCTGTTGAAAAAACATCTGTAACAGCTGCTTCTGCTAGTAATACAGCG  
 AAAGAAATGGGTGATACATCTGTAAAAAATGACAAACAGAAAGATGAATATTAGAAAGAG  
 TTATCTAAAAACCTTGATACGTCTAATTTGGGGGCTGATCTTGAAGAAAGATATCCCTCT  
 AAACCAGAGACAACCAACAATAAAGAAAGCAATGTAGTAACAAATGCTTCACTGCAATA  
 GCACAGAAAGTTCCTCAGCATATGAAGAGGTGAAGCCAGAAAGCAAGTCATCGCTTGCT  
 GTTCTTGATACATCTAAAAATAACAAATTAACAAGCCATAACCAAGAGGAAAGGGAAAT  
 GTAGTAGCTATTATGATACCTGGCTTTGATATTAACCATGATATTTTTCGTTTAGATAGC  
 CCAAAAGATGATAAGCACAGCTTTAAAACTAAGACAGAAATTTGAGGAATTAAGCAAAAA  
 CATAATATCACTTATGGGAAATGGGTAAACGATAAGATTGTTTTGACATAACTACGCC  
 AACAAATACAGAAACGGTGGCTGATATTGCAGCAGCTATGAAGATGGTTATGGTTAGAA  
 GCAAGAAATATTTCCCATGGTACACACGTTGCTGGTATTTTGTAGGTAAATAGTAACAGT  
 CCAGCAATCAATGGTCTTCTTTTAGAAGGTGCAGCGCCAAATGCTCAAGTCTTATTAAATG  
 CGTATTCAGATGATAAATGATTGCGACAAATTTGGTGAAGCATATGCTAAAGCAATCACA  
 GACGCTGTTAATCTAGGAGCAAAACGATTAAATAGGATTTGAAAAACAGCTGATTCT  
 TTAATGCTCTCAATGATAAAGTTAAATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTT  
 GCAGTTGTTGGCTGCCGAAATGAAGCGCATTTGGTATGGATTATAGCAAAACATT  
 TCAACTAATCCTGACTACGGTAAATAGTCCAGCTATTTCTGAAGATACCTTTGAGT  
 GTTGCTAGCTATGAATCACTTAAACTATCAGTGAGGTGCTGAACAACTATTGAAGGT  
 AAGTTAGTTAAGTTGCCGATTTGTGACTTCTAAACCTTTTGACAAAGGTAAAGGCTACGAT  
 TGGTTTATGCCAATTTATGGTGCAAAAAAGACTTTGAAGGTAAGGACTTTAAAGGTAAG  
 ATTGCATTAATGAGCGTGGTGGGACTTGTATTTATGACTAAATCACTCATGTCTACA  
 AATGCAGGTGTTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTTGGAATTTTCTA  
 ATTCTTACCGTGAATCACCTGTGGGGATTATTAGTAAAGTAGATGGCGAGCGTATAAAA  
 AATACTTCAAGTCAGTTAAACATTTAACCAGAGTTTGTAAAGTAGTTGATAGCCAAAGTGGT  
 AATCGTATGCTGGAACAAATCAAGTTGGGGCGTGACAGCTGAAGGAGCAATCAAGCTGAT  
 GTAACAGCTTCTGGCTTTGAAATTTATCTTCAACCTATAATAATCAATCAAAACAAATG  
 TCTGGTACAAGTATGGCTTACCACATGTTGCAGGATTATGACAAATGCTTCAAGTCAT  
 TTGGCTGAGAAATATAAGGGATGAATTTAGATTCTAAAAAATTGCTAGAAATGTCTAAA  
 AACATCCTCATGAGCTCAGCAACAGCATTTATAGTGAAGAGGATAAGGCGTTTATTCA  
 CCACGTCAGCAAGGTGCAGGTGATGTTGATGCTGAAAAAGCTATCAAGCTCAATATTAT  
 ATTACTGGAACCATGGCAAGCTAAATTAATCTCAACCAAGTGGGAGATAAATTTGAT  
 ATCAGATTACAATTATAAACTTGTAGAAGGTGTCAAGAAATTTGATTTATCAAGCTAAT  
 GTAGCAACAGAAACAGTAAATAAAGGTAAATTTGCCCTTAAACCAAGCCCTTGCTAGAT  
 ACTAATTGGCAGAAAGTAATCTTCTGTGATAAAGAAACCAAGTTTCGATTACTATTGAT  
 GCTAGTCAATTTAGTCAAGAAATTAAGAAACAGATGGCAATGGTTATTTCTAGAAGGT  
 TTTGTACGTTTAAAGAGGCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGT  
 GAAAGAGATGCAGGCAATTAATCCATATTTGCCATTTCTCCAAATAAAGATGGAATAGG  
 GACGAAATCACTCCCGAGGCACTTTCTTAAGAAATTTAAGGATATTTCTGCTCAAGTT  
 CTAGATCAAAATGGAATGTTATTTGGCAAGTAAGGTTTACCATCTTATCGTAAAAAT  
 TTCCATTAATTAATCCAAAGCAAGTGTGCTGATGATGCTTCTCAGTGGAGT  
 GGTTTAGATAAGGATGGCAAGTTGTAGCAGATGGTTTATATCTTATCGCTTACGTTTAC  
 ACACAGTAGCAGGAAGGAGCAATAGTCAGGAGTCAGACTTTAAAGTACAAGTAAGTACT  
 AAGTCACCAATCTTCTTACAGGCTCAGTTTGTAGAACTAATCGAACATTAAAGCTTA  
 GCCATGCTAAGCAAGTAGTTATGTTTCTACATATCGTTTACAAATAGTTTATCTCAT  
 GTTGTAAAAGATGAAGAAATATGGGATGAGACTTCTTACCATTATTTCCATATAGATCAA  
 GAAGTTAAAGTGACACTTCTTAAACCGTTAAGATAGGAGAGAGTGAAGTTGCGGTAGAC  
 CCTAAGGCCTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTGCAACCGTAAATTTG  
 TCTGATCTCTTGAATAGGCAAGTATCAGAGAAAGAAACGCTATAGTAATTTCTAAC  
 AGTTTCAAAATATTTGATACTTGAAGAAAGAACCTATGTTTATTTCTAAAAAGAAAAA  
 GTAGTAAACAGAAATCTAGAAGAAATTAATTTAGTTAAGCCGCAAACTACAGTTACTACT  
 CAATCATTTGTCTAAAGAAATACTAAATCAGGAAATGAGAAAGTCTCACTTCTACAAAC  
 AATAATAGTAGCAGAGTAGCTAAGATCATATCACTAAACATAACGGGGATTCTGTTAAC  
 CATACCTTACCTAGTACATCAGATAGAGCAACGAATGGTCTATTTGTTGGTACTTTGGCA  
 TTGTTATCTAGTTTACTTCTTTATTTGAAACCCAAAGACTAAAAATAATAGTAAA

SEQ ID NO. 4402  
**STRAIN 090**  
 GAGGAGCAAGAAATTAATAAACCAAGAGCAATCACCTGTAATTGCT  
 AATGTTGCTCAACAGCCATCGCCATCGGTAACCTACTAATATGTTGAAAA  
 AACATCTGTAACAGCTGCTTCTGCTAGTAATACAGTGAAGAAATGGGTG  
 ATACATCTGTAAAAAATGACAAACAGAAAGATGAATATTAGAAAGATT  
 TCTAAAAACCTTGATACGTCTAATTTGGGGGCTGATCTTGAAGAAATA  
 TCCCTCTAAACAGAGACAACCAACAATAAAGAAAGCAATGTAGTAACAA  
 ATGCTTCAACTGCAATAGCACAGAAAGTTCCTCAGCGTATGAAGAGGT  
 AAGCCAGAAAGCAAGTCATCGCTTGCTGTTTGTATACATCTAAATAAC  
 AAAATTGCAAGCCATAACCCAAAGAGGAAAGGGAATGTAGTAGCTATTA  
 TTGATACTGGCTTTGATATTAACCATGATATTTTCGTTTAGATAGCCCA  
 AAAGATGATAAGCACAGCTTTAAACTAAAGCAGAAATCGAGGAATTA  
 AGCAAAACATAATACCTTATGGGAAATGGGTAAACGATAAGATTGTTT  
 TTGCACATAACTACGCCAACATAACAGAAACGGTGGCTGATATTGCAGAC  
 GCTATGAAAGATGGTTATGGGTGAGAGCAAGAAATATTTCGCATGGTAC  
 ACACGTTGCTGGTATTTTGTAGGTAAATAGTAAACGCTCCAGCAATCAATG  
 GTCTTCTTTTAGAAGGTGCAGCGCCAAATGCTCAAGTCTTATTAAATGCGT

**Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)**

ATTCCAGATAAAATTGATTCCGACAAAATTGGAGAAGCATATGCTAAAGC  
 AATCAGACAGCGTGTtTAATCTAGGAGCAAAAaCGATTAAATATGAGCCTTG  
 GAAAAACAGCAGATTCTTTAAAttGCaCTCAATGATAAAGTTAAATTAGCA  
 CTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTGTGGCTGCCGAAA  
 TGAAGGTGCATTGGTATGGATTATAGCAAACCATTTATCAACTAATcCTG  
 ACTACGGTACGGTTAAATAGTCCAGCTATTTCTGAAGATACTtTGAGTGT  
 GCTAGCTATGAATCACTTAAAACTATCAGTGAGGTCGTGAAACAACTAT  
 TGaaGGTAAGTTAGTTAAGTTGCCGATTGTGACTTCTAAACCTTTtGACA  
 AAGGTAAGGCCCTACGATGTGGTTTATGCCAATTATGGTGCAaaaaAAGAC  
 TTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAAAtGAGCGTGGtGG  
 TGGACTTGATTtTTATGACTAAaatCACTcATGCTACAAATGCAGGTGTG  
 tTGGTATCGTtATtTtTAACgAtCAAGAAaAACGtGGAATTTTtTAATT  
 CCTTACCCTGAATTACCTGTGGGGTTATTAGTAAAGTAGATGGCGAGCG  
 TATAAAAAATACTTCAAGTCAGTTAACATTTAACCAGAGTTTtGAAGTAG  
 TTGATAGCCAAAGTGGCAATCGTATGCTGGAAACAAATCAAGTTGGGGCGTG  
 ACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTGGCTTTGAAT  
 TTTATCTTCAACCTATAATAATCAATACCAACCAATGTCTGGTACAAGTA  
 TGGCTTCACCACATGTTGCAGGATTAAAGACAATGCTTCAAAGTCATTG  
 GCTGAGAAATATAAAGGGATGAATTTAgATTCTTAAAAAATTGCTAGAATT  
 GTCTAAaACATCCTCATGAGCTCAGCAaCAGCATTATATAGTgAAGAgG  
 ATAAAGCGTtTtATTcACCAAGTCAGCAAGGtGCAGGtGTAGTTGATGCT  
 GAAAAAGCTATCCAAGCTCAATATTATGTTACTGGAAACGATGGCAAGC  
 TAAAAATTAACTCTCAAAACGAGTGGGAGATAAAATTTGATATCACAGTTACA  
 TTTCAAACTTGTAGAAGGTGTCAAAGAATTGTATTATCAAGCTAATGTA  
 GCAACAGAAcAAGTAAATAAAGGTAATTTGCCCTTAAACCAACAGCctT  
 GCTAGATACTAATTGGCAGAAAGTAATTCTTcGTGATAAAGAAACACAAG  
 TTcGATTTACTATTGATGCTAGTCAATTTAGTCAGAAATTTAAAGAACAG  
 ATGGCAAAATGGTTATTtTCTTagAAGGTTTGTACGTTTAAAGAAGCCAA  
 GGATAGtAATCAGGAGTTAaTGAGTATTCCTTtTGTAAGTtTAAATGGTG  
 ATTtTGGCAACTTACAAGCACTTGAAACACCGATTATAAGACGCTTTCT  
 AAAGGTAGTTTCTACTATAAACCAAAATGATACAACTCATAAAGCCAATT  
 GGAGTACAATGAATCAGCTCCTTTTGAAGCAACAACCTATAGTGCCTTGT  
 TAACCAATCAGCGTCTTGGGGCTATGTTGATTATGTCAAAATGGTGGG  
 GAGTTAGAATTAGCACCGGAGAGTcCAAAAAGAATTATTtTAgAACTTT  
 TGAGAATAAGGTTGAGGATAAAAACAATTCATCTTTTGGAAAGAGATGCA  
 GcAATAATCCATATTtTGCCATTCTCCAATTAAGATGGAATAGGGAAT  
 GAATCACTCCCAGGCACTTCTTAAGAAATGTTAAGGATATTtCTGTC  
 TCAAGTTCTAGATCAAAATGGAATGTTATTtGGCAAGTAAGGTTTtTAC  
 CATCTTATCGTAAAAATTTCCATAAATCTCAAAGCAAAGTGATGGTCAT  
 TATCGTATGGATGCCTTTCACTGGAGTGGTTAGATAAGGATGGCAAGT  
 TGTAAGCAGATGGTTTtTATACCTTATCGCCTACGTTACACACAGTAGCAG  
 AAGGAGCAAAATAGTCAGGAGTCAGACTTTAAAGTTCAAGTAAGTACTAAG  
 TCACCAATCTTCTTtTACTAGCTCAGTTTGTAGAACTAATCGAACATT  
 AAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTTACATATCGTTTAC  
 AATTAGTTTtTATCTCATGTTGTAAGAGATGAAGAATATGGGGATGAGACT  
 TCTTACCATTATTtCCATATAGATCAAGAAAGTAAAGTGACACTTCCTAA  
 AACGGTTAAGATAGGAGAGAGTGGGTTGCACTAGACCTTAAGGCTTGA  
 CACTTGTGTGGAAGATAAAGCTGGTAATTtTGCAACGGTAAATTTGTCT  
 GACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAACGCTATAGTAAT  
 TTCTAACAGTTTCAAATATTtTGATAACTTGAAAAAGAACTATAGTTTA  
 TTTCTAAAGAAAGAAAGTAGTAAACAGAATCTAGAAGAAATAACATTA  
 GTTAAGCCGCAAACTACAGTTACTACTCAATCATTTGCTTAAAGAAATAAC  
 TAAATCAGGAAATGAGAAAGTCTCACTTCTACAAACAAATAATAGTAGCA  
 GAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTTAACCAT  
 ACC

SEQ ID NO. 4403

STRAIN A909

GAGGAGCAAGAATTAAAAAACCAAGAGCAAT  
 CACCTGTAATTGCTAAATGTTGCTCAACAGCCATCGCCATCGGTAACACT  
 AATACTGTTGAAAAACATCTGTAAACATCTGCTTCTGCTAGTAATACAGC  
 GAAAGAAATGGGTGATACATCTGTAAAAATGACAAAACAGAAGATGAAT  
 TATTAGAAGAGTTATCTAAAAACCTTGATACGCTCAATTTGGGGCTGAT  
 CTTGAAGAAGAAATATCCCTCTAAACAGAGACAACCAACAATAAAGAAAG  
 CAATGTAGTAACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCTCAG  
 CATATGAAGAGGTGAAGCCAGAAAGCAAGTCATCACTTGCTGTTCTTGAT  
 ACATCTAAATAACAAATTTGCAAGCCATAACCCAAAGAGGAAAGGGAAA  
 TGTAGTAGCTATTATTGATACCTGGCTTGATATTAAACCATGATATTtTTC  
 GTTTAGATAGCCCAAAAGATgaTAAGCACAGCTTTaAACTAAGGCAGAA  
 TTTGAGGAATTAAAGCAAAACATAATATCACTTATGGGAAATGGGTTAA  
 CGATAAGATTGt:TTTGCACATAACTACGCCaCAATACAGAAACGGTGG  
 CTGATATTGCAGCAGCTATGAAAGATGGTTATGGGTGAGAAGCAAGAAT  
 ATTTCCGATGGTACACAGCTTGCTGGTATTtTGTAGGTAATAGTAAAGC  
 TCCAGCAATCAATGGTCTTCTTTAGAAGGTGCAGCGCCAAATGCTCAAG  
 TCTTATTAAATGCGTATTCCAGATAAAATTTGATTCGGACAAATTTGGTGAA  
 GCATATGCTAAAGCAATCACAGACGCTGTTAATCTAGGAGCAAAAACGAT  
 TAATATGAGCCTTGGAAAAACAGCAGATTCTTAAATTGCTCTCAATGATA  
 AAGTTAAATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTT  
 GTGGCTGCCGAAATGAAGGTGCATTGGTATGGATTATAGCAAAACCAT  
 ATCAACTAACTCCTGACTACGGTACGGTTAAATAGTCCAGCTATTtCTGAAG  
 ATACTTTGAGTGTGCTAGCTATGAATCACTTAAAACTATCAGTGAGGTC  
 GTTGAAACAACTATTGAAGGTAAGTTAGTTAAGTTGCCGATTGTGACTTC  
 TAAACCTTtTGACAAAGGTAAGGCCTACGATGTGGTTTATGCCAATTATG

**Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)**

GTGCAAAAAAGACTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATT  
 AATTGAGCGTGGTGGTGGACTTGATTTTATGACTAAAATCACTCATGCTA  
 CAAATGCAAGGTGTTGTTGGTATCGTTAATTTTAAACGATCAAGAAAAACGT  
 GGAATTTTCTAATTCCTTACCGTGAATACCTGTGGGGGTATTAGTAA  
 AGTAGATGGCGAGCGTATAAAAAATACCTCAAGTCAGTTAACATTTAAC  
 AGAGTTTGAAGTAGTTGATAGCCAAAGGTGGCAATCGTATGCTGGAACAA  
 TCAAGTTGGGGCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAAACAGC  
 TTCTGGCTTTGAAATTTATTTCTCAACCTATAATAATCAATACCAACAA  
 TGCTGGTACAGATATGGCTTACCACATGTGTCAGGATTAAATGACAAATG  
 CTTCAAGTCATTTGGCTGAGAAATATAAAGGATGAATTTAGATTCTAA  
 AAAATTGCTAGaATTGTCTAAAAACATcCTCATGAGCTCAGCAACAGCAT  
 TATATAGTGAAGAGGATAAGGCGTTTATTTACCACGTCAGCAAGGTGCA  
 GGTGTAGTTGATGCTGAAAAAGCTATCCAAAGCTCAATATTATGTTACTGG  
 AAACGATGGCAAAGCTAAATTAATCTCAAACGAGTGGGAGATAAATTTG  
 ATATCACAGTTACAATTCAAACTTGTAGAAGGTGTCAAAGAATTGTAT  
 TATCAAGCTAATGTAGCAACAGAACAGTAAATAAAGGTAATTTGCCTT  
 TAAACCaCAAGCCTTGCTAGATACTAATTGGCAGAAAGTAATTTCTGCTG  
 ATAAAGAAACACAAGTTCCGATTACTATGATTCTAGTCAATTTAGTCAG  
 AAATTAAGAAACAGATGGCAATGTTATTTCTAGAAGGTTTGTACG  
 TTTTAAAGAAAGCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTG  
 TAGGATTTAATGGTATTTTGGCACTTACAAGCACTTGAACACCGGATT  
 TATAAGACGCTTTCTAAAGGTAGTTTCTACTATAAACCAATGATACAAC  
 TCATAAAGACCAATTGGAGTACAATGAATCAGCTCCTTTTGAAAGCAACA  
 ACTATACCTCTGTGTAACACAAATCAGCGTCTTGGGGCTATGTTGATTAT  
 GTCAAAAATGGTGGGGAGTTAGAATTAGCACCGGAGAGTCCAAAAAGAA  
 TATTTTAGGAACCTTTGAGAATAAGGTGAGGATAAAACAAATTCATCTTT  
 TGGAAGAGATGCAGCGAATAATCCATATTTTGCCATTCTCCAAATAAA  
 GATGAAATAGGGATGAAATCACTCCCCAGGCAACTTTCTAAGAAATGT  
 TAAGGATATTTCTGCTCAAGTTCTAGATCAAAATGGAAATGTTATTTGGC  
 AAAGTAAGGTTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAAG  
 CAAAGTGATGGTCATTATCGTATGGATGCCCTTCAGTGGAGTGGTTAGA  
 TAAGGATGGCAAAGTTGTAGCAGATGGTTTATATCTATCGTTACGTT  
 ACACACCGTAGCAGAAGGAGCAATAGTCAGGAGTCAGACTTTAAAGTT  
 CAAGTAAGTACTAAGTCACCAAACTCTTCTTACGAGCTCAGTTTGTATGA  
 AACTAATCGAACATTAAAGCTTAGCCATGCCCTAAGGAAAGTAGTTATGTTT  
 CTACATATCGCTACAAATAGTTTATCTCATGTTGTAAAAGATGAAGAA  
 TATGAGATGAGAGCTTCTTACCATTATTTCCATATAGATCGAGAAGGTAA  
 AGTGACACTTCTTAAACAGTTAAGATAGGAGAGAGTGGGTTGAGTAG  
 ACCCTAAGACCTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTGCGA  
 ACGGTAAAATTGTCTGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGA  
 AAACGCTATAGTAATTTCTAACAAATTTCAAATATTTGATAACTTGAAAA  
 AAGAACCTATGTTTATTTCTAAAGAAAGGAAAGTAGTAAACAGAACTTA  
 GAAGAAATAGCATTAGTTAAGCCGCAAACTACAGTTACTACTCAATCATT  
 GTCTAAAGAAATAACTCAATCAGGAAATGAGAAAGTCTCACTTCTACAA  
 ACAATAATAGTAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGG  
 GATTCTGTTAACCATACC

SEQ ID NO. 4404

STRAIN H3B

GAGGAGCAAGAAATTA AAAAACCAGAGCAATCACCTGTAATTGC  
 TAATGTTGCTCAACAGCCATCGCCATCGGTAACTACTAATACTGTTGAAA  
 AAACATCTGTAAACATCTGCTTCTGCTAGTAATACAGCGAAAGAAATGGGT  
 GATACATCTGTAAAAATGACAAACAGAAAGATGAATATTAGAAGAGTT  
 ATCTAAAAACCTTGATACGCTCAATTTGGGGGCTGATCTTGAAGAAGAA  
 ATCCCTCTAAACAGAGACAAACCAATAAAGAAAGCAATGTAGTAACA  
 AATGCTTCAACTGCAATAGCACAGAAaGTTCCTCAGCATATGAAGAGGT  
 GAAGCCAGAAAGCAAGTCATCACTTGCTGTTCTTGATACATCTAAATAA  
 CAAAATTGCAAGCCATAACCCAAAGAGGAAAGCGAAATCTAGTAGCTATT  
 ATTGATACCTGGCTTTGATATTAAACCATGATATTTTCGTTTAGATAGCCC  
 AAAAGATGATAAGCACAGCTTTAAACCTAAGGCAGAAATTTGAGGAATTAA  
 AAGCAAAACATAATATCACTTATGGGAAATGGGTTAACGATAAGATTGTT  
 TTTGCACATAACTACGCCaCAATAACAGAAACGGTGGCTGATATTGCAGC  
 AGCTATGAAAGATGGTTATGGGTGAGAAGCAAGAAATTTTCGATGGTA  
 CACACGTTGCTGGTAATTTTGTAGGTAATAGTAAACGTCAGCAATCAAT  
 GGTCTTCTTTAGAAGGTGCAGCGCAAAATGCTCAAGTCTTATTAATGCG  
 TATTCAGATAAAATTTGATTGGGCAAAATTTGGTGAAGCATATGCTAAAG  
 CAATCACAGACGCTGTTAATCTAGGAGCAAAACGATTAATATGAGCCTT  
 GGA AAAACAGCAGATTCTTTAATTGCTCTCAATGATAAAGTTAAATTAGC  
 ACTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTTGTGGCTGCCGGA  
 ATGAAGGTGCATTGGTATGGATTATAGCAAACCATATCACTAATCCT  
 GACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGTACTTTGAGTGT  
 TGCTAGCTATGAATCACTTAAACCTATCAGTGAGGTGCGTTGAAACAACTA  
 TTGAAGGTAAGTTAGTTAAGTTGCCGATTGTGACTCTAAACCTTTGAC  
 AAAGGTAAGGCCTACGATGTGGTTTATGCCAATTATGGTGCAAAAAAGA  
 CTTTGAAGGTAAAGACTTTAAGGTAAGATTGCATTAATTGAGCGTGGT  
 GTGGACTGATTTTATGACTAAAACTCACTCATGCTACAAATGCAGGTGTT  
 GTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTGGAATTTTCTAAT  
 TCCCTTACCGTGAATTACCTGTGGGGGTATTAGTAAGTAGATGGCGAGC  
 GTATAAAAATACTTCAAGTCAGTTAACATTTAACAGAGTTTGTGAAGTA  
 GTTGATAGCCAAAGGTGGCAATCGTATGCTGGAACCAATCAAGTTGGGGCGT  
 GACAGCTGAAGGAGCAATCAAGCCTGATGTAAACGCTTCTGGCTTTGAAA  
 TTTATTTCTTCAACCTATAATAATCAATACCAACAAATGTCTGGTACAGT  
 ATGGCTTCAACCATGTTGCAGGATTAATGACAAATGCTTCAAGTCATTT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

GGCTGAGAAATATAAAGGGATGAATTTAGATTCTAAAAAATTGCTAGAAT  
 TGTCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATATAGTGAAGAG  
 GATAAGGCGTTTTATTCCACCACGTCAGCAAGGTGCAGGTGTAGTTGATGC  
 TGAAAAAGCTATCCAAGCTCAATATTATGTTACTGGAAACGATGGCAAAG  
 CTAATAATTAATCTCAACAGAGTGGGAGATAAATTGATATCACAGTTACA  
 ATTCTAAACTTGTAGAAGGTGTCAAAGAATTGTATTATCAAGCTAATGT  
 AGCAACAGAACAGTAAATAAAGGTAAATTTGCCCTTAAACCcAAGCCT  
 TGCTAGATACTAATTGGCAGAAAGTAATTCTTCGTGATAAAGAAACAA  
 GTTCGATTCTACTATTGATTCTAGTCAATTTAGTCAGAAATTTAAAGAACA  
 GATGGCAAATGGTTATTCTTAGAAGGTTTGTACGTTTAAAGAAGCCA  
 AGGATAGTAATCAGGAGTTAATGAGTATTCCTTTGTAGGATTTAATGGT  
 GATTTTGCAGACTcACAAGCACTTGAACACCGATTTATAAGACGCTTTC  
 TAAAGGTAGTTTCTACTATAAACCAAATGATACAACTCATAAGACCAAT  
 TGGAGTACAATGAATCAGCTCCTTTTGAAGCAACCACTATCTACTGCCCTG  
 TTAACCAATCAGCGCTCTTGGGGCTATGTTGATTATGTCAAAAAATGGTGG  
 GGAGTTAgAATTAgCACCGGAGAGTCCAAAAGAAATTATTTAGGAACCTT  
 TTGAGAATAAGGTTGAGGATAAAACAATTCTCTTTTGGAAAGAGATGCA  
 CGGAATAATCCATATTTGCCATTTCTCCAATAAAGATGGAAATAGGGA  
 TGAAATCACTCCCAGGCAACTTTCTTAAGAAATGTTAAGGATATTTCTG  
 CTCAAGTTCTAGATCAAAATGGAATGTTAATTGGCAAAGTAAGGTTTAA  
 CCATCTTATCGTAAAAATTTCCATAATAATCCAAAGCAAAGTGATGGTCA  
 TTATCGTATGGATGCCCTTCAGTGGAGTGGTTTAGATAAGGATGGCAAAG  
 TTGTAGCAGATGGTTTTTATACCTTATCGTTTACGTTACACACCACTAGCA  
 GAAGGAGCAATAGTCAGGAGTCAGACTTTAAAGTTCAAGTAAGTACTAA  
 GTCACCAAACTCTCCTTCAGGAGCTCAGTTTGTATGAACTAATCGAACAT  
 TAAGCTTAGCCATGCCCTAAGGAAAGTAGTTATGTTCTCATATCGTCTA  
 CAATTAGTTTATCTCATGTTGTAAAAGATGAAGAATATGGAGATGAGAC  
 TTCTTACCATTAATTTCCATATAGATCAAGAAGGTAAAGTGACACTTCTTA  
 AAACAGTTAAGATAGGAGAGAGTGGGTTGCAGTAGACCTTAAGACCTTG  
 ACACCTGTTGTGGAAGATAAAGCTGGTAATTTTCGCAACGGTAAAAATTGTC  
 TGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAACGCTATAGTAA  
 TTTCTAACAATTTCAAATATTTTGATAACTTGAAAAAGAACTATGTTT  
 ATTTCTAAAGAAGGAAAGTAGTAAACAAGAATCTAGAAGAAATAGCAAT  
 AGTTAAGCCGCAAACTACAGTTACTACTCAATCATTTGTCTAAAGAAATAA  
 CTCAATCAGGAAATGAGAAAGTCTCACTTCTACAAACAATAATAGTAGC  
 AGAGTAGCTAAGATCATATCACCTAAACATAACGGGATTTCTGTTAACCA  
 TACC

SEQ ID NO. 4405

STRAIN 18RS21

GAGGAGCAAGAAATAAAAACCAAGAGCAATCACC  
 TGTAAATGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACCTACTAATA  
 CTGTTGAAAAAACATCTGTAAACAGCTGCTTCTGCTAGTAAATACAGCGAAA  
 GAAATGGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAATTATT  
 AGAAGAGTTATCTAAAAACCTTGATACGCTCTAATTTGGGGGCTGATCTTG  
 AAGAAGATATCCCTCTAAACCAGAGACAACCAACAATAAAGAAAGCAAT  
 GTAGTAACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCATA  
 TGAAGAGGTGAAGCCAGAAAGCAAGTCATCGCTTGTGTTCTTGATACAT  
 CTAAATAACAAAAATTACAAGCCATAACCCAAGAGGAAAGGAAATGTA  
 GTAGCTATTATTGATAGTGGCTTTGATATTAAACATGATATTTTTCGTTT  
 AGATAGCCCAAAAGATGATAAGCAAGCTTTAAAACTAAGACAGAATTTG  
 AGGAATTAAGCAAAACATAATATCACTTATGGGAAATGGGTTAACGAT  
 AAGATTGTTTTGACATAAATACGCCAACAAATACAGAAACGGTGGCTGA  
 TATTGACGAGCTATGAAGATGGTTATGGTTCAGAAGCAAGAAATATT  
 CGCATGGTACACAGCTTGTCTGTTATTTTGTAGCTAATAGTAAACGTTCCA  
 GCAATCAATGGTCTTCTTTAGAAGGTGCAGCGCCAAATGCTCAAGTCTT  
 ATTAATGCGTATTCAGATAAAATTGATTCCGACAAATTTGGTGAAGCAT  
 ATGCTAAAGCAATCAGACGCTGTTAATCTAGGAGCAAAACGATTAAT  
 ATGAGTATTGGAACCAAGCTGATTCTTTAATTGCTCTCAATGATAAAGT  
 TAAATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGAGTTGTTGTGG  
 CTGCCGGAATGAAGGCGCATTTGGTATGGATTATAGCAAAACATTATCA  
 ACTAATCCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATAC  
 TTTGAGTGTGCTAGCTATGAATCACTTAAAACTATCAGTGAGGTGCTTG  
 AAACAACCTATTGAAGGTAAGTTAGTTAAGTTGCCGATTTGACTTTCTAAA  
 CCTTTTGACAAAGGTAAGGCTACGATGTGGTTTATGCCAATATGGTGC  
 AAAAAAGACTTTGAAGGTAAGGACTTTAAGGTAAGATTGCATTAAATTG  
 AGCGTGGTGGTGGACTTGATTTTATGACTAAAATCACTCATGCTACAAT  
 GCAGGTGTTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTGGAAA  
 TTTTCTAATTCCTTACCCTGAATTACCTGTGGGATTTATTAGTAAAGTAG  
 ATGGCGAGCGTATAAAAAATCACTTCAAGTCAGTTAAACATTAAACAGAGT  
 TTTGAAGTAGTTGATAGCCAGGTGGAATCGTATGCTGGAACCAATCAAG  
 TTGGGGCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTG  
 GCTTTGAATTTATTCTTCAACCTATAATAATCAATACCAaCAATGTCT  
 GGTACAAGTATGGCTTCAACACATGTTGCAGGATTAATGACAATGCTTCA  
 AAGTCATTGGCTGAGAAATATAAAGGATGAATTTAGATTCTAAAAAAT  
 TGCTAGAATTGTTCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATAT  
 AGTGAAGAGGATAAGGCGTTTATTACCACGTCAGCAAGGTGAGGTGT  
 AGTTGATGCTGAAAAAGCTATCCAAGCTCAATATATATATTACTGGAAACG  
 ATGGCAaAGCTAAAAATTAATCTCAACGAATGGGAGATAAATTTGATATC  
 ACAGTTACAATTCAaAACTTGTAGAAGGTGTCAAAGAATTGTATTATCA  
 AGCTAATGTAGCAACAGAAACAAGTAAATAAAGTAAATTTGCCCTTaAAC  
 CACAAGCCTTGCTAGATACTAATTGGCAGAAAGTAATTTCTTcGTGATAAA  
 GAAACCAAGTTCGATTACTATTGATGCTAGTCAATTTAGTCAGAAAT

**Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)**

AAAAGAACAGATGGCAAATGGTTATTTCTTAgAAGGTTTTGTACGTTTTA  
 AAGAAGCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTAGGA  
 TTTAATGGTGATTTTGCGAACCTTACAAGCACTTGAAACACCGATTATAA  
 GACGATTTCTAAAGGTAGTTTCTACTATAAACCAATGATACAACTCATA  
 AAGACCAATTTGGAGTACAATGAATCAGCTCCTTTTGAAGCAACAATAT  
 ACTGCCTTGTAAACAATCAGCGTCTTGGGGCTATGTTGATTATGTCAA  
 AAATGGTGGGAGTTAGAAATAGCaCCGGAGAGTCCAAAAGAAATTTATTT  
 TAGGAACCTTTTGAGAAATAAGGTTGAGGATAAAACAATTCATCTTTTGGA  
 AGAGATGCAGCGAATAATCCATATTTTGCCATTTCTCCAAATAAGATGG  
 AAATAGGGACGAAATCACTCCCCAGGCAACCTTTCTTAAGAAATGTTAAGG  
 ATATTTCTGCTCAAGTTCTAGATCAAAATGGAAATGTTATTTGGCAAAGT  
 AAGGTTTACCACCTTATCGTAAAAATTTCCATAATAATCCAAAGCAAAG  
 TGATGGTCATTATCGTATGGATGCTCTTCAGTGGAGTGGTTTAGATAAGG  
 ATGGCAAAGTTGTAGCAGATGGTTTTTATACCTTATCGCTTACGTTACACA  
 CCAGTAGCAGAAGGAGCAATAGTCAGGAGTCAGACTTTAAAGTACAAGT  
 AAGTACTAAGTCACCAATCTTCCTTCACGAGCTCAGTTTGTGAACTA  
 ATCGAACATTAAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTTACA  
 TATCGTTTACAATTAGTTTATCTCATGTTGTAAAGATGAAGAAATATGG  
 GGATGAGACTTCTTACCATTATTTCCATATAGATCAAGAAGGTAAAGTGA  
 CACTTCTTAAACCGGTTAAGATAGGAGAGAGTGAAGTTGCGGTAGACCTT  
 AAGGCCTTGACACTTGTGTGGAAGATAAAGCTGGTAAATTCGCAACGGT  
 AAAATGTCTGATCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAACG  
 CTATAGTAATTTCTAACAGTTTCAAATATTTTGATACTTGAAGAAAGAA  
 CCTATGTTTATTTCTAAAGAAAGAAAGTAGTAAACAAGAACTTAGAAGA  
 AATAATATTAGTTAAGCCGCAAACTACAGTTACTACTCAATCATTTGTCTA  
 AAGAAATACTAAATCAGGAAATGAGAAAGTCTCACITCTACAAACAAT  
 AATAGTAGCAGAGTAGCTAAGATCATATCACTTAAACATAACGGGGATTCT  
 TGTTAACCATACC

SEQ ID NO. 4406

STRAIN M732

CAGGAGCAAGAATTAAAAACCAAGAGCAATCACCT  
 GTAATTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACTACTAATAT  
 TGTGTAAGAAACATCTGTAAACAGCTGCTTCTGCTAGTAATACAGTGAAG  
 AAATGGGTGATACATCTGTAAAAAATGACAAACAGAGATGAATTATTA  
 GAAGAGTTATCTAAAAACCTTGATACGTCTAATTTGGGGCTGATCTTGA  
 AGAAGAAATATCCCTCTAAACCAAGAGACCAACAATAAAGAAAGCAATG  
 TAGTAACAAATGCTTCAACTGCAATAGCACAGAAAGTCCCTCAGCATAT  
 GAAGAGGTGAAGTCAGAAAGCAAGTCATCGCTTGCTGTTCTTGATACATC  
 TAAATAACAAAAATTACAGGCCACAACCCAAAGAGGAAAGGAAATGTAG  
 TAGCTATTTATGATAGTGGCTTTGATATTAAACCATGATATTTTTCGTTTA  
 GATAGCCCAAGAGATGATAAGCAGAGCTTTAAACTAAGGCAGAAATTTGA  
 GGAATTAAGCAAAACATAATATCACTTATGGGAATGGGTTAAGGATA  
 AGATTGTTTTTGCACATAACTACGCCAACATAACAGAAACGGTGGCTGAT  
 ATTGCAGCAGCTATGAAAGATGGTTATGGGTGCAAGCAAGAAATATTTT  
 GCATGGTACACAGCTTGTCTGGTATTTTGTAGGTAATAGTAAACGCTCCAG  
 CAATCAATAGTCTCTTTTGAAGGTGACAGCGCAAAATGCTCAAGTCTTA  
 TTAATGCGTATTCAGATAAAATGATTCGGACAAATTTGGAGAAGCATA  
 TGCTTAAAGCAATCATAGACGCTGTTAATCTAGGAGCAAAACGATTAAATA  
 TGAGCCTGGGAAAAACGGCTGATTCTTTAATTGCTCTCAATGATAAAGTT  
 AAATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAAGTTGTTGTCG  
 TGCCGAAATGAAGGTGCAATTTGGTATGGATTATAGCAAAACCATTTCAA  
 CTAATCCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATACT  
 TTGAGTGTGCTAGCTATGAATCACTTAAACTATCAGTGAGGTGCTTGA  
 AACAACTATTGAAGGTAAGTTAGTTAAGTTGCCGATTTGTGACTTCTAAAC  
 CTTTGACAAAGGTAAAGCCTACGATGTGGTTTATGCCAATTATGGTGCA  
 AAAAAGATTTTGAAGGTAAAGACTTTAAAGGTAAGATGCAATTAATTGAG  
 CGTGGTGGTGGACTTGATTTTATGACTAAAATCACTCATGCTACAAATGC  
 AGGTGTTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTGGAAAT  
 TTCTAATTCCTTACCGTGAATTACCTGTGGGGGTTATTAGTAAAGTAGAT  
 GCGAGCGGTATAAAAAATACTTCAAGTCAGTTAACATTTAACCAGAGTTT  
 TGAAGTAGTTGATAGCCAAGGTGGCAATCGTATGCTGGAACAATCAAGTT  
 GGGGCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTGTC  
 TTTGAAATTTATTTCTCAACCTATAATTAATCAATACTAAACAATGTCTGG  
 TACAAGTATGGCTTCAACCATGTTGCAAGATTAATGACAAATGCTTCAAA  
 GTCAATTTGGCTGAGAAATATAAAGGGATGAATTTAGATTCTAAAAAATTG  
 CTAGAAATGCTTAAAAACATCCTCATGAGCTCAGCAACAGCATTATATAG  
 TGAAGAGGATAAGGCGTTTTATTCACCAGCTCAGCAAGGTGCAAGGTGATG  
 TTGATGCTGAAAAAGCTATCCAAGCTCAATATTATGTTACTGGAACAGAT  
 GGCAAGTTAAAAATTAATCTCAACAGGAGGGAGATAAATTTGATATCAC  
 AGTTACAATTCATaAACTTGTAGAAGGTGTCAAAGAAATTTGATTATCAAG  
 CTAATGTAGCAACAGAAaCAAGTAAATAAAGGTAATTTGCCCTTAAACCA  
 CAAGCCTTGCTAGATACTAATTTGGCAGAAAGTAATTTCTCGTATAAAGA  
 AACACAAGTTTCGATTTACTATTGATGCTAGTCAATTTAGTCAGAAATTA  
 AAGACAGATGGCAAATGGTTATTTCTTAGAAGGTTTGTACGTTTAAAA  
 GAAGCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTGTAGGAT  
 TAATGGTGATTTTGCGAACCTTACAAGCACTTGAAACaCCGATTATATAAG  
 CGCTTTCTAAAGGTAGTTTCTACTATAAACCAATGATACAACTCATAAA  
 GACCAATTTGAGTACAATGAATCAGCTCCTTTTGAAGCAACAATATAC  
 TGCTTTGTTAACCAATCAGCGCTTGGGGCTATGTTGATTATGTCAAAA  
 ATGTTGGGGAGTTAGAAATTAGCACCGGAGAGTCCAAAAGAAATTTATTTA  
 GGAACCTTTTGAAGATAAGGTTGAGGATAAAACAATTCATCTTTTGAAGAG  
 AGATGCAGCGAATAATCCATATTTTGCCATTTCTCCAATAAAGATGGAA

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

ATAGGGACGAAATCACTCCCCAGGCAACTTTCTTAAGAAATGTTAAGGAT  
 ATTTCTGCTCAAGTTCTAGATCAAAATGGAAATGTTATTGGCAAAGTAA  
 GGTTTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAGCAAAGTG  
 ATGGTCATTATCGTATGGATGCTCTTCAGTGGAGTGGTTTAGATAAGGAT  
 GGCAAAGTTGTAGCAGATGGTTTTTATACCTTATCGCTTACGTTACACACC  
 AGTAGCAGAAGGAGCaAATAGTCAGGAGTCAGACTTTAAAGTTCAAGTAA  
 GTACTAAGTCACCAAACTTTCCTTCACGAGCTCAGTTTGTAGAACTAAT  
 CGAACATTAAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTACATA  
 TCGTTTACAATTAGTTTATCTCATGTTGTAAAAGATGAAGAATATGGGG  
 ATGAGACTTCTTACCATTAATTTCCATATAGATCAAGAAGGTAAAGTGACA  
 CTTCTTAAACGGTTAAGATAGGAGAGAGTGAGGTTGCGGTAGACCTTAA  
 GGCCTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTTGCAACGGTAA  
 AATTGCTGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAACCGCT  
 ATAGTAAATTTCTAACAGTTTCAAATATTTTGATAACTTGAAGAAAGAACCC  
 TAGTTTATTCTTAAAGAAAGGAAAGTAGTAAACAAGAATCTAGAAGAAA  
 TAACATTAGTTAAGCCTCAAACTACAGTTACTACTCAATCATGTCTTAA  
 GAAATAACTAAATCAGGAAATGAGAAAGTCCTCACTTCTCAAAACAATA  
 TAGTAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTG  
 TTAACCATACC

SEQ ID NO. 4407

STRAIN COH1

GAGGAGCAAGAATTAAAAACCAAGAGCAATCACCTGT  
 AATTGCTAATGTTGCTCAACAGCCATCGCCATCGGTaACTACTAATATTG  
 TTGAAAAAACATCTGTAAACAGCTGCTTCTGCTAGTAATACAGTGAAAGAA  
 ATGGGcGATACATCTGTAAAAAATGACAAAACAGAAGATGAATTATTAGA  
 AGAGTTATCTAAAAACCTTGATACGCTCTAATTTGGGGGCTGATCTTGAAG  
 AAGAATATCCCTCTAAACAGAGaCAACCAACAATAAAGAAAGCAATGTA  
 GTAACAAATGCTTCACTGCAATAGCACAGAAAGTTCCTCAGCATATGA  
 AGAGGTGAAGTCAGAAAGCAAGTCATCGCTTGTGTTCTTGATACATCTA  
 AAATAACAAATTACAAGCCCAACCCAAAGAGGAAAGGGAATAGTAGTA  
 GCTATTATTGATACTGGCTTTGATATTAAACCATGATATTTTCGTTTGA  
 TAGCCCAAAAGATGATAAGCACAGCTTTAAACTAAGGCAGAAATTGAGG  
 AATTAAGCAAAACATAATATCACTTATGGGAATGGGTTAACGATAAG  
 ATTGTTTTTGCACATAACTACGCCaCAATACAGAAACGGTGGCTGATAT  
 TGCAGCAGCTATGAAAGATGGTTATGGGTGAGAAGCAAGAATATTTTGC  
 ATGGTACACACGTTGCTGGTATTTTGTAGGTAATAGTAAACGTCACGCA  
 ATCAATAGTCTTCTTTAGAGGTGACAGCGCCAAATGCTCAAGTCTTATT  
 AATGCGTATTCCAGATAAAATGATTCTGGACAAATTTGGAGAAGCATATG  
 CTAAGCAATCATAGACGCTGTTAATCTAGGAGCAAAACGATTAAATATG  
 AGCCTGGGAAAAACGGCTGATTCTTTAATTGCTCTCAATGATAAAGTTAA  
 ATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAAGTTGTGTGGCTG  
 CCGGAATGAAGGTGCAATTGGTATGGATTATAGCAAAACCATTTATCACT  
 AATCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATACTTT  
 GAGTGTGTGCTAGCTATGAATCACTTAAACTATCAGTGAGGTGCTTGA  
 CAATATTGAAGGTAAGTTAGTTAAGTTGCGGATTGTGACTTCTAAACCT  
 TcTGACAAAGGTAAGGCCTACGATGTGGTTTATGCCAATTATGGTGCAAA  
 AAGATTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAAATTGAGCG  
 TGGTGGTGGACTTGATTATTATGACTAAATCACTCATGCTACAAATGCA  
 GTGTTGTTGGTATCGTTATTTTAAACGATCAAGAAACAGTGGAAATTTT  
 CTAATTCCTTACCGTGAATTACCTGTGGGGTTATTAGTAAAGTAGATGG  
 CGAGCGTATAAAAAACTTCAAGTCAGTTAAACATTTAAACAGAGTTTGA  
 AAGTAGTTGATAGCCAAAGGTGGCAATCGTATGCTGGAAACATCAAGTTGG  
 GCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTGGCTT  
 TGAaATTTATTCTTCAACCTATAATAATCAATACTAAACAATGTCTGGTA  
 CRAAGTATGGCTTCAACACATGTTGCAGGATTAATGACAATGCTTCAAAGT  
 CATTTGGCTGAGAAATATAAGGGATGAATTTAGATTCTaAAAAATTGCT  
 AGaATTGCTCTaAAACATCCTCATGAGCTCAGCAACAGCATTATATAGT  
 AAGAGGATAAGGCGTTTTATTACCACGTCAGCAAGGTGCAGGTGTAGTT  
 GATGCTGAAAAAGCTATCCAAGCTCAATATATGTTACTGGAAACGATGG  
 CAAAGTTAAATTAATCTCAAAACGAGAGGGAGATAAATTTGATATCACAG  
 TTACAATTCATaAACTTGTAAGAGGTGTCAGAAATTTGATTATCAAGCT  
 AATGTAGCAaCAGAACAAAGTAAATAAAGGTAAATTTGCCCTTAAACCA  
 AGCCTTGCTAGATACTAATTGGCAGAAAGTAATTTCTTcGTGATAAGAAA  
 CACAAGTTCGATTACTATTGATGCTAGTCAATTTAGTCAGAAATTA  
 GAACAGATGGCAAAATGGTTATTTCTTAGAAGGTTTGTACGTTTAAAGA  
 AGCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTAGGATT  
 ATGGTATTGCGAAGCTTACAAGCACTTGAACACCGATTATAAGACG  
 CTTTCTAAAGGTAGTTTCTACTATAAACCAATGATACAACTCATAAAGA  
 CCAATTGGAGTACAATGAATCAGTCTCTTTTGAAGCAACAACCTATACTG  
 CCTTGTATAACACAAATCAGCGCTTTGGGGCTATGTTGATTATGTCAAAAAT  
 GGTGGGGAGTTAGAAATAGCACCGGAGAGTCCAAAAAGAAATTTTATAGG  
 aACTTTTGAAGATAAGGTTGAGGATAAAACAATTCATCTTTTGAAGAG  
 ATGCAGCGAATAATCCATATTTTGCCATTTCTCCAATAAAGATGGAAT  
 AGGAGCGAAATCACTCCCCAGGCaCTTTCTTAAGAAATGTTAAGGATAT  
 TTCTGCTCAAGTCTTAGATCAAAATGGAAATGTTATTGGCAAAGTAAGG  
 TTTTACCATCTTATCGTAAAAATTTCCATAATaATCCAAGCAAGTGAT  
 GGTCAATTATCGTATGGATGCTCTTCAGTGGAGTGGTTAGATAAGGATGG  
 CAAAGTTGTAgCAGATGGTTTATATACTTATCGCTTACGTTACACACCAG  
 TAGCAGAAGGAGCAAAATAGTCAGGAGTCAGACTTTaAGTTCAAGTAAGT  
 AcTAAGTCACCAATCTTCTTTCACGAGCTCAGTTTGATGaAACTAATCG  
 AACATTAAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTCATATC  
 GTTACAATTAGTTTATCTCATCTTTGTAAGAGTAGAAGATATGGGAT

**Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)**

GAGACTTCTTACCATTATTTCCATATAGATCAAGAAGGTAAAGTGACACT  
 TCCTAAACGGTTAAGTAGGAGAGAGTGAGGTTGCGGTAGACCCCTAAGG  
 CCTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTTGCAACGGTAAAA  
 TTGCTGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAAACGCTAT  
 AGTAATTTCTAACAGTTTCAAAATATTTTGATAACTTGAAAGAAAGAACCTA  
 TGTTTATTTCTAAAGAAGGAAAAGTAGTAAACAGAATCTAGAAGAAATA  
 ACATTAGTTAAGCCTCAAACTACAGTTACTACTCAATCATTTGTCTAAAGA  
 AATAACTAAATCAGGAAATGAGAAAGTCTCACTTCTACAAACAATAATA  
 GTAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTT  
 AACCATAACC

SEQ ID NO. 4408

STRAIN M781

GAGGAGCAAGAATTAAAAACCAAGAGCAATCACCTGT  
 AATTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACCTACTAATATTG  
 TTGAAAAAACATCTGTAACAGCTGCTTCTGCTAGTAATACAGTGAAAGAA  
 ATGGGTGATACATCTGTAAAAATGACAAACAGAGATGAATTAATTAGA  
 AGAGTTATCTAAAAACCTTGATACGTTCTAATTTGGGGCTGATCTTGAAG  
 AAGAATATCCCTCTAAACAGAGACAACCAACATAAAGAAAGCAATGTA  
 GTAACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCATATGA  
 AGAGGTGAAGTCAGAAAGCAAGTCATCGCTTGTCTGTTCTTGATACATCTA  
 AAATAACAAAAATACAGGCCACAACCCAAAGAGGAAAGGAAATGTAGTA  
 GCTATTATTGATACCTGGCTTTGATATTAACCATGATATTTTTCGTTTGA  
 TAGCCCAAAAGATGATAAGCACAGCTTTAAACTAAGGCAGAAATTTGAGG  
 AATTAAGCAAAAACATAATATCACTTATGGGAAATGGGTTAACGATAAG  
 ATTGTTTTTGCACATAACTACGCCAAACAATACAGAAACGGTGGCTGATAT  
 TGCAGCAGCTATGAAAGATGGTTATGGGTGAGAGCAAGAAATATTTTGC  
 ATGGTACACACGTTGCTGGTATTTTGTAGGTAATAGTAACCGTCCAGCA  
 ATCAATAGTCTTCTTTAGAAGGTGCAGCGCCAAATGCTCAAGTCTTATT  
 AATGGGTATTTCCAGATAAAATTGATTCGGAACAATTTGGAGAAGCATATG  
 CTAAAGCAATCATAGACGCTGTTAATCTAGGAGCAAAAACGATTAATATG  
 AGCCTGGGAAAAACGGCTGATTCTTAAATGCTCTCAATGATAAAGTTAA  
 ATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAATTGTTGGGCTG  
 CCGGAAATGAAGGTGCAATTTGGTATGGATTATAGCAAAACCATTATCAaCT  
 AATCCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATACTTT  
 GAGTGTGCTAGCTATGAATCACTTAAACTATCAGTGAGGTGCTTGAAG  
 CAACATTGAAGGTAAAGTTAGTTAAGTTGCCGATTGTGACTCTCAaCCT  
 TTTGCAAAAGGTAAGGCTACGATGTGGTTTATGCCAATTATGGTGCAAA  
 AAAGATTTTGAAGGTAAGGACTTTAAAGGTAAAGTTGCATTAATTGAGCG  
 TGGTGGTGGACTTGATTTTATGACTAAAAATCACTCATGCTACAAATCAG  
 GTGTTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTGGAAATTTT  
 cTAATTCCTTACCGTGAATTACCTGTGGGGTTATTAGTAAAGTAGATGG  
 CGAGCGTATAAAAAATACTTCAAGTCAGTTAACATTAAACAGAGTTTg  
 AAGTAGTTGATAGCCAAAGGTGGCAATCGTATGCTGGAACAATCAAGTTGG  
 GCGGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAAACAGCTTCTGGCTT  
 TGAAATTTATCTTCAACCTATAAATCAATCACTAAACAATGTCTGGTA  
 CAAGTATGGCTTCACCACATGTTGAGGATTAATGACAATGCTTCAAAGT  
 CATTTGGCTGAGAAATATAAAGGGATGAATTTAGATTCTAAAAAATTGCT  
 AGAATTGTCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATATAGTG  
 AAGAGGATAAGGCGTTTTATTACCACGTCAGCAAGGTGCAGGTGTAGTT  
 GATGCTGAAAAAGCTATCCAAAGCTCAATATTATGTTACTGGAACCGATGG  
 CAAAGTTAAAAATTAATCTCAAACGAGAGGGAGATAAATTTGATATCAG  
 TTACAATTCATaaACTTGTAGAAGGTGTCAAAGAATTGTATTATCAAGCT  
 AATGTAGCaaCAGAAACAGTAAATaaAGGTAATTTGCCCTTaaACCaaCA  
 AGCCTTGCTAGATATAATTGGCAGaaAGTaaATTCTTcGTGATAAAGAAA  
 CACAAGTTcGATTACTATcTGATGCTAGTCAATTTAGTCAGAAATTAAAA  
 GAACAGATGGCAAAATGGTTATTCTTGAAGGTTTGTACGTTTAAAGA  
 AGCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTAGGATTTA  
 ATGGTGATTTTGCAGAACTcACAAGCACTTGAACACCGATTTATAAGACG  
 CTTTCTAAAGGTAGTTCTACTATAaaCCAAATGATCAAACTCATAAAGA  
 CCAATTGGAGTACAATGAATCAGCTCCTTTTGAAGCAACAACCTATACTG  
 CCTTGTTAAACAATCAGCGTCTTGGGCTATGTTGATTATGTCAAAAAT  
 GGTGGGGAGTTAGAATTAGCACCGGAGAGTCCAAAAAGAAATTTTTAGG  
 AACTTTTGAGAATAAGGTTGAGGATAAAACAATTCATCTTTGGAAGAG  
 ATGCAGCGAATAATCCATATTTTGCATTTCTCCAATAAAGATGGAAAT  
 AGGAGCgaATCACTCCCCAGGCaACTTCTTAAGAAATGTTAAGGATAT  
 TTCTGCTCAAGTCTTAGATCAAAATGGAATGTTATTTGGCAAAGTAAGG  
 TTTTACCATCTTATCGTAAAAATTTCCATAATaATCCAAAGCAAGTGAT  
 GGTCAATTATCGTATGGATGCTCTTCACTGGAGTGGTTTAGATAAGGATGG  
 CAAAGTTGTAGCAGATGGTTTATACTTATCGCTTACGTTACACACCAG  
 TAGCAGAGGAGCAAAATAGTCAGGAGTCAGACTTTAAAGTTCAAGTAAGT  
 ACTAAGTCACCAATCTTCCCTTACGAGCTCAGTTTGATGAAACTAATCG  
 AACATTAAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTCATATC  
 GTTTACAATTAGTTTATCTCATGTGTGTAAGATGAAGAATATGGGGAT  
 GAGACTTCTTACCATTATTTCCATATAGATCAAGAAGGTAAAGTGACACT  
 TCCTAAACCGGTTAAGATAGGAGAGAGTGAGGTTGCGGTAGACCCCTAAGG  
 CCTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTTGCAACGGTAAAA  
 TTGCTGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAAACGCTAT  
 AGTAATTTCTAACAGTTTCAAAATTTTGTATAACTGAAAGAAAGAACCTA  
 TGTTTATTTCTAAAGAAGGAAAAGTAGTAAACAAGAATCTAGAAGAAATA  
 ACATTAGTTAAGCCTCAAACTACAGTTACTACTCAATCATTTGTCTAAAGA  
 AATAACTAAATCAGGAAATGAGAAAGTCTCACTTCTACAAACAATAATA  
 GTAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTT



Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

AACCATACC

SEQ ID NO. 4409

STRAIN CJB110

GAGGAGCAAGAATTAAAAACCAAGAGCAATCACCTGTAA  
 TTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACACTAATATTGTT  
 GAAAAACATCTGTAnCAGCTGCTTCTGCTAGTAATACAGCGAAAGAAAT  
 GGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAATTATTAGAAG  
 AGTTATCTAAAAACCTTGATACGTCTAATWGGGGCTGATCTTGAAGAA  
 GAATATCCCTCTAAACCAGAGACAAACCAATAAAGAAAGCAATGTAGT  
 AACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCGTATGAAG  
 AGGTGaAGCCAGAAAGCAAGTCATCGCTTGCTGTTTTTGATACATCTAAA  
 ATAACAAAATTGCAAGCCATAACCCAAAGAGGAAAGGAAATGTAGTAGC  
 TATTATTGATCTGGCTTTGATATTAAACCATGATATTTTCGTTTAGATA  
 GCCCAAAGATGATAAGCACAGCTTTAAACTTAAAGCAGAATTCGAGGAA  
 tTAAAGCAAAACATAATATCACTTATGGGAATGGGTTAACGATAAGAT  
 TGTTTTTGACATAACTACGCCAACATACAGAAACGGTGGCTGATATTG  
 CAGCAGCTATGAAAGATGGTTATGGGTGAGAAGCAAGAAATATTTGCAAT  
 GGTACACACGTTGCTGGTATTTTGTAGGTAAATAGTAAACGTCAGCAAT  
 CAATGGTCTTTCTTTAGAGGTGCGCGCAATGCTCAAGTCTTATTA  
 TGCGTATTCAGATAAAATTGATTGCGGCAAAATTTGGAGAAGCATATGCT  
 AAAGCAATCACAGACGCTCTTAATCTAGGAGCAAAACGATTAAATATGAG  
 CCTTGGAAAAACAGCAGATTCTTTAATTGCACCTCAATGATAAAGTTAAAT  
 TAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAAGTGTGTGGCTGCC  
 GGAATGAAGGTGCAATTTGGTATGGATTATAGCAAAACATTATCAACTAA  
 TcCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATACTTTGA  
 GTGTTGCTAGCTATGAATCACTTAAACTATCAGTGAGGTGCTTGAACA  
 ACTATTGAAGGTAAGTTAGTTAAGTTGCGGATTTGTGACTTCTAAACCTTT  
 TGACAAAGGTAAAGCCTACGATGTGGTTTATGCCAATTATGGTGCAAAAA  
 AAGACTTTGAAGGTAAGGACTTTAAGGTAAGATTGCATTAATTTAGCGT  
 GGTGGTGCACTTGAATTTATGACTAAAATCACTCATGCTACAAATGCAGG  
 TGTTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTGGAATTTTc  
 TAATTCCTTACCGTGAATTACCTGTGgGGGTTATTAGTAAAGTAGATGGC  
 GAGCGTATAAAAAATACITCAAGTCAGTTAATTTAACCAgAGTTTGA  
 AGTAGTTGATAGCCAAgGTGGCAATCGTATGCTGGAACCAATCAAGTGGG  
 CGGTGACAGCTGAAGGAGCAATCAAGCCGTGATGTACAGCTTCTGGCTTT  
 GAAATTTTATTCTTCAACCTATAATAATCAATACCAAAACAAATGTCTGTAC  
 AAGTAGGCTTCAACCATGTGTCAGGATTAATGACAAATGCTTCAAAATC  
 ATTTGGCTGAGAAATATAAAGGGATGAATTTAGATTCTAAAAAATTGCTA  
 GAATTTGCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATATAGTGA  
 AGAGGATAAGGCGTTTATTCAACAGCTCAGCAAGGTGCGAGGTGATGTTG  
 ATGCTGAAAAAGCTATCCAAGCTCAATATTATGTTACTGGAACAGATGGC  
 AAAGCTAAAAATTAATCTCAACGAGTGGGAGATAAATTTGATATCACAGT  
 TACAATTATAAACTTGTAGAAGGTGTCAAAGAATTGTATTATCAAGCTA  
 ATGTAGCAACAGAACAGTAAATAAAGTAAATTTGCCCTTaAACCAAA  
 GCCTTGCTAGATACTAATTGGCAGAAAGTAATTTCTcGTGATAAAGAAAC  
 ACAAGTTGATTTACTATcTGATGCTAGTCAATTTAGTCAGAAATTAAGAG  
 AACAGATGGCAAAATGGTTATTTCTAGaAGGTTTGTACGTTTAAAGAA  
 GCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTGTAGGATTTAA  
 TGGTGATTTTGCGAACtLACAGCACTTGAACACCGATTATAAGACGC  
 TTTCTAAAGGTAGTctCTACTATAAACCAATGATACAACTCATAAGAC  
 CAATTTGGAGTACAATGAATCAGCTCctTTTGAAAGCAACAACTATACTGC  
 CTTGTTAACCAATCAGCGTCTTGGGGCTATGTTGATTATGTCAAAAATG  
 GTGGGAGTTAGAATTAGCACCGGAGAGTCCAAAAGAAATTTATTTAGGA  
 ACTTTTGAGAATAAGGTTGAGGATAAAACAAATTCATCTTTTGGAAGAGA  
 TGCAGCAATAATCCATATTTTGCCATTCTTCCAATAAAGATGGAATA  
 GGGATGaAATCACTCCCAGGCAACtTTCTTAAGAAATGTTAAGGATATT  
 TCTGCTCAAGTTCTAGATCAAAATGGAATGTTATTTGGCAAAGTAAGGT  
 TTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAAGCAAAGTGATG  
 GTCAATTATCGTATGGATGCCCTTTCAGTGGAGTGGTTAgATAAgGATGGC  
 AAAGTTGTAGCAGATGGTTTTTATACTTATCGCCTACGTTACACACCAGT  
 AGCAGAAgGAGCAATAGTCAGGAGTCaGACITTAAGTTCAAGTAAGTA  
 CTAAGTCACCAATCTTCTTTACTAGCTCAGTTTGATGAAACTAATCGA  
 ACATTAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTCATATATCG  
 TTTACAATTAGTTTATCTCATGTTGTAAAAGATGAAGAATATGGGGATG  
 AGACTTCTTACCATTATTTCCATATAGATCAAGAAGGTAAAGTGACACTT  
 CCTAAAAAGGTTAAGATAGGAGAGAGTGGGTTGAGTAGACCTTAAGGC  
 CTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTTGCAACGGTaAAAT  
 TGTCTGACCTCTTGAaTAAGcCAGTAGTATCAGAGAAAGAAAACGCTATA  
 GTAATTTCTAACAGTTTCAATATTTTGATAACTTGAAAAAGAACTAT  
 GTTTATTCTTAAAGAAGGAAAGTAGTAAACAAGAATCTAGAAGAAATAA  
 CATTAGTTAAGCCGCAaACTACAGTTACTACTCAATCATTTGTCTAAAGAA  
 ATAACATAATCAGGAAATGAGAAAGTCTCACTCTACAAACAATAATAG  
 TAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTTA  
 ACCATACC

SEQ ID NO. 4410

STRAIN 1169NT

GAGGAGCAAGAATTAAAAACCAAGAGCAATC

ACCTGTAATGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACACTA  
 ATATTGTTGAAAAACATCTGTAAACAGCTGCTTCTGCTAGTAATACAGCG  
 AAAGAAATGGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAAT  
 ATTAGAAGAGTTATCTAAAAACCTTGATACGCTAATATGGGGGCTGATC

**Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)**

TTGAAGAAGAAATATCCCTCTAAACCAGAGACAACCAACAATAAGGAAAGC  
 AATGTAGTAACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGC  
 ATATGAAGAGGTGAAGCCAAAAGCAAGTCAATCGCTTGCTGTTCTTGATA  
 CATCTTAAATAACAAATATGCAAGCCATAACCCAAAGAGGAAAGGAAAT  
 GTAGTAGCTATTATTGATACTGGCTTTGATATTAAACCATGATATTTTCG  
 TTTAGATAGCCCAAAAGATGATAAGCACAGCTTTAAAAATAAGGCAGAAAT  
 TCGAGGAATTAAGCAAAACATAATATCACTTATGGGAAATGGGTTAAC  
 GATAAGATTGTTTTTGCACATAAATACGCCAACAAATACAGAAACGGTGGC  
 TGATATTGCAGCAGCTATGAAAGATGGTTATGGTTCAGAAGCAAAAGAAAT  
 TTTCCGATGGTACACACGTTGCTGGTATTTTGTAGGTAATAGTAACGTT  
 CCAGCAATCAATGGTCTTCTTTTGAAGGTGCAGCGCCAAATGCTCAAGT  
 CTTATTATGGCTATTCAGATAAAAATGATTCGGACAAATTCGGAGAAG  
 CATATGCTAAAGCAATCACAGACGCTGTTAATCTAGGAGCTAAAAACGATT  
 AATATGAGTATTGAAAAACAGCTGATTCTTTAATTTGCTCTCAATGATAA  
 AGTTAAATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAAGTTGTTG  
 TGGCTGCGGAAATGAAGGCGCAATTTGGTATGGATTATAGCAAAACCGTTA  
 TCAACTAATCTGACTACGGTACGGTAAATAGTCCAGCTATTTCTGAAGA  
 TACTTTGAGTGTGCTAGCTATGAATCACTTAAACATATCAGTGAAGGTCG  
 TTGAACCAACTATTGAAGGTAAAGTTAGTTAAGTTCGCCGATTGCGACTTCT  
 AAACCTTTTACAAAGGTAAAGGCTACGATGTGGTTTATGCCAATTATGG  
 TGCAAAAAAGACTTTGAAGGTAAAGGCTTTAAAGGTAAAGTTGCAATTA  
 TTGAGCGTGGTGGTGGACTTGATTTATGACTAAATCACTCATGCTACA  
 AATGCAGGTGTGTGGTATCGTTATTTTAAAGATCAAGAAAAACGTGG  
 AAATTTTCTAATTCCTTACCGTGAATACCTGTGGGGGTTATTAGTAAAG  
 TAGATGGCGAGCGTATAAAAAATACCTTCAAGTCAAGTTAAACATTTAACCA  
 AGATTTGAAGTAGTTGATAGCCAAAGTGGCAATCGTATGCTGGAACCAATC  
 aagTtGGGGCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAAACAGCTT  
 CTGGCTTCGAATTTATTTCTTCTCaaCCTATAATAATCAATACCAAAACATG  
 TCTGGTACAAGTATGGCTTCAACACATGTTGCAGGATTAATGACAATGCT  
 TCAAGTCATTGGCTGAGaAATATAAGGGATGAATTTAGATTCTAAaAA  
 AATTTGCTAGAATTGTTCTAAAAACATCCCTCATGAGCTCAGCAACAGCATT  
 TATAGTGAAGAGGATAAGGCGTTTTATTCAACAGTCAAGCAAGGtGCAGG  
 TGATGTTGATGCTGAAAAAGCTATCCAAGCTCAATATTATGTTACTGGAA  
 ACGATGGCAAGCTAAATTAATCTCAACAGAGTGGGAGATAAATTTGAT  
 ATCAGCTTACNATTCTATAAATTTGTAGAAGGTGTCAAGAATTTGATTA  
 TCAAGCTAATGTAGCAACAGAACAGTAAATAAAGGTAAATTTGCCCTTA  
 AACCAAGGCTTGTAGATACTAATTGGCAGAAAGTAATTTCTTCTGAT  
 AAAGAAACACAAGTTGATTTACTATTGATGCTAGTCAATTTAGTCAAGAA  
 ATTAAAAAGAACAGATGGCAAAATGGTTATTTCTTGAAGGTTTTGTACGTT  
 TTAAGAAGCTAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTA  
 GGATTTAATGGTGAATTTTGGAGCTTACAAGCACTTGAACACCGATTTA  
 TAAGACGCTTTCTAAAGGTAGTTTCTACTATAAACCAATGATACAATC  
 ATAAAGCAATTTGGAGTATAATGAATCAGCTCCTTTTGAAAGCAACAAC  
 TATATGCTGCTTTAAACACAATCAGCGTCTTGGGGCTATGTTGATATGT  
 CaAAAAATGGTGGGAGTTAGAATTAGCACCGGAGAGTcCAAAAAGAATTA  
 TTTTAGGAACCTTTTGAATAAAGGTTGAGGATAAAACAATTCATCTTTTG  
 GAAAGAGATGCAGCGAATAATCCATATTTTGCCTTTCTCCAATAAAGA  
 TGGAAATAGGGATGAAATCACTCCCAAGGCAACTTTCTTAAGAAATGTTA  
 AGGATATTTCTGCTCAAGTTCTAGATCAAAATGGAAATGTTATTGGCAA  
 AGTAAGGTTTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAAGCA  
 AGTGATGGTCAATTATCGTATGGATGCCCTTCAGTGGAGTGGTTTAgATA  
 AGGATGGCAAGTTGTAGCAGATGGTTTTTACTTATCGCTTACGTTAC  
 ACACAGTAGCAGAAGGAGCAAAATAGTCAGGAGTCAGACTTTAAAGTTCA  
 AGTAAGTACTAAGTCACCAATCTTCTTCAAGAGCTCAGTTTGTAGaAA  
 CTAATCGAACATTAAAGCTTAGCCATGCCCTAAGGGAAGTAGTTATGTTCT  
 ATATATCGCTACCAATTAGTTTATCTCATGTTGTAAAGATGAAGAATA  
 TGGAGATGAGACTTCTACTATTATTTCCATATAGATCAAGAAGGTAAAG  
 CGACACTTCTTAAACCGGTTAAGATAGGAGAGAGTGAGGTTGCAGTAGAC  
 CCTAAGGCCCTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTCCGCaC  
 GGTAAATTTGCTGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAA  
 ACGCTATAGTAATTTCTAACAGTTTCAAATATTTTGATAACTTGAAAAAA  
 GAACCTATGTTTATTTCTAAAAAGAAAAAGTAGTAAACAAGAACTTAGA  
 AGAaATAATATTAGTTAAGCCGCaCACTACAGTTACTACTCaaTCAATTGT  
 CTAAGAATAAATACTAAATCAGGAAATGAGAAAGTCTCACTTCTACAAAC  
 AATAATAGTAGTAGAGTAGCTAAATCATATCACCTTAAACATAATGGGGA  
 TTCGTTTAAACATACC

SEQ ID NO. 4411

STRAIN **JM9130013**

GAGGAGCAAGAATTAACCAAGAGCAATCACCTGTAA  
 TTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACCTACTAATCTGTT  
 GAAAAACATCTGTAAAGCTGCTTCTGCTAGTAAATACAGCGAAAGAAAT  
 GGGTGATACATCTGTAATAAATGACAAAACAGAAATGAATATTAGAA  
 AGTTATCTAAAAACCTTGATACGTCTAATTTGGGGGCTGATCTGAAGAA  
 GAATATCCCTCTAAACAGAGACAACCAACAATAAAGAAAGCAATGTAGT  
 AACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCATATGAAG  
 AGGTGAAGCCAGAAAGCAAGTCATCGCTTGTCTTCTTGATACATCTAAA  
 ATAAACAAAATTAAGGCCATAACCAAGAGGAAAGGGAAATGTAGTAGC  
 TATTATTGATACCTGGCTTGTATTTAAACATGATATTTTCGTTTAGATA  
 GCCCAAGAGATGATAAGCACAGCTTAAACTAAGACAGAAATTTGAGGAA  
 TTAAGCAAAACATAATATCACTTATGGGAAATGGGTTAACGATAAGAT  
 TGTTTTTGCACATAACTACGCCAACAAATACAGAAACGGTGGCTGATATTG  
 CAGCAGCTATGAAGATGGTTATGGTTCAAGAGCAAGAAATTTTCGCAAT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

GGTACACACGTTGCTGGTATTTTGTAGGTAATAGTAAACGTCAGCAAT  
 CAATGGTCTCTTTTGAAGGTCAGCGCCAAATGCTCAAGTCTTATTA  
 TGCGTATCCAGATAAAATTGATTCGGACAAATTGGTGAAGCATATGCT  
 AAAGCAATCACAGACGCTGTTAATCTAGGAGCAAAAACGATTAAATGAG  
 TATTGAAAAACAGCTGATTCTTTAATTTGCTCTCAATGATAAAGTTAAAT  
 TAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTTGTGGCTGCC  
 GGAAATGAAGGCGCATTTGGTATGGATTATAGCAAAACATTATCAACTAA  
 TCCTGACTACGGTACGGTTAATAGTCCAGCTATTCTGAAGATACTTTGA  
 GTGTTGCTAGCTATGAATCACTTAAAACTATCAGTGAGGTCGTTGAAACA  
 ACTATTGAAGGTAAGTTAGTTAAGTTGCCGATTGTGACTTCTAAACCTTT  
 TGACAAAGGTAAGGCCCTACGATGTGGTTTATGCCAATTATGGTGCAAAAA  
 AAGACTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAAATGAGCGT  
 GGTGGTGGACTTGATTATGACTAAAATCACTCATGTACAAATGCAGG  
 TGTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTGGAAATTTTC  
 TAATTCCTTACCGTGAATTACCTGTGGGGATTATTAGTAAAGTAGATGGC  
 GAGCGTATAAAAAATACCTTCAAGTCAGTTAACATTTAACCCAGAGTTTGA  
 AGTAGTTGATAGCAAGGTCGTAATCGTATGCTGGAACAAATCAAGTTGGG  
 GCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTGGCTTT  
 GAAATTTATTTCTCAACCTATAATAATCAATACCAAAACATGTCTGGTAC  
 AAGTATGGCTTACCACATGTTGCAGGATTATGACAATGCTTCAAAGTC  
 ATTTGGCTGAGAATATAAAGGGATGAATTTAGATTCTAAAAAATTGCTA  
 GAATTTGCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATATAGTGA  
 AGAGGATAAGGCGCTTTTATTCACCAAGTCAGCAAGGTCAGGTTAGTTG  
 ATGCTGAAAAAGCTATCCAAAGCTCAATATATATTTACTGGAACGATGGC  
 AAAGCTAAAAATTAATCTCAACGAATGGGAGATAAATTTGATATCACAGT  
 TACAATTCATAAATCTGTAGAAGGTGTCAAGAAATGTATTATCAAGCTA  
 ATGTAGCAACAGAACAGTAAATAAAGGTAAATTTGCCCTTAAACCAAA  
 GCCTTGCTAGATACTAATTTGGCAGAAAGTAATTTCTCGTGATAAAGAAC  
 ACAAGTTTCGATTACTATTGATGCTAGTCAATTTAGTCAGAAATTAAGG  
 AACAGATGGCAAAATGGTTATTTCTTGAAGGTTTGTACGTTTAAAGAA  
 GCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTGTAGGATTAA  
 TGGTATTTTGGCACTTACAAGCACTTGAACACCCGATTATAAGACGC  
 TTTCTAAAGGTAGTTTCTACTATAAACCAATGATACAACCTATAAGAC  
 CAATTTGAGTACAATGAATCAGCTCCTTTTGAAGCAACAACTATATGCT  
 CTGTTTAAACAAATCAGCGTCTTGGGGCTATGTTGATTATGTCAAAATG  
 GTGGGAGTTAGAAATAGCACCCGAGAGTCCAAAAAGAAATTTATTTAGGA  
 ACTTTTGAGAATAAGGTTGAGGATAAAACAATTCATCTTTTGGAAGAGA  
 TGCAGGGAATAATCCATATTTGCCATTTCTCAAAATAAGATGGAATA  
 GGCACGAATCACTCCCGAGCACTTTCTTAAAGAAATGTTAAGGATATT  
 TCTGCTCAAGTTCTAGATCAAAATGGAATGTTATTTGGCAAGTAAGGT  
 TTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAAGCAAAGTGATG  
 GTCAATTATCGTATGGATGCTCTTCAAGTGGAGTGGTTTAGATAAGGATGGC  
 AAAGTTGTAGCAGATGGTTTATATCTATCGCTTACGTTACACACCACT  
 AGCAGAAGGAGCAAAATAGTCAGGAGTCAGACTTAAAGTACAAGTAAGTA  
 CTAAGTCACCAAAATCTTCTTACGAGCTCAGTTTGATGAACTAATCGA  
 ACATTAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTACATATCG  
 TTTACAATTAGTTTATCTCATGTTGTAAAGATGAAGAAATATGGGGATG  
 AGACTTCTTACCATTATTTCCATATAGATCAAGAAGGTAAGTGACACTT  
 CCTAAAAACGGTTAAGATAGGAGAGAGTGAGGTTGCGGTAGACCCCTAAGGC  
 CTGTGACACTTGTGTGAAGATAAAGCTGGTAATTTGCGCAACGGTAAAT  
 TGTCTGATCTCTGAATAAGGCAGTAGTATCAGAGAAAGAAACGCTATA  
 GTAATTTCTAACAGTTTCAAAATATTTTGATAACTTGAAGAAAGAACCTAT  
 GTTTATTTCTAAAAAGAAAAAGTAGTAAACAAGAATCTAGAAGAAATAA  
 TATTAGTTAAGCCGCAAACTACAGTTACTACTCAATCATTGTCTAAAGAA  
 ATAACATAATCAGGAAATGAGAAAGTCTCACTTCTACAAACAATAATAG  
 TAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGATTTCTGTTA  
 ACCATACC

PRETTY of: /biotmp/msa183564.2{\*} May 13, 2003 03:28 ...

	1	50
msa183564.2{147_COH1}	-----	-----
msa183564.2{147_M732}	-----	-----
msa183564.2{147_M781}	-----	-----
msa183564.2{147_2603}	gtggataaac atcactcaaa aaaggctatt ttaaagttaa cacttataac	
msa183564.2{147_JM9130013}	-----	-----
msa183564.2{147_18RS21}	-----	-----
msa183564.2{147_090}	-----	-----
msa183564.2{147_CJB110}	-----	-----
msa183564.2{147_A909}	-----	-----
msa183564.2{147_H36B}	-----	-----
msa183564.2{147_1169NT}	-----	-----
Consensus	*****	*****
	51	100
msa183564.2{147_COH1}	-----	GAGGAGCAAG
msa183564.2{147_M732}	-----	GAGGAGCAAG
msa183564.2{147_M781}	-----	GAGGAGCAAG
msa183564.2{147_2603}	aactagtatt ttattaatgc atagcaatca agtgaatgca	GAGGAGCAAG
msa183564.2{147_JM9130013}	-----	GAGGAGCAAG
msa183564.2{147_18RS21}	-----	GAGGAGCAAG
msa183564.2{147_090}	-----	GAGGAGCAAG
msa183564.2{147_CJB110}	-----	GAGGAGCAAG

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_A909}	-----	-----	-----	-----	GAGGAGCAAG
msa183564.2{147_H36B}	-----	-----	-----	-----	GAGGAGCAAG
msa183564.2{147_1169NT}	-----	-----	-----	-----	GAGGAGCAAG
Consensus	*****	*****	*****	*****	*****
101					
msa183564.2{147_COH1}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_M732}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_M781}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_2603}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_JM9130013}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_18RS21}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_090}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_CJB110}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_A909}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_H36B}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_1169NT}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
Consensus	*****	*****	*****	*****	*****
151					
msa183564.2{147_COH1}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_M732}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_M781}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_2603}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_JM9130013}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_18RS21}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_090}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_CJB110}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_A909}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_H36B}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_1169NT}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAAACAT	CTGTAAcAgC
Consensus	*****	*****	*****	*****	*****
201					
msa183564.2{147_COH1}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_M732}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_M781}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_2603}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_JM9130013}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_18RS21}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_090}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_CJB110}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_A909}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_H36B}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_1169NT}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
Consensus	*****	*****	*****	*****	*****
251					
msa183564.2{147_COH1}	ATGACAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_M732}	ATGACAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_M781}	ATGACAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_2603}	ATGACAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_JM9130013}	ATGACAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_18RS21}	ATGACAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_090}	ATGACAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_CJB110}	ATGACAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_A909}	ATGACAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_H36B}	ATGACAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_1169NT}	ATGACAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
Consensus	*****	*****	*****	*****	*****
301					
msa183564.2{147_COH1}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_M732}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_M781}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_2603}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_JM9130013}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_18RS21}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_090}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_CJB110}	ACGTCTAATw	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_A909}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_H36B}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_1169NT}	ACGTCTAATA	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
Consensus	*****	*****	*****	*****	*****
351					
msa183564.2{147_COH1}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAG
msa183564.2{147_M732}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAG
msa183564.2{147_M781}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAG
msa183564.2{147_2603}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAG
msa183564.2{147_JM9130013}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAG
msa183564.2{147_18RS21}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAG
msa183564.2{147_090}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAG

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_CJB110}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAA	
msa183564.2{147_A909}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAA	
msa183564.2{147_H36B}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAA	
msa183564.2{147_1169NT}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAA	
Consensus	*****	*****	*****	*****	*****	
msa183564.2{147_COH1}	401	TAGCACAGAA	AGTTCCTCTCA	GCaTATGAAG	AGGTGAAGtC	AgAAAGCAAG
msa183564.2{147_M732}	TAGCACAGAA	AGTTCCTCTCA	GCaTATGAAG	AGGTGAAGtC	AgAAAGCAAG	
msa183564.2{147_M781}	TAGCACAGAA	AGTTCCTCTCA	GCaTATGAAG	AGGTGAAGtC	AgAAAGCAAG	
msa183564.2{147_2603}	TAGCACAGAA	AGTTCCTCTCA	GCaTATGAAG	AGGTGAAGcC	AgAAAGCAAG	
msa183564.2{147_JM9130013}	TAGCACAGAA	AGTTCCTCTCA	GCaTATGAAG	AGGTGAAGcC	AgAAAGCAAG	
msa183564.2{147_18RS21}	TAGCACAGAA	AGTTCCTCTCA	GCaTATGAAG	AGGTGAAGcC	AgAAAGCAAG	
msa183564.2{147_090}	TAGCACAGAA	AGTTCCTCTCA	GCGtATGAAG	AGGTGAAGcC	AgAAAGCAAG	
msa183564.2{147_CJB110}	TAGCACAGAA	AGTTCCTCTCA	GCaTATGAAG	AGGTGAAGcC	AgAAAGCAAG	
msa183564.2{147_A909}	TAGCACAGAA	AGTTCCTCTCA	GCaTATGAAG	AGGTGAAGcC	AgAAAGCAAG	
msa183564.2{147_H36B}	TAGCACAGAA	AGTTCCTCTCA	GCaTATGAAG	AGGTGAAGcC	AgAAAGCAAG	
msa183564.2{147_1169NT}	TAGCACAGAA	AGTTCCTCTCA	GCaTATGAAG	AGGTGAAGcC	AaAAAGCAAG	
Consensus	*****	*****	**-----	*****	*-----*	
msa183564.2{147_COH1}	451	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc
msa183564.2{147_M732}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc	
msa183564.2{147_M781}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc	
msa183564.2{147_2603}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc	
msa183564.2{147_JM9130013}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc	
msa183564.2{147_18RS21}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc	
msa183564.2{147_090}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TgCAAGCCAc	
msa183564.2{147_CJB110}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TgCAAGCCAc	
msa183564.2{147_A909}	TCATCaCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TgCAAGCCAc	
msa183564.2{147_H36B}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TgCAAGCCAc	
msa183564.2{147_1169NT}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TgCAAGCCAc	
Consensus	*****	*****	*****	*****	*****	*-----*
msa183564.2{147_COH1}	501	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG
msa183564.2{147_M732}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG	
msa183564.2{147_M781}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG	
msa183564.2{147_2603}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG	
msa183564.2{147_JM9130013}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG	
msa183564.2{147_18RS21}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG	
msa183564.2{147_090}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG	
msa183564.2{147_CJB110}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG	
msa183564.2{147_A909}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG	
msa183564.2{147_H36B}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG	
msa183564.2{147_1169NT}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG	
Consensus	*****	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	551	ATATTAAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC
msa183564.2{147_M732}	ATATTAAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC	
msa183564.2{147_M781}	ATATTAAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC	
msa183564.2{147_2603}	ATATTAAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC	
msa183564.2{147_JM9130013}	ATATTAAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC	
msa183564.2{147_18RS21}	ATATTAAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC	
msa183564.2{147_090}	ATATTAAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC	
msa183564.2{147_CJB110}	ATATTAAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC	
msa183564.2{147_A909}	ATATTAAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC	
msa183564.2{147_H36B}	ATATTAAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC	
msa183564.2{147_1169NT}	ATATTAAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC	
Consensus	*****	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	601	AGCTTTAAAA	cTAAGgCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_M732}	AGCTTTAAAA	cTAAGgCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT	
msa183564.2{147_M781}	AGCTTTAAAA	cTAAGgCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT	
msa183564.2{147_2603}	AGCTTTAAAA	cTAAGaCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT	
msa183564.2{147_JM9130013}	AGCTTTAAAA	cTAAGaCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT	
msa183564.2{147_18RS21}	AGCTTTAAAA	cTAAGaCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT	
msa183564.2{147_090}	AGCTTTAAAA	cTAAGgCAGA	ATTcGAGGAA	TTAAAAGCAA	AACATAATAT	
msa183564.2{147_CJB110}	AGCTTTAAAA	cTAAGgCAGA	ATTcGAGGAA	TTAAAAGCAA	AACATAATAT	
msa183564.2{147_A909}	AGCTTTAAAA	cTAAGgCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT	
msa183564.2{147_H36B}	AGCTTTAAAA	cTAAGgCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT	
msa183564.2{147_1169NT}	AGCTTTAAAA	aTAAGgCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT	
Consensus	*****	-***-****	***-*****	*****	*****	*****
msa183564.2{147_COH1}	651	CACCTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_M732}	CACCTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG	
msa183564.2{147_M781}	CACCTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG	
msa183564.2{147_2603}	CACCTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG	
msa183564.2{147_JM9130013}	CACCTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG	
msa183564.2{147_18RS21}	CACCTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG	

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_090}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_CJB110}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_A909}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_H36B}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_1169NT}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_M732}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_M781}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_2603}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_JM9130013}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_18RS21}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_090}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_CJB110}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_A909}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_H36B}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_1169NT}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	TATGGGTCAG	AAGCAAAGAA	TATTTtGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_M732}	TATGGGTCAG	AAGCAAAGAA	TATTTtGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_M781}	TATGGGTCAG	AAGCAAAGAA	TATTTtGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_2603}	TATGGGTCAG	AAGCAAAGAA	TATTTtGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_JM9130013}	TATGGGTCAG	AAGCAAAGAA	TATTTtGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_18RS21}	TATGGGTCAG	AAGCAAAGAA	TATTTtGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_090}	TATGGGTCAG	AAGCAAAGAA	TATTTtGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_CJB110}	TATGGGTCAG	AAGCAAAGAA	TATTTtGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_A909}	TATGGGTCAG	AAGCAAAGAA	TATTTtGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_H36B}	TATGGGTCAG	AAGCAAAGAA	TATTTtGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_1169NT}	TATGGGTCAG	AAGCAAAGAA	TATTTtGCAT	GGTACACACG	TTGCTGGTAT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCCT	CTTTTAGAAG
msa183564.2{147_M732}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCCT	CTTTTAGAAG
msa183564.2{147_M781}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCCT	CTTTTAGAAG
msa183564.2{147_2603}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCCT	CTTTTAGAAG
msa183564.2{147_JM9130013}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCCT	CTTTTAGAAG
msa183564.2{147_18RS21}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCCT	CTTTTAGAAG
msa183564.2{147_090}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCCT	CTTTTAGAAG
msa183564.2{147_CJB110}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCCT	CTTTTAGAAG
msa183564.2{147_A909}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCCT	CTTTTAGAAG
msa183564.2{147_H36B}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCCT	CTTTTAGAAG
msa183564.2{147_1169NT}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCCT	CTTTTAGAAG
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_M732}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_M781}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_2603}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_JM9130013}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_18RS21}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_090}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_CJB110}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_A909}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_H36B}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_1169NT}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	GATTTCGGACA	AATTTGGaGA	AGCATATGCT	AAAGCAATCA	tAGACGCTGT
msa183564.2{147_M732}	GATTTCGGACA	AATTTGGaGA	AGCATATGCT	AAAGCAATCA	tAGACGCTGT
msa183564.2{147_M781}	GATTTCGGACA	AATTTGGaGA	AGCATATGCT	AAAGCAATCA	tAGACGCTGT
msa183564.2{147_2603}	GATTTCGGACA	AATTTGGtGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_JM9130013}	GATTTCGGACA	AATTTGGtGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_18RS21}	GATTTCGGACA	AATTTGGtGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_090}	GATTTCGGACA	AATTTGGaGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_CJB110}	GATTTCGGACA	AATTTGGaGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_A909}	GATTTCGGACA	AATTTGGtGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_H36B}	GATTTCGGACA	AATTTGGtGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_1169NT}	GATTTCGGACA	AATTTGGaGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	TAATCTAGGA	GCaAAAACGA	TTAATATGAG	ccTgGGAAAA	ACgGcTGATT
msa183564.2{147_M732}	TAATCTAGGA	GCaAAAACGA	TTAATATGAG	ccTgGGAAAA	ACgGcTGATT
msa183564.2{147_M781}	TAATCTAGGA	GCaAAAACGA	TTAATATGAG	ccTgGGAAAA	ACgGcTGATT
msa183564.2{147_2603}	TAATCTAGGA	GCaAAAACGA	TTAATATGAG	taTtGGAAAA	ACaGcTGATT
msa183564.2{147_JM9130013}	TAATCTAGGA	GCaAAAACGA	TTAATATGAG	taTtGGAAAA	ACaGcTGATT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_18RS21}	TAATCTAGGA	GCaAAAACGA	TAAATATGAG	taTtGGAAAA	ACaGcTGATT
msa183564.2{147_090}	TAATCTAGGA	GCaAAAACGA	TAAATATGAG	ccTtGGAAAA	ACaGcAGATT
msa183564.2{147_CJB110}	TAATCTAGGA	GCaAAAACGA	TAAATATGAG	ccTtGGAAAA	ACaGcAGATT
msa183564.2{147_A909}	TAATCTAGGA	GCaAAAACGA	TAAATATGAG	ccTtGGAAAA	ACaGcAGATT
msa183564.2{147_H36B}	TAATCTAGGA	GCaAAAACGA	TAAATATGAG	ccTtGGAAAA	ACaGcAGATT
msa183564.2{147_1169NT}	TAATCTAGGA	GCTAAAACGA	TAAATATGAG	taTtGGAAAA	ACaGcTGATT
Consensus	*****	**-----*	*****	-_*-----*	**--*-----*
1001					
msa183564.2{147_COH1}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_M732}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_M781}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_2603}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_JM9130013}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_18RS21}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_090}	CTTTAATTGC	aCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_CJB110}	CTTTAATTGC	aCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_A909}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_H36B}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_1169NT}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
Consensus	*****	-----*	*****	*****	*****
1051					
msa183564.2{147_COH1}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTTGG
msa183564.2{147_M732}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTTGG
msa183564.2{147_M781}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTTGG
msa183564.2{147_2603}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GcGCATTTGG
msa183564.2{147_JM9130013}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GcGCATTTGG
msa183564.2{147_18RS21}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GcGCATTTGG
msa183564.2{147_090}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTTGG
msa183564.2{147_CJB110}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTTGG
msa183564.2{147_A909}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTTGG
msa183564.2{147_H36B}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTTGG
msa183564.2{147_1169NT}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GcGCATTTGG
Consensus	*****	*****	*****	*****	*-----*
1101					
msa183564.2{147_COH1}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_M732}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_M781}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_2603}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_JM9130013}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_18RS21}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_090}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_CJB110}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_A909}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_H36B}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_1169NT}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
Consensus	*****	*****	*****	*****	*****
1151					
msa183564.2{147_COH1}	ATAGTCCAGC	TATTTCTGAA	GATACITTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_M732}	ATAGTCCAGC	TATTTCTGAA	GATACITTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_M781}	ATAGTCCAGC	TATTTCTGAA	GATACITTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_2603}	ATAGTCCAGC	TATTTCTGAA	GATACITTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_JM9130013}	ATAGTCCAGC	TATTTCTGAA	GATACITTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_18RS21}	ATAGTCCAGC	TATTTCTGAA	GATACITTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_090}	ATAGTCCAGC	TATTTCTGAA	GATACITTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_CJB110}	ATAGTCCAGC	TATTTCTGAA	GATACITTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_A909}	ATAGTCCAGC	TATTTCTGAA	GATACITTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_H36B}	ATAGTCCAGC	TATTTCTGAA	GATACITTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_1169NT}	ATAGTCCAGC	TATTTCTGAA	GATACITTGA	GTGTTGCTAG	CTATGAATCA
Consensus	*****	*****	*****	*****	*****
1201					
msa183564.2{147_COH1}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_M732}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_M781}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_2603}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_JM9130013}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_18RS21}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_090}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_CJB110}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_A909}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_H36B}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_1169NT}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
Consensus	*****	*****	*****	*****	*****
1251					
msa183564.2{147_COH1}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_M732}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_M781}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_2603}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_JM9130013}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_18RS21}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_090}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_CJB110}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_A909}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_H36B}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_1169NT}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGACTTTG	AAGGTAAGGA
msa183564.2{147_M732}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGACTTTG	AAGGTAAGGA
msa183564.2{147_M781}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGACTTTG	AAGGTAAGGA
msa183564.2{147_2603}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGACTTTG	AAGGTAAGGA
msa183564.2{147_JM9130013}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGACTTTG	AAGGTAAGGA
msa183564.2{147_18RS21}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGACTTTG	AAGGTAAGGA
msa183564.2{147_090}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGACTTTG	AAGGTAAGGA
msa183564.2{147_CJB110}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGACTTTG	AAGGTAAGGA
msa183564.2{147_A909}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGACTTTG	AAGGTAAGGA
msa183564.2{147_H36B}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGACTTTG	AAGGTAAGGA
msa183564.2{147_1169NT}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGACTTTG	AAGGTAAGGA
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_M732}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_M781}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_2603}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_JM9130013}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_18RS21}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_090}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_CJB110}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_A909}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_H36B}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_1169NT}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_M732}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_M781}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_2603}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_JM9130013}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_18RS21}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_090}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_CJB110}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_A909}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_H36B}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_1169NT}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_M732}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_M781}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_2603}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_JM9130013}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_18RS21}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_090}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_CJB110}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_A909}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_H36B}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_1169NT}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	ACCTGTGGGG	GTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_M732}	ACCTGTGGGG	GTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_M781}	ACCTGTGGGG	GTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_2603}	ACCTGTGGGG	GTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_JM9130013}	ACCTGTGGGG	GTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_18RS21}	ACCTGTGGGG	GTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_090}	ACCTGTGGGG	GTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_CJB110}	ACCTGTGGGG	GTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_A909}	ACCTGTGGGG	GTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_H36B}	ACCTGTGGGG	GTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_1169NT}	ACCTGTGGGG	GTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	CAAGTCAGTT	AACATTAAAC	CAGAGTTTGG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_M732}	CAAGTCAGTT	AACATTAAAC	CAGAGTTTGG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_M781}	CAAGTCAGTT	AACATTAAAC	CAGAGTTTGG	AAGTAGTTGA	TAGCCAAGGT



Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_2603}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_JM9130013}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_18RS21}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_090}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_CJB110}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_A909}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_H36B}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_1169NT}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTG	AAGTAGTTGA	TAGCCAAGGT
Consensus	*****	*****	*****	*****	*****
1601	1650				
msa183564.2{147_COH1}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_M732}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_M781}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_2603}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_JM9130013}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_18RS21}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_090}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_CJB110}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_A909}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_H36B}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_1169NT}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
Consensus	*****	*****	*****	*****	*****
1651	1700				
msa183564.2{147_COH1}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_M732}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_M781}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_2603}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_JM9130013}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_18RS21}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_090}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_CJB110}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_A909}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_H36B}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_1169NT}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
Consensus	*****	*****	*****	*****	*****
1701	1750				
msa183564.2{147_COH1}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_M732}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_M781}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_2603}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_JM9130013}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_18RS21}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_090}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_CJB110}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_A909}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_H36B}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_1169NT}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
Consensus	*****	*****	*****	*****	*****
1751	1800				
msa183564.2{147_COH1}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_M732}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_M781}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_2603}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_JM9130013}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_18RS21}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_090}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_CJB110}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_A909}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_H36B}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_1169NT}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
Consensus	*****	*****	*****	*****	*****
1801	1850				
msa183564.2{147_COH1}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_M732}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_M781}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_2603}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_JM9130013}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_18RS21}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_090}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_CJB110}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_A909}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_H36B}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_1169NT}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
Consensus	*****	*****	*****	*****	*****
1851	1900				
msa183564.2{147_COH1}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTAT
msa183564.2{147_M732}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTAT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_M781}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_2603}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_JM9130013}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_18RS21}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_090}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_CJB110}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_A909}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_H36B}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_1169NT}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
Consensus	*****	*****	*****	*****	*****
1901					
msa183564.2{147_COH1}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_M732}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_M781}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_2603}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_JM9130013}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_18RS21}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_090}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_CJB110}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_A909}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_H36B}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_1169NT}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
Consensus	*****	*****	*****	*****	*****
1951					
msa183564.2{147_COH1}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_M732}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_M781}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_2603}	AGCTCAATAT	TATaTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_JM9130013}	AGCTCAATAT	TATaTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_18RS21}	AGCTCAATAT	TATaTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_090}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_CJB110}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_A909}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_H36B}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_1169NT}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
Consensus	*****	***-*****	*****	*****-*****	*****
2001					
msa183564.2{147_COH1}	AACGAgagGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_M732}	AACGAgagGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_M781}	AACGAgagGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_2603}	AACGAatGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_JM9130013}	AACGAatGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_18RS21}	AACGAatGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_090}	AACGAggGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_CJB110}	AACGAggGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_A909}	AACGAggGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_H36B}	AACGAggGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_1169NT}	AACGAggGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
Consensus	*****-****	*****	*****	*****	*****
2051					
msa183564.2{147_COH1}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_M732}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_M781}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_2603}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_JM9130013}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_18RS21}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_090}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_CJB110}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_A909}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_H36B}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_1169NT}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
Consensus	*****	*****	*****	*****	*****
2101					
msa183564.2{147_COH1}	AAATAAAGGT	AAATTTGCCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_M732}	AAATAAAGGT	AAATTTGCCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_M781}	AAATAAAGGT	AAATTTGCCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_2603}	AAATAAAGGT	AAATTTGCCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_JM9130013}	AAATAAAGGT	AAATTTGCCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_18RS21}	AAATAAAGGT	AAATTTGCCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_090}	AAATAAAGGT	AAATTTGCCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_CJB110}	AAATAAAGGT	AAATTTGCCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_A909}	AAATAAAGGT	AAATTTGCCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_H36B}	AAATAAAGGT	AAATTTGCCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_1169NT}	AAATAAAGGT	AAATTTGCCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
Consensus	*****	*****	*****	*****	*****
2151					
msa183564.2{147_COH1}	GGCAGAAAGT	AATTCCTTCGT	GATAAAGAAA	CACAAGTTCG	ATTACTATT
2200					

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_M732}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTTCG ATTTACTATT	
msa183564.2{147_M781}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTTCG ATTTACTATT	
msa183564.2{147_2603}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTTCG ATTTACTATT	
msa183564.2{147_JM9130013}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTTCG ATTTACTATT	
msa183564.2{147_18RS21}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTTCG ATTTACTATT	
msa183564.2{147_090}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTTCG ATTTACTATT	
msa183564.2{147_CJB110}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTTCG ATTTACTATT	
msa183564.2{147_A909}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTTCG ATTTACTATT	
msa183564.2{147_H36B}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTTCG ATTTACTATT	
msa183564.2{147_1169NT}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTTCG ATTTACTATT	
Consensus	*****	*****
msa183564.2{147_COH1}	2201 GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	2250
msa183564.2{147_M732}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_M781}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_2603}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_JM9130013}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_18RS21}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_090}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_CJB110}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_A909}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_H36B}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_1169NT}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
Consensus	*****	*****
msa183564.2{147_COH1}	2251 TTTCTTAGAA GGTITTTGTAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	2300
msa183564.2{147_M732}	TTTCTTAGAA GGTITTTGTAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
msa183564.2{147_M781}	TTTCTTAGAA GGTITTTGTAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
msa183564.2{147_2603}	TTTCTTAGAA GGTITTTGTAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
msa183564.2{147_JM9130013}	TTTCTTAGAA GGTITTTGTAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
msa183564.2{147_18RS21}	TTTCTTAGAA GGTITTTGTAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
msa183564.2{147_090}	TTTCTTAGAA GGTITTTGTAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
msa183564.2{147_CJB110}	TTTCTTAGAA GGTITTTGTAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
msa183564.2{147_A909}	TTTCTTAGAA GGTITTTGTAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
msa183564.2{147_H36B}	TTTCTTAGAA GGTITTTGTAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
msa183564.2{147_1169NT}	TTTCTTAGAA GGTITTTGTAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
Consensus	*****	*****
msa183564.2{147_COH1}	2301 AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	2350
msa183564.2{147_M732}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_M781}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_2603}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_JM9130013}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_18RS21}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_090}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_CJB110}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_A909}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_H36B}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_1169NT}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
Consensus	*****	*****
msa183564.2{147_COH1}	2351 CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	2400
msa183564.2{147_M732}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_M781}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_2603}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_JM9130013}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_18RS21}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_090}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_CJB110}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_A909}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_H36B}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_1169NT}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
Consensus	*****	*****
msa183564.2{147_COH1}	2401 CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	2450
msa183564.2{147_M732}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_M781}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_2603}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_JM9130013}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_18RS21}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_090}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_CJB110}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_A909}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_H36B}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_1169NT}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
Consensus	*****	*****

2451

2500

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_COH1}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_M732}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_M781}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_2603}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_JM9130013}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_18RS21}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_090}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_CJB110}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_A909}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_H36B}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_1169NT}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
Consensus	*****	*****	*****	*****	*****
2501					
msa183564.2{147_COH1}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_M732}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_M781}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_2603}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_JM9130013}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_18RS21}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_090}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_CJB110}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_A909}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_H36B}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_1169NT}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
Consensus	*****	*****	*****	*****	*****
2551					
msa183564.2{147_COH1}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_M732}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_M781}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_2603}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_JM9130013}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_18RS21}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_090}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_CJB110}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_A909}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_H36B}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_1169NT}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
Consensus	*****	*****	*****	*****	*****
2601					
msa183564.2{147_COH1}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_M732}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_M781}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_2603}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_JM9130013}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_18RS21}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_090}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_CJB110}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_A909}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_H36B}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_1169NT}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
Consensus	*****	*****	*****	*****	*****
2651					
msa183564.2{147_COH1}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_M732}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_M781}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_2603}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_JM9130013}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_18RS21}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_090}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_CJB110}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_A909}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_H36B}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_1169NT}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
Consensus	*****	*****	*****	*****	*****
2701					
msa183564.2{147_COH1}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_M732}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_M781}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_2603}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_JM9130013}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_18RS21}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_090}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_CJB110}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_A909}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_H36B}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_1169NT}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
Consensus	*****	*****	*****	*****	*****
2750					

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

		2751			2800
msa183564.2{147_COH1}	AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
msa183564.2{147_M732}	AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
msa183564.2{147_M781}	AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
msa183564.2{147_2603}	AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
msa183564.2{147_JM9130013}	AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
msa183564.2{147_18RS21}	AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
msa183564.2{147_090}	AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
msa183564.2{147_CJB110}	AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
msa183564.2{147_A909}	AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
msa183564.2{147_H36B}	AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
msa183564.2{147_1169NT}	AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
Consensus	*****	*****	*****	*****	*****
		2801			2850
msa183564.2{147_COH1}	AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
msa183564.2{147_M732}	AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
msa183564.2{147_M781}	AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
msa183564.2{147_2603}	AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
msa183564.2{147_JM9130013}	AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
msa183564.2{147_18RS21}	AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
msa183564.2{147_090}	AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
msa183564.2{147_CJB110}	AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
msa183564.2{147_A909}	AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
msa183564.2{147_H36B}	AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
msa183564.2{147_1169NT}	AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
Consensus	*****	*****	***-*****	*****	*****
		2851			2900
msa183564.2{147_COH1}	tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_M732}	tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_M781}	tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_2603}	tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_JM9130013}	tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_18RS21}	tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_090}	tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_CJB110}	tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_A909}	tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_H36B}	tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_1169NT}	tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
Consensus	--*****	*****	*****	*****	*****
		2901			2950
msa183564.2{147_COH1}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_M732}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_M781}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_2603}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_JM9130013}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_18RS21}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_090}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_CJB110}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_A909}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_H36B}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_1169NT}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
Consensus	*****	***-*****	*****	*****	*****
		2951			3000
msa183564.2{147_COH1}	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAAATCTTCC
msa183564.2{147_M732}	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAAATCTTCC
msa183564.2{147_M781}	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAAATCTTCC
msa183564.2{147_2603}	CAGGAGTCAG	ACTTTAAAGT	aCAAGTAAGT	ACTAAGTCAC	CAAAATCTTCC
msa183564.2{147_JM9130013}	CAGGAGTCAG	ACTTTAAAGT	aCAAGTAAGT	ACTAAGTCAC	CAAAATCTTCC
msa183564.2{147_18RS21}	CAGGAGTCAG	ACTTTAAAGT	aCAAGTAAGT	ACTAAGTCAC	CAAAATCTTCC
msa183564.2{147_090}	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAAATCTTCC
msa183564.2{147_CJB110}	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAAATCTTCC
msa183564.2{147_A909}	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAAATCTTCC
msa183564.2{147_H36B}	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAAATCTTCC
msa183564.2{147_1169NT}	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAAATCTTCC
Consensus	*****	*****	-*****	*****	*****
		3001			3050
msa183564.2{147_COH1}	TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAAGC	TTAGCCATGC
msa183564.2{147_M732}	TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAAGC	TTAGCCATGC
msa183564.2{147_M781}	TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAAGC	TTAGCCATGC
msa183564.2{147_2603}	TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAAGC	TTAGCCATGC
msa183564.2{147_JM9130013}	TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAAGC	TTAGCCATGC
msa183564.2{147_18RS21}	TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAAGC	TTAGCCATGC
msa183564.2{147_090}	TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAAGC	TTAGCCATGC
msa183564.2{147_CJB110}	TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAAGC	TTAGCCATGC
msa183564.2{147_A909}	TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAAGC	TTAGCCATGC
msa183564.2{147_H36B}	TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAAGC	TTAGCCATGC
msa183564.2{147_1169NT}	TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAAGC	TTAGCCATGC
Consensus	**--*****	*****	*****	*****	*****

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

	3051		3100
msa183564.2{147_COH1}	CTAAGGaAAG TAGTTATGTT CCTAcATATC GTtTACAATT AGTtTTATCT		
msa183564.2{147_M732}	CTAAGGaAAG TAGTTATGTT CCTAcATATC GTtTACAATT AGTtTTATCT		
msa183564.2{147_M781}	CTAAGGaAAG TAGTTATGTT CCTAcATATC GTtTACAATT AGTtTTATCT		
msa183564.2{147_2603}	CTAAGGaAAG TAGTTATGTT CCTAcATATC GTtTACAATT AGTtTTATCT		
msa183564.2{147_JM9130013}	CTAAGGaAAG TAGTTATGTT CCTAcATATC GTtTACAATT AGTtTTATCT		
msa183564.2{147_18RS21}	CTAAGGaAAG TAGTTATGTT CCTAcATATC GTtTACAATT AGTtTTATCT		
msa183564.2{147_090}	CTAAGGaAAG TAGTTATGTT CCTAcATATC GTtTACAATT AGTtTTATCT		
msa183564.2{147_CJB110}	CTAAGGaAAG TAGTTATGTT CCTAcATATC GTtTACAATT AGTtTTATCT		
msa183564.2{147_A909}	CTAAGGaAAG TAGTTATGTT CCTAcATATC GTcTACAATT AGTtTTATCT		
msa183564.2{147_H36B}	CTAAGGaAAG TAGTTATGTT CCTAcATATC GTcTACAATT AGTtTTATCT		
msa183564.2{147_1169NT}	CTAAGGaAAG TAGTTATGTT CCTAcATATC GTcTACAATT AGTtTTATCT		
Consensus	*****	*****	*****
	3101		3150
msa183564.2{147_COH1}	CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT AccATTATTT		
msa183564.2{147_M732}	CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT AccATTATTT		
msa183564.2{147_M781}	CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT AccATTATTT		
msa183564.2{147_2603}	CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT AccATTATTT		
msa183564.2{147_JM9130013}	CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT AccATTATTT		
msa183564.2{147_18RS21}	CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT AccATTATTT		
msa183564.2{147_090}	CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT AccATTATTT		
msa183564.2{147_CJB110}	CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT AccATTATTT		
msa183564.2{147_A909}	CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT AccATTATTT		
msa183564.2{147_H36B}	CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT AccATTATTT		
msa183564.2{147_1169NT}	CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT AccATTATTT		
Consensus	*****	*****	*****
	3151		3200
msa183564.2{147_COH1}	CCATATAGAT CaAGAAGGTA AAGtGACACT TCCTAAAACg GTTAAGATAG		
msa183564.2{147_M732}	CCATATAGAT CaAGAAGGTA AAGtGACACT TCCTAAAACg GTTAAGATAG		
msa183564.2{147_M781}	CCATATAGAT CaAGAAGGTA AAGtGACACT TCCTAAAACg GTTAAGATAG		
msa183564.2{147_2603}	CCATATAGAT CaAGAAGGTA AAGtGACACT TCCTAAAACg GTTAAGATAG		
msa183564.2{147_JM9130013}	CCATATAGAT CaAGAAGGTA AAGtGACACT TCCTAAAACg GTTAAGATAG		
msa183564.2{147_18RS21}	CCATATAGAT CaAGAAGGTA AAGtGACACT TCCTAAAACg GTTAAGATAG		
msa183564.2{147_090}	CCATATAGAT CaAGAAGGTA AAGtGACACT TCCTAAAACg GTTAAGATAG		
msa183564.2{147_CJB110}	CCATATAGAT CaAGAAGGTA AAGtGACACT TCCTAAAACg GTTAAGATAG		
msa183564.2{147_A909}	CCATATAGAT CgAGAAGGTA AAGtGACACT TCCTAAAACa GTTAAGATAG		
msa183564.2{147_H36B}	CCATATAGAT CaAGAAGGTA AAGtGACACT TCCTAAAACa GTTAAGATAG		
msa183564.2{147_1169NT}	CCATATAGAT CaAGAAGGTA AAGcGACACT TCCTAAAACg GTTAAGATAG		
Consensus	*****	*****	*****
	3201		3250
msa183564.2{147_COH1}	GAGAGAGTGA GGTTCGcGTA GACCCTAAGg CCTTGACACT TGTGTGGAA		
msa183564.2{147_M732}	GAGAGAGTGA GGTTCGcGTA GACCCTAAGg CCTTGACACT TGTGTGGAA		
msa183564.2{147_M781}	GAGAGAGTGA GGTTCGcGTA GACCCTAAGg CCTTGACACT TGTGTGGAA		
msa183564.2{147_2603}	GAGAGAGTGA GGTTCGcGTA GACCCTAAGg CCTTGACACT TGTGTGGAA		
msa183564.2{147_JM9130013}	GAGAGAGTGA GGTTCGcGTA GACCCTAAGg CCTTGACACT TGTGTGGAA		
msa183564.2{147_18RS21}	GAGAGAGTGA GGTTCGcGTA GACCCTAAGg CCTTGACACT TGTGTGGAA		
msa183564.2{147_090}	GAGAGAGTGA GGTTCGcGTA GACCCTAAGg CCTTGACACT TGTGTGGAA		
msa183564.2{147_CJB110}	GAGAGAGTGA GGTTCGcGTA GACCCTAAGg CCTTGACACT TGTGTGGAA		
msa183564.2{147_A909}	GAGAGAGTGA GGTTCGcGTA GACCCTAAGa CCTTGACACT TGTGTGGAA		
msa183564.2{147_H36B}	GAGAGAGTGA GGTTCGcGTA GACCCTAAGa CCTTGACACT TGTGTGGAA		
msa183564.2{147_1169NT}	GAGAGAGTGA GGTTCGcGTA GACCCTAAGg CCTTGACACT TGTGTGGAA		
Consensus	*****	*****	*****
	3251		3300
msa183564.2{147_COH1}	GATAAAGCTG GTAATTTtGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA		
msa183564.2{147_M732}	GATAAAGCTG GTAATTTtGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA		
msa183564.2{147_M781}	GATAAAGCTG GTAATTTtGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA		
msa183564.2{147_2603}	GATAAAGCTG GTAATTTtGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA		
msa183564.2{147_JM9130013}	GATAAAGCTG GTAATTTtGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA		
msa183564.2{147_18RS21}	GATAAAGCTG GTAATTTtGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA		
msa183564.2{147_090}	GATAAAGCTG GTAATTTtGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA		
msa183564.2{147_CJB110}	GATAAAGCTG GTAATTTtGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA		
msa183564.2{147_A909}	GATAAAGCTG GTAATTTtGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA		
msa183564.2{147_H36B}	GATAAAGCTG GTAATTTtGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA		
msa183564.2{147_1169NT}	GATAAAGCTG GTAATTTtGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA		
Consensus	*****	*****	*****
	3301		3350
msa183564.2{147_COH1}	GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTtCT AACAgTTTCA		
msa183564.2{147_M732}	GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTtCT AACAgTTTCA		
msa183564.2{147_M781}	GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTtCT AACAgTTTCA		
msa183564.2{147_2603}	GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTtCT AACAgTTTCA		
msa183564.2{147_JM9130013}	GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTtCT AACAgTTTCA		
msa183564.2{147_18RS21}	GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTtCT AACAgTTTCA		
msa183564.2{147_090}	GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTtCT AACAgTTTCA		
msa183564.2{147_CJB110}	GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTtCT AACAgTTTCA		
msa183564.2{147_A909}	GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTtCT AACAgTTTCA		
msa183564.2{147_H36B}	GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTtCT AACAgTTTCA		
msa183564.2{147_1169NT}	GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTtCT AACAgTTTCA		

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

Consensus	*****	*****	*****	*****	*****
	3351				3400
msa183564.2{147_COH1}	AATATTTTGA	TAACCTGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_M732}	AATATTTTGA	TAACCTGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_M781}	AATATTTTGA	TAACCTGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_2603}	AATATTTTGA	TAACCTGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_JM9130013}	AATATTTTGA	TAACCTGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_18RS21}	AATATTTTGA	TAACCTGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_090}	AATATTTTGA	TAACCTGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_CJB110}	AATATTTTGA	TAACCTGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_A909}	AATATTTTGA	TAACCTGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_H36B}	AATATTTTGA	TAACCTGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_1169NT}	AATATTTTGA	TAACCTGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
Consensus	*****	*****	*****	*****	*****
	3401				3450
msa183564.2{147_COH1}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_M732}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_M781}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_2603}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_JM9130013}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_18RS21}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_090}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_CJB110}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_A909}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_H36B}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_1169NT}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
Consensus	*****	*****	*****	*****	*****
	3451				3500
msa183564.2{147_COH1}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_M732}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_M781}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_2603}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_JM9130013}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_18RS21}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_090}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_CJB110}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_A909}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_H36B}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_1169NT}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
Consensus	*****	*****	*****	*****	*****
	3501				3550
msa183564.2{147_COH1}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaAGATC
msa183564.2{147_M732}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaAGATC
msa183564.2{147_M781}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaAGATC
msa183564.2{147_2603}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaAGATC
msa183564.2{147_JM9130013}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaAGATC
msa183564.2{147_18RS21}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaAGATC
msa183564.2{147_090}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaAGATC
msa183564.2{147_CJB110}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaAGATC
msa183564.2{147_A909}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaAGATC
msa183564.2{147_H36B}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaAGATC
msa183564.2{147_1169NT}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaAGATC
Consensus	*****	*****	*****	*****	*****
	3551				3600
msa183564.2{147_COH1}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_M732}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_M781}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_2603}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_JM9130013}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_18RS21}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_090}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_CJB110}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_A909}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_H36B}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_1169NT}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
Consensus	*****	*****	*****	*****	*****
	3601				3650
msa183564.2{147_COH1}	-----	-----	-----	-----	-----
msa183564.2{147_M732}	-----	-----	-----	-----	-----
msa183564.2{147_M781}	-----	-----	-----	-----	-----
msa183564.2{147_2603}	atcagataga	gcaacgaatg	gtctatttgg	tggtactttg	gcattgttat
msa183564.2{147_JM9130013}	-----	-----	-----	-----	-----
msa183564.2{147_18RS21}	-----	-----	-----	-----	-----
msa183564.2{147_090}	-----	-----	-----	-----	-----
msa183564.2{147_CJB110}	-----	-----	-----	-----	-----
msa183564.2{147_A909}	-----	-----	-----	-----	-----
msa183564.2{147_H36B}	-----	-----	-----	-----	-----

**Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)**

msa183564.2{147_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	3651				3700
msa183564.2{147_COH1}	-----	-----	-----	-----	-----
msa183564.2{147_M732}	-----	-----	-----	-----	-----
msa183564.2{147_M781}	-----	-----	-----	-----	-----
msa183564.2{147_2603}	-----	-----	-----	-----	-----
msa183564.2{147_JM9130013}	-----	-----	-----	-----	-----
msa183564.2{147_18RS21}	-----	-----	-----	-----	-----
msa183564.2{147_090}	-----	-----	-----	-----	-----
msa183564.2{147_CJB110}	-----	-----	-----	-----	-----
msa183564.2{147_A909}	-----	-----	-----	-----	-----
msa183564.2{147_H36B}	-----	-----	-----	-----	-----
msa183564.2{147_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****

**SEQ ID NO. 4412****STRAIN 2603**

VDKHHSSKAILKLTITLTTISILLMHSNQVNAEEQELKNQEQSPVIANVAQQPSPSVTTNTIV  
 EKTSTVTAASANTAKEMGDTSVKNDKTEDELEELSKNLDTSNLGADLEEEYPSKPKETTIN  
 NKESNVVTNASTAIAQKVPAYEEVKEPKSSSLAVLDTSKITKLQAITQRGKGNVVAIID  
 TGFDINHDI FRLDSPKDDKHSFKTKTEFEELKAKHNITYGKWNVDKI VFAHNYANNNTETV  
 ADIAAAMKDGYSSEAKNISHGTHVAGIFVGNKRPAINGLLLEGAAPNAQVLLMRIPDKI  
 DSDKFGEAYAKAITDAVNLGAKTINMSIGKTADSLIALNDKVKLALKLASEKGVAVVVAA  
 GNEGAFGMDYSKPLSTNPDYGTVNSPAISEDTLSVASYESLKTISEVVETITEGKLVKLP  
 IVTSKPFDKGKAYDVVYANYGAKKDFEGKDFGKIALIERGGGLDFMTKITTHATNAGVVG  
 IVI FNDQEKRGNFILPYRELPGVIISKVDGERIKNTSSQLTFNQSFVVDQSQGNRMLEQ  
 SSWGVTABGAIKPDVTASGFIEYSSSTYNNQYQTMSTGSMASPHVAGLMTMLQSHLAEKYK  
 GMLNLSKLLLELSKNILMSSATALYSEEDKAFYSPRQQGAGVVDAAEKAIQAQYYITGNDG  
 KAKINLKRMGDKFDTITVTIHKLVGVKELYQANVATEQVNGKGFALKPQALLDNTWQKV  
 ILRDKETQVRFTIDASQFSQKLKEQMANGYFLEGFVRFEAKDSNQELMSIPFVGFGNDF  
 ANLQALETPITYKTLKGSFYKPNDDTHKDQLEYNESAPFESNNYTALLTQSASWGYVDY  
 VKNGGELELAPESPKRIILGTFFENKVEDKTIHLLERDAANNPYFAISPNDGNGRDEITPQ  
 ATFLRNVDKISAQVLDQNGNVIWQSKVLPSYRKNFHNPKQSDGHYRMDALQWSGLDKDG  
 KVVADGFYTYRLRYTPVAEGANSQESDFKVQVSTKSPNLPRAQFDETNRTLSLAMPKES  
 SYVPTYRLQLVLSHVVKDEEYGDTSYHYFHIHQEGKVTLPKTVKIGESEVAVDPKALTL  
 VVEDKAGNFATVKLSDDLKAVVSEKENAIVISNSFKYFDNLKKEPMFISKKEKVVNKNL  
 BEIILVKPQTITVTITQSLSEITKSGNEKVLSTNNNSSRVAKII SPKHNGDSVNHTLPST  
 SDRATNGLVGLTALLSSLLLYLKPKTKNNKS

**SEQ ID NO. 4413****STRAIN A909**

EEQELKNQEQSPVIANVAQQPSPSVTTNTVEKTSVTSASANTAKEMGDTSVKNDKTEDE  
 LLEELSKNLDTSNLGADLEEEYPSKPKETTNNKESNVVTNASTAIAQKVPAYEEVKEPKES  
 SSLAVLDTSKITKLQAITQRGKGNVVAIIDTGFDINHDI FRLDSPKDDKHSFKTKAEFEE  
 LKAKHNITYGKWNVDKI VFAHNYANNNTETVADIAAAMKDGYSSEAKNISHGTHVAGIFVG  
 NSKRPAINGLLLEGAAPNAQVLLMRIPDKIDSDFGEAYAKAITDAVNLGAKTINMSLGK  
 TADSLIALNDKVKLALKLASEKGVAVVVAAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE  
 DTLVASYESLKTISEVVETITEGKLVKLP IVTSKPFDKGKAYDVVYANYGAKKRL.R.G  
 L.R.DCIN.AWWT.FYD.NHSCYKCRCCWYRYF.RSRKTWKFNSNLP.ITCGGY..SRW  
 RAYKIFYKSVNT.PEF.SS..PRWQSYAGTIKLGDRS.RSNQA.CNSFWL.NLFFNL..S  
 IPNNVWYKGYFTTCCIRINDNASKSFG.EI.RDEFRF.KIARIV.KHPHELSNSII..RG.  
 GVLFTTSARCRC.S.C.KSYPSSILCYWKRWQS.N.SQTSGR.I.YHSYNS.TCRRCORIV  
 LSS.CSNRTSK.R.ICP.TTSLARY.LAESNSS..RNTSSIIY.F.SI.SEIKRTDGKWL  
 FLRRFCTF.RSQQ..SGVNEYSFCRI.W.FCELTST.NTDL.DAF.R.FLL.TK.YNS.R  
 PIGVQ.ISSF.KQQLYCLVNTISVLGLC.LCQKWGWVRI STGESKKNYFRNF.E.G.G.N  
 NSSFGKRCSE.SIFCHFSK.RWK.G.NHSPGNFLKCC.GYFCSSSRSKWKCYLAK.GFTI  
 LS.KFP..SKAK.WLSYGCPSVEWFR.GWQCSRWFYLSFTLHTSSRRSK.SGVRL.S  
 SSKY.VTKSSFTSSV..N.SNIKLSHA.GK.LCSYISSTISFISCKR.RIWR.DFLPLF  
 PYRSRR.SDTS.NS.DRRE.GCSR.P.DLTCCGR.SW.FRNGKIV.PLE.GSSIRERKRY  
 SNF.QFQIF..LEKRTYVYF.RRKSSQESRRNSIS.AANYSSYIIV.RNNSIRK.ESP  
 HFYKQ...QSS.DHIT.T.RGFC.PY

**SEQ ID NO. 4414****STRAIN H36B**

EEQELKNQEQSPVIANVAQQPSPSVTTNTVEKTSVTSASANTAKEMGDTSVKNDKTEDE  
 LLEELSKNLDTSNLGADLEEEYPSKPKETTNNKESNVVTNASTAIAQKVPAYEEVKEPKES  
 SSLAVLDTSKITKLQAITQRGKGNVVAIIDTGFDINHDI FRLDSPKDDKHSFKTKAEFEE  
 LKAKHNITYGKWNVDKI VFAHNYANNNTETVADIAAAMKDGYSSEAKNISHGTHVAGIFVG  
 NSKRPAINGLLLEGAAPNAQVLLMRIPDKIDSDFGEAYAKAITDAVNLGAKTINMSLGK  
 TADSLIALNDKVKLALKLASEKGVAVVVAAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE  
 DTLVASYESLKTISEVVETITEGKLVKLP IVTSKPFDKGKAYDVVYANYGAKKDFEGK  
 FKGKIALIERGGGLDFMTKITTHATNAGVVGIVIFNDQEKRGNFILPYRELPGVIISKVDG  
 ERIKNTSSQLTFNQSFVVDQSQGNRMLEQSSWGVTABGAIKPDVTASGFIEYSSSTYNNQ  
 YQTMSTGSMASPHVAGLMTMLQSHLAEKYKGMNLSKLLLELSKNILMSSATALYSEEDK  
 AFYSPRQQGAGVVDAAEKAIQAQYYITGNDGKAKINLKRVDKFDITVTIHKLVGVKELY  
 YQANVATEQVNGKGFALKPQALLDNTWQKVIILRDKETQVRFTIDSSQFSQKLKEQMANGY  
 FLEGFVRFEAKDSNQELMSIPFVGFGNDFANLQALETPITYKTLKGSFYKPNDDTHKD  
 QLEYNESAPFESNNYTALLTQSASWGYVDYVKNGGELELAPESPKRIILGTFFENKVEDKTI  
 HLLERDAANNPYFAISPNDGNGRDEITPQATFLRNVDKISAQVLDQNGNVIWQSKVLPS  
 YRKNFHNPKQSDGHYRMDALQWSGLDKDGKVVADGFYTYRLRYTPVAEGANSQESDFKV  
 QVSTKSPNLPRAQFDETNRTLSLAMPKESYVPTYRLQLVLSHVVKDEEYGDTSYHYF



**Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)**

HIDQEGKVTLPKTVKIGESEVAVDPKTLTLVVEDKAGNFATVKLSDLLNKAVVSEKENAI  
 VTSNNFKYFDNLKKEPMFI SKKGVVNNKLEBIALVKPQTIVTTQSLSKETITQSGNEKVL  
 TSTNNSSSRVAKI ISPKHNGDSVNHT

**SEQ ID NO. 4415****STRAIN 18RS21**

EEQELKNQEQSPVIANVAQOPSPSVTNTVEKTSVTAASASNTAKEMGDTSVKNDKTEDE  
 LLEELSKNLDTSNLGADLEEEYPSKPETTNKESNVVNTASTAIAQKVPSAYEEVKPESK  
 SSLAVLDTSKITKLQATTQRGKGNVVAI IDTGFDINHDI FRLDSPKDDKHSFKTKTEFEE  
 LKAKHNTYGGKWNVDKI VFAHNYANNNTETVADIAAAMKDGYGSEAKNISHGTHVAGIFVG  
 NSKRPAINGLLLEGAAPNAQVLLMRIPDKIDSDFGEAYAKA IDAVNLGAKTINMSIGK  
 TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE  
 DTLSVASYESLTKTISEVVETITIEGKLVKLP IVTSKPFDDKGKAYDVVYANYGAKKDFEGKD  
 FKGKIALIERGGGLDMTKI THATNAGVVGIV I FNDQEKRGNFILPYRELPVGI ISKVDG  
 BRIKNTSSQLTFNQSFVVDSDQGNRMLEQSSWGVTAEGA IKPDVTAAGFEIYSSYNNQ  
 YQTMSTGSMASPHVAGLMTMLQSHLAEKYKGMNLDSSKLLLELSKNILMSSATALYSEEDK  
 AFYSPRQOQAGVVDAAEKAIQAQYITGNDGKAKINLKRMDGKDFITVTIHLKVEGVKELY  
 YQANVATEQVNVKGFALKPQALLDTNWQKVLIRDKETQVRFT IDASQFSQKLKEQMANGY  
 FLEGVFRFKEAKDSNQLMSI PFVGFNGDFANLQALETP IYKTI SKGSFYYPNDTTHKD  
 QLEYNESAPFESNNY TALLTQSASWGYVDVYKNGGELELAPESPKRI ILGTFFENKVEDKT  
 IHLLERDAANNPYFAISPNDGGRDEITPQATFLRNVDI SAQVLDQNGNVIWQSKVLP  
 YRKNPHNNPKQSDGHRMDALQWGLDKDKGVVADGFYTYRLRYTPVAEGANSQESDFKV  
 QVSTKSPNLPRAQFDETNRITSLAMPKESYVPTYRLQLVLSHVVDKEEYGDSTSYHYF  
 HIDQEGKVTLPKTVKIGESEVAVDPKALTTLVVEDKAGNFATVKLSDLLNKAVVSEKENAI  
 VTSNNFKYFDNLKKEPMFI SKKGVVNNKLEBIALVKPQTIVTTQSLSKETITQSGNEKVL  
 TSTNNSSSRVAKI ISPKHNGDSVNHT

**SEQ ID NO. 4416****STRAIN M732**

EEQELKNQEQSPVIANVAQOPSPSVTNTVEKTSVTAASASNTAKEMGDTSVKNDKTEDE  
 LLEELSKNLDTSNLGADLEEEYPSKPETTNKESNVVNTASTAIAQKVPSAYEEVKSEK  
 SSLAVLDTSKITKLQATTQRGKGNVVAI IDTGFDINHDI FRLDSPKDDKHSFKTKAEFEE  
 LKAKHNTYGGKWNVDKI VFAHNYANNNTETVADIAAAMKDGYGSEAKNISHGTHVAGIFVG  
 NSKRPAINGLLLEGAAPNAQVLLMRIPDKIDSDFGEAYAKA IDAVNLGAKTINMSIGK  
 TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE  
 DTLSVASYESLTKTISEVVETITIEGKLVKLP IVTSKPFDDKGKAYDVVYANYGAKKILKVRT  
 LKVRILH. LSVVVDLIL. LKSLMLQMQVLLVSLFLT IKKNVEIF. FLTVNVLWGLLVK. MA  
 SV. KILQVS. HLTRVLK. LIAKVAIVCWNQVGA. QLKEQSSLM. QLLALKFILQPII IN  
 TKQCLVQVWLHMLQD. .QCFKVIWLRNIG. I. ILKNC. NCLKTSS. AQQHYIVKRI  
 RFIHHVSKVQV. LMLKKLSKLNIMLETMAKLLISNEREINLISQLQFINL. KVSKNCI  
 IKLM. QONK. IKVNLPLNHKPC. ILIGRK. FFVKKHFDLLMLVNLVRN. KNRWQMI  
 S. KVLVVLKPRIVIRS. .VFL. DLMVILRTYKHLKHFIRRFKVVSTINQMIQLIKT  
 NWSTMNQLLLKATTILPC. HNQLGAMLIMSKMVG. N. HRRVQKELF. ELLRIRLRIKQ  
 FIFWKEMQRIIHLPLFLQIKMEIGTKSLPRQLS. EMLRIFLLKF. IKMEMLFGKVRFYHL  
 IVKISII IQSKVMVI IVWMLFSGVV. IRMAKL. QMVFI LIAVTHQ. QKEQIVRSQTLKF  
 K. VLSHQIFLHLSLMKLIH. A. PCLRKVVMFLHIVYN. FYLML. KMKNMGMRLLTII S  
 I. IKKVK. HFLKRLR. ERVRLR. TLRP. HLLWKIKLVILQR. NCLTS. IRQ. YQKKTIL.  
 .FLTVSNILIT. RKNLCLFLKKEK. .TRI. KK. H. LSLKLQLLLNHLCK. LNQEMRKSS  
 LLQTIIVAE. LRSYHLNITGILITI

**SEQ ID NO. 4417****STRAIN COH1**

EEQELKNQEQSPVIANVAQOPSPSVTNTVEKTSVTAASASNTAKEMGDTSVKNDKTEDE  
 LLEELSKNLDTSNLGADLEEEYPSKPETTNKESNVVNTASTAIAQKVPSAYEEVKSEK  
 SSLAVLDTSKITKLQATTQRGKGNVVAI IDTGFDINHDI FRLDSPKDDKHSFKTKAEFEE  
 LKAKHNTYGGKWNVDKI VFAHNYANNNTETVADIAAAMKDGYGSEAKNISHGTHVAGIFVG  
 NSKRPAINGLLLEGAAPNAQVLLMRIPDKIDSDFGEAYAKA IDAVNLGAKTINMSIGK  
 TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE  
 DTLSVASYESLTKTISEVVETITIEGKLVKLP IVTSKPFDDKGKAYDVVYANYGAKKILKVRT  
 LKVRILH. LSVVVDLIL. LKSLMLQMQVLLVSLFLT IKKNVEIF. FLTVNVLWGLLVK. MA  
 SV. KILQVS. HLTRVLK. LIAKVAIVCWNQVGA. QLKEQSSLM. QLLALKFILQPII IN  
 TKQCLVQVWLHMLQD. .QCFKVIWLRNIG. I. ILKNC. NCLKTSS. AQQHYIVKRI  
 RFIHHVSKVQV. LMLKKLSKLNIMLETMAKLLISNEREINLISQLQFINL. KVSKNCI  
 IKLM. QONK. IKVNLPLNHKPC. ILIGRK. FFVKKHFDLLMLVNLVRN. KNRWQMI  
 S. KVLVVLKPRIVIRS. .VFL. DLMVILRTYKHLKHFIRRFKVVSTINQMIQLIKT  
 NWSTMNQLLLKATTILPC. HNQLGAMLIMSKMVG. N. HRRVQKELF. ELLRIRLRIKQ  
 FIFWKEMQRIIHLPLFLQIKMEIGTKSLPRQLS. EMLRIFLLKF. IKMEMLFGKVRFYHL  
 IVKISII IQSKVMVI IVWMLFSGVV. IRMAKL. QMVFI LIAVTHQ. QKEQIVRSQTLKF  
 K. VLSHQIFLHLSLMKLIH. A. PCLRKVVMFLHIVYN. FYLML. KMKNMGMRLLTII S  
 I. IKKVK. HFLKRLR. ERVRLR. TLRP. HLLWKIKLVILQR. NCLTS. IRQ. YQKKTIL.  
 .FLTVSNILIT. RKNLCLFLKKEK. .TRI. KK. H. LSLKLQLLLNHLCK. LNQEMRKSS  
 LLQTIIVAE. LRSYHLNITGILITI

**SEQ ID NO. 4418****STRAIN M781**

EEQELKNQEQSPVIANVAQOPSPSVTNTVEKTSVTAASASNTAKEMGDTSVKNDKTEDE  
 LLEELSKNLDTSNLGADLEEEYPSKPETTNKESNVVNTASTAIAQKVPSAYEEVKSEK  
 SSLAVLDTSKITKLQATTQRGKGNVVAI IDTGFDINHDI FRLDSPKDDKHSFKTKAEFEE  
 LKAKHNTYGGKWNVDKI VFAHNYANNNTETVADIAAAMKDGYGSEAKNISHGTHVAGIFVG  
 NSKRPAINGLLLEGAAPNAQVLLMRIPDKIDSDFGEAYAKA IDAVNLGAKTINMSIGK  
 TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE  
 DTLSVASYESLTKTISEVVETITIEGKLVKLP IVTSKPFDDKGKAYDVVYANYGAKKILKVRT  
 LKVRILH. LSVVVDLIL. LKSLMLQMQVLLVSLFLT IKKNVEIF. FLTVNVLWGLLVK. MA

**Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)**

SV.KILQVS.HLTRVLK.LIAKVAIVCWNQVGA.QLKEQSSLM.QLLALKFILQPIIIN  
TKQCLVQVWLHMLQD..QCCKVILWRNIKG.I.ILKNC.NCLKTSS.AQQOYHIVKRIR  
RFIHHVSKVQV.LMLKKLSKLNIMLLETMAKLKLSNEREINLISQLQFINL.KVSKNCI  
IKLM.QQNK.IKVNPLPLNHKPC.ILIGRK.FFVIKKHKFDLLMLVNLVRN.KNRWQMI  
S.KVLYVLKKPRIVIRS..VPLL.DLMVILRTYKHLKHFIRFLKVVSTINQMIQLIKT  
NWSTMNQLLLKATTILPC.HNQLGAMLIMSKMVG.S.N.HRRVQKELF.ELLRIRLRIKQ  
IFPWKEMQRIIHLFPFLQIKMEIGTKSLPRQLS.EMLRIFLLKF.IKMEMFGKVRFYHL  
IVKISII IQSKVMVIVVMFLSGVV.IRMAKL.QMVFIILAIYVTHQ.QKEQIVRSQTLKF  
K.VLSHQIFLHLSMLKLIBH.A.PCLRKVVMLHIVYN.FYLM.L.KMKMGMRLLTIIS  
I.IKKVK.HFLKRLR.ERVRLR.TLRP.HLLWKIKLVILQR.NCLTS.IRQ.YQRKKTIL.  
.FLTVSNILIT.RKNLCLFLKKEK..TRI.KK.H.LSLKLQLLNHCLKK.LNQEMRKSS  
LLQTIIVAE.LRSYHLNITGILLTI

SEQ ID NO. 4419

STRAIN JM9130013

EEQELKNQEQSPVIANVAQQPSPSVTTNTVEKTSVTAASANTAKEMGDTSVKNDKTEDE  
LLEELSKNLDTSNLGADLEEYPSKPEPTNNKESNVVNTASTAIAQKVP SAYEEVKPESK  
SSLAVFDTSKITKLQAITQRGKGNVVAIIDTGFDINHDI.FRLDSPKDDKHSFKTKTEFEE  
LKAKHNITYGKWVNDKIVFAHNYANNTETVADIAAAMKDGYGSEAKNISHGTHVAGIFVG  
NSKRPAINGLLLEGAAPNAQVLLMRI.PDKIDSDKFGEAYAKAITDAVNLGAKTINMSIGK  
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE  
DTLSVASYESLKITSEVVETIEGKLVKLP.IVTSKPPDKGKAYDVVYANYGAKKDFEGKD  
FKGKIALIERGGGLDFMTKITHATNAGVVGIVIFNDQEKGRGNFLIPYRELPGVISKVDG  
ERIKNTSSQTLTFNQSFVVDSQGGNRMLEQSSWGVTAEAGIKPDVTASGFEIYSSTYNNQ  
YQTMSTGSMASPHVAGLMTMLQSHLAEKYKGMNLD SKKLELSKNILMSSATALYSEEDK  
AFYSPPRQGGAGVDAEKAIQAQYYITGNDGKAKINLKRMDKFDITVTIHKLVEGVKELY  
YQANVATEQVNGKGFALKPQALLDTNWQKVLIRDKETQVRFTIDASQFSQKLKEQMANGY  
FLEGFVRFEKAKDSNQELMSIPFVGFGNDFANLQALETPITYKLSKGSFYKPNDTTHKD  
QLEYNESAPFESNNYTALLTQSASWGYVDYVKNNGGELELAPESPKRIILGTFFENKVEDKT  
IHLLERDAANNPYFAISPENKDGNRDEITPQATFLRNVDISAQVLDQNGNVIWQSKVLPS  
YRKNFHNPKQSDGHYRMDALQWSGLDKDGKVVADGFTYRLRYTPVAEGANSQESDFKV  
QVSTKSPNLPSRAQFDETNRTLSLAMPKESYVPTYRLQLVLSHVVKDEEYGDETS YHYF  
HIDQEGKVTLPTKTVKIGESEVAVDPKALTIVVEDKAGNFATVKLSDDLNKAVVSEKENAI  
VISNSFKYFNLKKEPMFISKEGKVVNKNLEEBITLVKPQTTVTTQSLSKETKSGNEKVL  
TSTNNSSSRVAKIISPKNHGDVSNHT

SEQ ID NO. 4420

STRAIN 090

EEQELKNQEQSPVIANVAQQPSPSVTTNTVEKTSVTAASANTVKEMGDTSVKNDKTEDE  
LLEELSKNLDTSNLGADLEEYPSKPEPTNNKESNVVNTASTAIAQKVP SAYEEVKPESK  
SSLAVFDTSKITKLQAITQRGKGNVVAIIDTGFDINHDI.FRLDSPKDDKHSFKTKAEFEE  
LKAKHNITYGKWVNDKIVFAHNYANNTETVADIAAAMKDGYGSEAKNISHGTHVAGIFVG  
NSKRPAINGLLLEGAAPNAQVLLMRI.PDKIDSDKFGEAYAKAITDAVNLGAKTINMSLGK  
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE  
DTLSVASYESLKITSEVVETIEGKLVKLP.IVTSKPPDKGKAYDVVYANYGAKKDFEGKD  
FKGKIALIERGGGLDFMTKITHATNAGVVGIVIFNDQEKGRGNFLIPYRELPGVISKVDG  
ERIKNTSSQTLTFNQSFVVDSQGGNRMLEQSSWGVTAEAGIKPDVTASGFEIYSSTYNNQ  
YQTMSTGSMASPHVAGLMTMLQSHLAEKYKGMNLD SKKLELSKNILMSSATALYSEEDK  
AFYSPPRQGGAGVDAEKAIQAQYYVTGNDGKAKINLKRVDKFDITVTIHKLVEGVKELY  
YQANVATEQVNGKGFALKPQALLDTNWQKVLIRDKETQVRFTIDASQFSQKLKEQMANGY  
FLEGFVRFEKAKDSNQELMSIPFVGFGNDFANLQALETPITYKLSKGSFYKPNDTTHKD  
QLEYNESAPFESNNYTALLTQSASWGYVDYVKNNGGELELAPESPKRIILGTFFENKVEDKT  
IHLLERDAANNPYFAISPENKDGNRDEITPQATFLRNVDISAQVLDQNGNVIWQSKVLPS  
YRKNFHNPKQSDGHYRMDAFQWSGLDKDGKVVADGFTYRLRYTPVAEGANSQESDFKV  
QVSTKSPNLPLLAQFDETNRTLSLAMPKESYVPTYRLQLVLSHVVKDEEYGDETS YHYF  
HIDQEGKVTLPTKTVKIGESEVAVDPKALTIVVEDKAGNFATVKLSDDLNKAVVSEKENAI  
VISNSFKYFNLKKEPMFISKEGKVVNKNLEEBITLVKPQTTVTTQSLSKETKSGNEKVL  
TSTNNSSSRVAKIISPKNHGDVSNHT

SEQ ID NO. 4421

STRAIN CJB110

EEQELKNQEQSPVIANVAQQPSPSVTTNTVEKTSVTAASANTAKEMGDTSVKNDKTEDE  
LLEELSKNLDTSNLGADLEEYPSKPEPTNNKESNVVNTASTAIAQKVP SAYEEVKPESK  
SSLAVFDTSKITKLQAITQRGKGNVVAIIDTGFDINHDI.FRLDSPKDDKHSFKTKAEFEE  
LKAKHNITYGKWVNDKIVFAHNYANNTETVADIAAAMKDGYGSEAKNISHGTHVAGIFVG  
NSKRPAINGLLLEGAAPNAQVLLMRI.PDKIDSDKFGEAYAKAITDAVNLGAKTINMSLGK  
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE  
DTLSVASYESLKITSEVVETIEGKLVKLP.IVTSKPPDKGKAYDVVYANYGAKKDFEGKD  
FKGKIALIERGGGLDFMTKITHATNAGVVGIVIFNDQEKGRGNFLIPYRELPGVISKVDG  
ERIKNTSSQTLTFNQSFVVDSQGGNRMLEQSSWGVTAEAGIKPDVTASGFEIYSSTYNNQ  
YQTMSTGSMASPHVAGLMTMLQSHLAEKYKGMNLD SKKLELSKNILMSSATALYSEEDK  
AFYSPPRQGGAGVDAEKAIQAQYYVTGNDGKAKINLKRVDKFDITVTIHKLVEGVKELY  
YQANVATEQVNGKGFALKPQALLDTNWQKVLIRDKETQVRFTIDASQFSQKLKEQMANGY  
FLEGFVRFEKAKDSNQELMSIPFVGFGNDFANLQALETPITYKLSKGSFYKPNDTTHKD  
QLEYNESAPFESNNYTALLTQSASWGYVDYVKNNGGELELAPESPKRIILGTFFENKVEDKT  
IHLLERDAANNPYFAISPENKDGNRDEITPQATFLRNVDISAQVLDQNGNVIWQSKVLPS  
YRKNFHNPKQSDGHYRMDAFQWSGLDKDGKVVADGFTYRLRYTPVAEGANSQESDFKV  
QVSTKSPNLPLLAQFDETNRTLSLAMPKESYVPTYRLQLVLSHVVKDEEYGDETS YHYF  
HIDQEGKVTLPTKTVKIGESEVAVDPKALTIVVEDKAGNFATVKLSDDLNKAVVSEKENAI  
VISNSFKYFNLKKEPMFISKEGKVVNKNLEEBITLVKPQTTVTTQSLSKETKSGNEKVL  
TSTNNSSSRVAKIISPKNHGDVSNHT

SEQ ID NO. 4422

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

**STRAIN 1169NT**

EEQELKNQEQSPVIANVAQQSPSVTTNI VEKTSVTAASANTAKEMGDTSVKNDKTEDE  
 LLEELSKNLDTSNMGADLEEYPSKPETTNNKESNVVTINASTAIAQKVPSAYEEVKPKSK  
 SSLAVLDTSKITKLQAITQRGKGNVVAIIDTGFDINHDI FRLDSPKDDKHSPFNKAEFEE  
 LKAKHNITYGKWVNDKIVFAHNYANTTETVADIAAAMKDGYSKAKNISHGTHVAGIFVG  
 NSKRPAINGLLLEGAAAPNAQVLLMRI PDKIDSDKFGEAYAKAITDAVNLGAKTINMSIGK  
 TADSLIALNDKVLKALASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE  
 DTLASVASYESLKTISEVVETITIEGKLVKLPVITVSKPFDKGAIDVYVANYGAKDFEGKD  
 FKOKIALIERGGGLDMFTKITHTATNAGVVGIVIFNDQEKRGNFILPYRELPGVVISKVDG  
 ERIKNTSSQLTFNQRFEVVDSSQGGNRMLEQSSWGVTAAGAIKPDVTASGFEIYSSTYNNQ  
 YQTMSTGSMASPHVAGLMTMLQSHLAEKYKGMNLDISKLLELSKNILMSSATALYSEEDK  
 AFYSPRQGGAGVVDAAEKAIQAQYVVTGNDGKAKINLKRVDGKFDITVTIHKLVEGVKELY  
 YQANVATEQVNGKGFALKPQALLDTNWQKVIILRDKETQVRFTIDASQFSQKLKEQMANGY  
 FLEGFVRFKKAKSDNQBLMSIPFVGFGNGDFASLQALETPITYKTLKSGSFYYKPNDTTHKD  
 QLEYNESAPPFESNNYATALLTQSSASWGYVDVYKNGGELELAPESPKRIILGTFENKVEDKT  
 IHLERDAANNPYFAISPNDGGRDEITPQATFLRNVDKIDSAQVLDQNGNVIWQSKVLPS  
 YRKNFHNPNKQSDGHYRMDALQWGLDKDKGVVADGFPYTLRYLRYTPVABGANSQESDPKV  
 QVSTKSPNLPSSRAQFDETNRTLSLAMPKGSYVPIYRLQLVLSHVVKDEYGEDTSYYYP  
 HLDQEGKATLPKTVKIGESEVAVDPKALTIVVEDKAGNFATVKLSDDLNKAVVSEKENAI  
 VISNSPKYFNDLKEPMFISKKEKVVNKNLEBIIIVKPHTTVTITQSLKEITKSGNEKVL  
 TSTNNSSRVAKIISPKNHGSVNHNT

PRETTY of: /biotmp/msa209368.2{\*} February 10, 2003 02:09 ..

	1	50
msa209368.2{147_COH1}	-----	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_M732}	-----	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_M781}	-----	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_18RS21}	-----	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_2603}	vdkhhskkai lkltlittsi lhmshngvna	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_JM9130013}	-----	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_090}	-----	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_CJB110}	-----	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_1169NT}	-----	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_H36B}	-----	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_A909}	-----	EEQELKNQEQ SPVIANVAQQ
Consensus	*****	*****

	51	100
msa209368.2{147_COH1}	PSPSVTtNiV EKTsvTaASA SNTvKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_M732}	PSPSVTtNiV EKTsvTaASA SNTvKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_M781}	PSPSVTtNiV EKTsvTaASA SNTvKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_18RS21}	PSPSVTtntV EKTsvTaASA SNTaKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_2603}	PSPSVTtntV EKTsvTaASA SNTaKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_JM9130013}	PSPSVTtntV EKTsvTaASA SNTaKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_090}	PSPSVTtntV EKTsvTaASA SNTvKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_CJB110}	PSPSVTtNiV EKTsvTaASA SNTaKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_1169NT}	PSPSVTtNiV EKTsvTaASA SNTaKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_H36B}	PSPSVTtntV EKTsvTaASA SNTaKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_A909}	PSPSVTtntV EKTsvTaASA SNTaKEMGDT SVKNDKTEDE	LLEELSKNLD
Consensus	*****	*****

	101	150
msa209368.2{147_COH1}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAIAQKVPS	AYEEVKseSK
msa209368.2{147_M732}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAIAQKVPS	AYEEVKseSK
msa209368.2{147_M781}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAIAQKVPS	AYEEVKseSK
msa209368.2{147_18RS21}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAIAQKVPS	AYEEVKpeSK
msa209368.2{147_2603}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAIAQKVPS	AYEEVKpeSK
msa209368.2{147_JM9130013}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAIAQKVPS	AYEEVKpeSK
msa209368.2{147_090}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAIAQKVPS	AYEEVKpeSK
msa209368.2{147_CJB110}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAIAQKVPS	AYEEVKpeSK
msa209368.2{147_1169NT}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAIAQKVPS	AYEEVKpeSK
msa209368.2{147_H36B}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAIAQKVPS	AYEEVKpeSK
msa209368.2{147_A909}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAIAQKVPS	AYEEVKpeSK
Consensus	***-*****	*****

	151	200
msa209368.2{147_COH1}	SSLAVLDTSK ITKLQAITQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_M732}	SSLAVLDTSK ITKLQAITQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_M781}	SSLAVLDTSK ITKLQAITQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_18RS21}	SSLAVLDTSK ITKLQAITQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_2603}	SSLAVLDTSK ITKLQAITQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_JM9130013}	SSLAVLDTSK ITKLQAITQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_090}	SSLAVLDTSK ITKLQAITQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_CJB110}	SSLAVLDTSK ITKLQAITQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_1169NT}	SSLAVLDTSK ITKLQAITQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_H36B}	SSLAVLDTSK ITKLQAITQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_A909}	SSLAVLDTSK ITKLQAITQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
Consensus	*****	*****

	201	250
msa209368.2{147_COH1}	SPKtKaEFEE LKAKHNITYG KWVNDKIVFA HNYANTTETV ADIAAAMKDG	

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa209368.2{147_M732}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_M781}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_18RS21}	SFKtKtEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_2603}	SFKtKtEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_JM9130013}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_090}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_CJB110}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_1169NT}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_H36B}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_A909}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
Consensus	*****-*****	*****-*****	*****-*****	*****-*****	*****-*****
msa209368.2{147_COH1}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_M732}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_M781}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_18RS21}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_2603}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_JM9130013}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_090}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_CJB110}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_1169NT}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_H36B}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_A909}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
Consensus	*****-*****	*****-*****	*****-*****	*****-*****	*****-*****
msa209368.2{147_COH1}	DSDKFGGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_M732}	DSDKFGGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_M781}	DSDKFGGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_18RS21}	DSDKFGGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_2603}	DSDKFGGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_JM9130013}	DSDKFGGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_090}	DSDKFGGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_CJB110}	DSDKFGGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_1169NT}	DSDKFGGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_H36B}	DSDKFGGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_A909}	DSDKFGGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
Consensus	*****-*****	*****-*****	*****-*****	*****-*****	*****-*****
msa209368.2{147_COH1}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_M732}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_M781}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_18RS21}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_2603}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_JM9130013}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_090}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_CJB110}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_1169NT}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_H36B}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_A909}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
Consensus	*****-*****	*****-*****	*****-*****	*****-*****	*****-*****
msa209368.2{147_COH1}	LKTISeVVET	TIEGKLvKlP	IVTSKPFdKG	KAYDVVYANY	GAKKilkvrt
msa209368.2{147_M732}	LKTISeVVET	TIEGKLvKlP	IVTSKPFdKG	KAYDVVYANY	GAKKilkvrt
msa209368.2{147_M781}	LKTISeVVET	TIEGKLvKlP	IVTSKPFdKG	KAYDVVYANY	GAKKilkvrt
msa209368.2{147_18RS21}	LKTISeVVET	TIEGKLvKlP	IVTSKPFdKG	KAYDVVYANY	GAKKdfegkd
msa209368.2{147_2603}	LKTISeVVET	TIEGKLvKlP	IVTSKPFdKG	KAYDVVYANY	GAKKdfegkd
msa209368.2{147_JM9130013}	LKTISeVVET	TIEGKLvKlP	IVTSKPFdKG	KAYDVVYANY	GAKKdfegkd
msa209368.2{147_090}	LKTISeVVET	TIEGKLvKlP	IVTSKPFdKG	KAYDVVYANY	GAKKdfegkd
msa209368.2{147_CJB110}	LKTISeVVET	TIEGKLvKlP	IVTSKPFdKG	KAYDVVYANY	GAKKdfegkd
msa209368.2{147_1169NT}	LKTISeVVET	TIEGKLvKlP	IVTSKPFdKG	KAYDVVYANY	GAKKdfegkd
msa209368.2{147_H36B}	LKTISeVVET	TIEGKLvKlP	IVTSKPFdKG	KAYDVVYANY	GAKKdfegkd
msa209368.2{147_A909}	LKTISeVVET	TIEGKLvKlP	IVTSKPFdKG	KAYDVVYANY	GAKKrl.r.g
Consensus	*****-*****	*****-*****	*****-*****	*****-*****	*****-*****
msa209368.2{147_COH1}	lkvrhlh.lsv	vvdlil.lks	lmlqmqvllv	slfltkiknv	eiF.fltvny
msa209368.2{147_M732}	lkvrhlh.lsv	vvdlil.lks	lmlqmqvllv	slfltkiknv	eiF.fltvny
msa209368.2{147_M781}	lkvrhlh.lsv	vvdlil.lks	lmlqmqvllv	slfltkiknv	eiF.fltvny
msa209368.2{147_18RS21}	fkgkialier	gggldfntki	thatnagvvg	ivifndqekr	gnFlippyrel
msa209368.2{147_2603}	fkgkialier	gggldfntki	thatnagvvg	ivifndqekr	gnFlippyrel
msa209368.2{147_JM9130013}	fkgkialier	gggldfntki	thatnagvvg	ivifndqekr	gnFlippyrel
msa209368.2{147_090}	fkgkialier	gggldfntki	thatnagvvg	ivifndqekr	gnFlippyrel
msa209368.2{147_CJB110}	fkgkialier	gggldfntki	thatnagvvg	ivifndqekr	gnFlippyrel
msa209368.2{147_1169NT}	fkgkialier	gggldfntki	thatnagvvg	ivifndqekr	gnFlippyrel
msa209368.2{147_H36B}	fkgkialier	gggldfntki	thatnagvvg	ivifndqekr	gnFlippyrel
msa209368.2{147_A909}	l.r.dcin.a	wwwt.fyd.n	hscykrcrcw	yyrf.rsrkt	wkFsnslp.i
Consensus	*****-*****	*****-*****	*****-*****	*****-*****	*****-*****

501

550

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa209368.2{147_COH1}	lwGllvk.ma	sv.Kilqvs.	hltrvlk.li	akvaivcwnn	qvga.qlkeq
msa209368.2{147_M732}	lwGllvk.ma	sv.Kilqvs.	hltrvlk.li	akvaivcwnn	qvga.qlkeq
msa209368.2{147_M781}	lwGllvk.ma	sv.Kilqvs.	hltrvlk.li	akvaivcwnn	qvga.qlkeq
msa209368.2{147_18RS21}	pvGiiskvdg	eriKntssql	tfngsfvvd	sqgggnrmleq	sswgvttaega
msa209368.2{147_2603}	pvGiiskvdg	eriKntssql	tfngsfvvd	sqgggnrmleq	sswgvttaega
msa209368.2{147_JM9130013}	pvGiiskvdg	eriKntssql	tfngsfvvd	sqgggnrmleq	sswgvttaega
msa209368.2{147_090}	pvGviskvdg	eriKntssql	tfngsfvvd	sqgggnrmleq	sswgvttaega
msa209368.2{147_CJB110}	pvGviskvdg	eriKntssql	tfngsfvvd	sqgggnrmleq	sswgvttaega
msa209368.2{147_1169NT}	pvGviskvdg	eriKntssql	tfngsfvvd	sqgggnrmleq	sswgvttaega
msa209368.2{147_H36B}	pvGviskvdg	eriKntssql	tfngsfvvd	sqgggnrmleq	sswgvttaega
msa209368.2{147_A909}	tcGgy..srw	rayKkyfksv	ni..pef..ss.	.prwqsyagt	iklgrds.rs
Consensus	-----	-----	-----	-----	-----
msa209368.2{147_COH1}	sslm.qllal	kfilqpiiin	tkqclvqvwl	hhmlqd..qc	fkviwlrnk
msa209368.2{147_M732}	sslm.qllal	kfilqpiiin	tkqclvqvwl	hhmlqd..qc	fkviwlrnk
msa209368.2{147_M781}	sslm.qllal	kfilqpiiin	tkqclvqvwl	hhmlqd..qc	fkviwlrnk
msa209368.2{147_18RS21}	ikpdvtasgf	eiyssstynnq	yqtmagtsma	sphvaglmtm	lqshlaekyk
msa209368.2{147_2603}	ikpdvtasgf	eiyssstynnq	yqtmagtsma	sphvaglmtm	lqshlaekyk
msa209368.2{147_JM9130013}	ikpdvtasgf	eiyssstynnq	yqtmagtsma	sphvaglmtm	lqshlaekyk
msa209368.2{147_090}	ikpdvtasgf	eiyssstynnq	yqtmagtsma	sphvaglmtm	lqshlaekyk
msa209368.2{147_CJB110}	ikpdvtasgf	eiyssstynnq	yqtmagtsma	sphvaglmtm	lqshlaekyk
msa209368.2{147_1169NT}	ikpdvtasgf	eiyssstynnq	yqtmagtsma	sphvaglmtm	lqshlaekyk
msa209368.2{147_H36B}	ikpdvtasgf	eiyssstynnq	yqtmagtsma	sphvaglmtm	lqshlaekyk
msa209368.2{147_A909}	nqa.cnsfwl	.nlffnl..s	ipnnvwykyg	fttccrindn	asksfg.ei.
Consensus	-----	-----	-----	-----	-----
msa209368.2{147_COH1}	g.i.ilknc.	nclktss.aq	qghyivkrir	rflhhvskvq	v.lmlkKlSk
msa209368.2{147_M732}	g.i.ilknc.	nclktss.aq	qghyivkrir	rflhhvskvq	v.lmlkKlSk
msa209368.2{147_M781}	g.i.ilknc.	nclktss.aq	qghyivkrir	rflhhvskvq	v.lmlkKlSk
msa209368.2{147_18RS21}	gmnlidskkl	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_2603}	gmnlidskkl	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_JM9130013}	gmnlidskkl	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_090}	gmnlidskkl	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_CJB110}	gmnlidskkl	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_1169NT}	gmnlidskkl	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_H36B}	gmnlidskkl	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_A909}	rdefrf.kia	riv.khphel	nsii...rg.	gvlfettsarc	rscs.c.Ksyp
Consensus	-----	-----	-----	-----	-----
msa209368.2{147_COH1}	lnimlletma	klklisnere	inlisqlqfi	nl.kvsknci	iklm.qgnk.
msa209368.2{147_M732}	lnimlletma	klklisnere	inlisqlqfi	nl.kvsknci	iklm.qgnk.
msa209368.2{147_M781}	lnimlletma	klklisnere	inlisqlqfi	nl.kvsknci	iklm.qgnk.
msa209368.2{147_18RS21}	aqyyitgndg	kakinlkrmg	dkfditvtih	klvegkely	yqanvateqv
msa209368.2{147_2603}	aqyyitgndg	kakinlkrmg	dkfditvtih	klvegkely	yqanvateqv
msa209368.2{147_JM9130013}	aqyyitgndg	kakinlkrmg	dkfditvtih	klvegkely	yqanvateqv
msa209368.2{147_090}	aqyyitgndg	kakinlkrmg	dkfditvtih	klvegkely	yqanvateqv
msa209368.2{147_CJB110}	aqyyitgndg	kakinlkrmg	dkfditvtih	klvegkely	yqanvateqv
msa209368.2{147_1169NT}	aqyyitgndg	kakinlkrmg	dkfditvtih	klvegkely	yqanvateqv
msa209368.2{147_H36B}	aqyyitgndg	kakinlkrmg	dkfditvtih	klvegkely	yqanvateqv
msa209368.2{147_A909}	ssilcywkrw	qs.n.sqtsg	r.i.yhsyns	.tcrrcqriv	lss.csnrts
Consensus	-----	-----	-----	-----	-----
msa209368.2{147_COH1}	ikvnlplnhk	pc.iligrk.	ffvikkhkfd	lllmlvnlvr	n.Knrwqmvi
msa209368.2{147_M732}	ikvnlplnhk	pc.iligrk.	ffvikkhkfd	lllmlvnlvr	n.Knrwqmvi
msa209368.2{147_M781}	ikvnlplnhk	pc.iligrk.	ffvikkhkfd	lllmlvnlvr	n.Knrwqmvi
msa209368.2{147_18RS21}	nkqkfalkpq	alldtnwqkv	ilrdketqvr	ftidasqfsq	klKegmangy
msa209368.2{147_2603}	nkqkfalkpq	alldtnwqkv	ilrdketqvr	ftidasqfsq	klKegmangy
msa209368.2{147_JM9130013}	nkqkfalkpq	alldtnwqkv	ilrdketqvr	ftidasqfsq	klKegmangy
msa209368.2{147_090}	nkqkfalkpq	alldtnwqkv	ilrdketqvr	ftidasqfsq	klKegmangy
msa209368.2{147_CJB110}	nkqkfalkpq	alldtnwqkv	ilrdketqvr	ftidasqfsq	klKegmangy
msa209368.2{147_1169NT}	nkqkfalkpq	alldtnwqkv	ilrdketqvr	ftidasqfsq	klKegmangy
msa209368.2{147_H36B}	nkqkfalkpq	alldtnwqkv	ilrdketqvr	ftidasqfsq	klKegmangy
msa209368.2{147_A909}	k.r.icp.tt	slary.laes	nss..rntss	iyf.f.si.s	eiKrtgdgkw
Consensus	-----	-----	-----	-----	-----
msa209368.2{147_COH1}	s.kvlyvlkk	privirs..v	flldlmvil	rtykhkhkrf	irrfkvvst
msa209368.2{147_M732}	s.kvlyvlkk	privirs..v	flldlmvil	rtykhkhkrf	irrfkvvst
msa209368.2{147_M781}	s.kvlyvlkk	privirs..v	flldlmvil	rtykhkhkrf	irrfkvvst
msa209368.2{147_18RS21}	flegfvrkke	akdsngelms	ipfvfgngdf	anlqaletpi	yktlskgsfy
msa209368.2{147_2603}	flegfvrkke	akdsngelms	ipfvfgngdf	anlqaletpi	yktlskgsfy
msa209368.2{147_JM9130013}	flegfvrkke	akdsngelms	ipfvfgngdf	anlqaletpi	yktlskgsfy
msa209368.2{147_090}	flegfvrkke	akdsngelms	ipfvfgngdf	anlqaletpi	yktlskgsfy
msa209368.2{147_CJB110}	flegfvrkke	akdsngelms	ipfvfgngdf	anlqaletpi	yktlskgsfy
msa209368.2{147_1169NT}	flegfvrkke	akdsngelms	ipfvfgngdf	anlqaletpi	yktlskgsfy
msa209368.2{147_H36B}	flegfvrkke	akdsngelms	ipfvfgngdf	anlqaletpi	yktlskgsfy
msa209368.2{147_A909}	flrrfctf.r	sqq..sgvne	ysfcrl.w.f	celtat.ntd	l.daf.r.fl
Consensus	-----	-----	-----	-----	-----

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

	801			850	
msa209368.2{147_COH1}	inqmiglikt	nwstmnglll	kattilpc.h	nqrlgamlim	skmvgs.n.h
msa209368.2{147_M732}	inqmiglikt	nwstmnglll	kattilpc.h	nqrlgamlim	skmvgs.n.h
msa209368.2{147_M781}	inqmiglikt	nwstmnglll	kattilpc.h	nqrlgamlim	skmvgs.n.h
msa209368.2{147_18RS21}	ykpnndtthkd	qleynesapf	esnnytalit	qsaswgyvdy	vknggelela
msa209368.2{147_2603}	ykpnndtthkd	qleynesapf	esnnytalit	qsaswgyvdy	vknggelela
msa209368.2{147_JM9130013}	ykpnndtthkd	qleynesapf	esnnytalit	qsaswgyvdy	vknggelela
msa209368.2{147_090}	ykpnndtthkd	qleynesapf	esnnytalit	qsaswgyvdy	vknggelela
msa209368.2{147_CJB110}	ykpnndtthkd	qleynesapf	esnnytalit	qsaswgyvdy	vknggelela
msa209368.2{147_1169NT}	ykpnndtthkd	qleynesapf	esnnytalit	qsaswgyvdy	vknggelela
msa209368.2{147_H36B}	ykpnndtthkd	qleynesapf	esnnytalit	qsaswgyvdy	vknggelela
msa209368.2{147_A909}	l.tk.yns.r	pigvq.issf	.kqglyclvn	tisvlglc.l	cqkwwgvriss
Consensus	-----	-----	-----	-----	-----
	851			900	
msa209368.2{147_COH1}	rrvqKelf.e	llrirlrikq	fifwkemqri	ihilpflqik	meigtkslpr
msa209368.2{147_M732}	rrvqKelf.e	llrirlrikq	fifwkemqri	ihilpflqik	meigtkslpr
msa209368.2{147_M781}	rrvqKelf.e	llrirlrikq	fifwkemqri	ihilpflqik	meigtkslpr
msa209368.2{147_18RS21}	pespKriilg	tfenkvedkt	ihlllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_2603}	pespKriilg	tfenkvedkt	ihlllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_JM9130013}	pespKriilg	tfenkvedkt	ihlllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_090}	pespKriilg	tfenkvedkt	ihlllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_CJB110}	pespKriilg	tfenkvedkt	ihlllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_1169NT}	pespKriilg	tfenkvedkt	ihlllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_H36B}	pespKriilg	tfenkvedkt	ihlllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_A909}	tgesKlNyfr	nf.e.g.g.n	nssfgkrcse	.sifchfsk.	rwk.g.nhsp
Consensus	-----	-----	-----	-----	-----
	901			950	
msa209368.2{147_COH1}	qls.emlrif	llkf.ikmem	lfgkvrifyhl	ivkisiisq	kvmviiivwml
msa209368.2{147_M732}	qls.emlrif	llkf.ikmem	lfgkvrifyhl	ivkisiisq	kvmviiivwml
msa209368.2{147_M781}	qls.emlrif	llkf.ikmem	lfgkvrifyhl	ivkisiisq	kvmviiivwml
msa209368.2{147_18RS21}	atflrnvkdi	saqvldqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_2603}	atflrnvkdi	saqvldqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_JM9130013}	atflrnvkdi	saqvldqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_090}	atflrnvkdi	saqvldqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_CJB110}	atflrnvkdi	saqvldqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_1169NT}	atflrnvkdi	saqvldqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_H36B}	atflrnvkdi	saqvldqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_A909}	gnflkkc.gy	fcssrsrskwk	cylak.gfti	ls.kfp..sk	ak.wslsygc
Consensus	-----	-----	-----	-----	-----
	951			1000	
msa209368.2{147_COH1}	fsgvv.irma	kl.qmvFili	ayvthq.qke	qivrsqtlkf	k.vlshqifl
msa209368.2{147_M732}	fsgvv.irma	kl.qmvFili	ayvthq.qke	qivrsqtlkf	k.vlshqifl
msa209368.2{147_M781}	fsgvv.irma	kl.qmvFili	ayvthq.qke	qivrsqtlkf	k.vlshqifl
msa209368.2{147_18RS21}	lqwsqldkdq	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstksnplp
msa209368.2{147_2603}	lqwsqldkdq	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstksnplp
msa209368.2{147_JM9130013}	lqwsqldkdq	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstksnplp
msa209368.2{147_090}	lqwsqldkdq	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstksnplp
msa209368.2{147_CJB110}	lqwsqldkdq	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstksnplp
msa209368.2{147_1169NT}	lqwsqldkdq	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstksnplp
msa209368.2{147_H36B}	lqwsqldkdq	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstksnplp
msa209368.2{147_A909}	psvewfr.gw	qscsrwFlly	sftlhtsarr	sk.sgvrl.s	ssky.vtkss
Consensus	-----	-----	-----	-----	-----
	1001			1050	
msa209368.2{147_COH1}	helslmkllie	h.a.pclrk	vmflhivyn.	fyml.Knkn	mgmrl1tiis
msa209368.2{147_M732}	helslmkllie	h.a.pclrk	vmflhivyn.	fyml.Knkn	mgmrl1tiis
msa209368.2{147_M781}	helslmkllie	h.a.pclrk	vmflhivyn.	fyml.Knkn	mgmrl1tiis
msa209368.2{147_18RS21}	sraqfdetnr	tlslampkes	syvptyrlql	vlshvvKdee	ygdetshyhf
msa209368.2{147_2603}	sraqfdetnr	tlslampkes	syvptyrlql	vlshvvKdee	ygdetshyhf
msa209368.2{147_JM9130013}	sraqfdetnr	tlslampkes	syvptyrlql	vlshvvKdee	ygdetshyhf
msa209368.2{147_090}	sraqfdetnr	tlslampkes	syvptyrlql	vlshvvKdee	ygdetshyhf
msa209368.2{147_CJB110}	sraqfdetnr	tlslampkes	syvptyrlql	vlshvvKdee	ygdetshyhf
msa209368.2{147_1169NT}	sraqfdetnr	tlslampkes	syvptyrlql	vlshvvKdee	ygdetshyhf
msa209368.2{147_H36B}	sraqfdetnr	tlslampkes	syvptyrlql	vlshvvKdee	ygdetshyhf
msa209368.2{147_A909}	ftssv..n.s	niklsha.gk	.lcsyissti	sfisccKr.r	iwr.dflplf
Consensus	-----	-----	-----	-----	-----
	1051			1100	
msa209368.2{147_COH1}	i.ikkvk.hf	lkrlr.ervr	lr.tlrp.hl	lwkiklvilq	r.nc1ts.ir
msa209368.2{147_M732}	i.ikkvk.hf	lkrlr.ervr	lr.tlrp.hl	lwkiklvilq	r.nc1ts.ir
msa209368.2{147_M781}	i.ikkvk.hf	lkrlr.ervr	lr.tlrp.hl	lwkiklvilq	r.nc1ts.ir
msa209368.2{147_18RS21}	hidqegkvtl	pktkvigese	vavdpkaltl	vvedkagnfa	tvklsdlnk
msa209368.2{147_2603}	hidqegkvtl	pktkvigese	vavdpkaltl	vvedkagnfa	tvklsdlnk
msa209368.2{147_JM9130013}	hidqegkvtl	pktkvigese	vavdpkaltl	vvedkagnfa	tvklsdlnk
msa209368.2{147_090}	hidqegkvtl	pktkvigese	vavdpkaltl	vvedkagnfa	tvklsdlnk
msa209368.2{147_CJB110}	hidqegkvtl	pktkvigese	vavdpkaltl	vvedkagnfa	tvklsdlnk
msa209368.2{147_1169NT}	hidqegkvtl	pktkvigese	vavdpkaltl	vvedkagnfa	tvklsdlnk
msa209368.2{147_H36B}	hidqegkvtl	pktkvigese	vavdpkaltl	vvedkagnfa	tvklsdlnk
msa209368.2{147_A909}	pyrsrr.sdt	s.ns.drre.	gcsrp.dldt	ccgr.sw.fr	ngkiv.ple.
Consensus	-----	-----	-----	-----	-----

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

	1101			1150
msa209368.2{147_COH1}	q.yqrkktl.	.fltvsnili	t.rKnlclfl	kkeK..tri. kk.h.lslkl
msa209368.2{147_M732}	q.yqrkktl.	.fltvsnili	t.rKnlclfl	kkeK..tri. kk.h.lslkl
msa209368.2{147_M781}	q.yqrkktl.	.fltvsnili	t.rKnlclfl	kkeK..tri. kk.h.lslkl
msa209368.2{147_18RS21}	avvsekenai	visnsfkyfd	nlkKepmfis	kkeKvvknkl eeilvvpqt
msa209368.2{147_2603}	avvsekenai	visnsfkyfd	nlkKepmfis	kkeKvvknkl eeilvvpqt
msa209368.2{147_JM9130013}	avvsekenai	visnsfkyfd	nlkKepmfis	kkeKvvknkl eeilvvpqt
msa209368.2{147_090}	avvsekenai	visnsfkyfd	nlkKesmfis	kegKvvknkl eeitlvkpqt
msa209368.2{147_CJB110}	avvsekenai	visnsfkyfd	nlkKesmfis	kegKvvknkl eeitlvkpqt
msa209368.2{147_1169NT}	avvsekenai	visnsfkyfd	nlkKepmfis	kkeKvvknkl eeilvvpqt
msa209368.2{147_H36B}	avvsekenai	visnnfkyfd	nlkKepmfis	kegKvvknkl eeialvvpqt
msa209368.2{147_A909}	gssirerkry	snf.qfqif.	.leKrtvyvf	.rrKsskqes rrnsis.aan
Consensus	-----	-----	---*-----	---*-----
	1151			1200
msa209368.2{147_COH1}	qlllnhclkk	.lngemrkss	llqtiivae.	lrsyhlnitg illti-----
msa209368.2{147_M732}	qlllnhclkk	.lngemrkss	llqtiivae.	lrsyhlnitg illti-----
msa209368.2{147_M781}	qlllnhclkk	.lngemrkss	llqtiivae.	lrsyhlnitg illti-----
msa209368.2{147_18RS21}	tvttqslske	itksgnekvl	tstnnssrv	akiispkhng dsvnhT-----
msa209368.2{147_2603}	tvttqslske	itksgnekvl	tstnnssrv	akiispkhng dsvnhTlpst
msa209368.2{147_JM9130013}	tvttqslske	itksgnekvl	tstnnssrv	akiispkhng dsvnhT-----
msa209368.2{147_090}	tvttqslske	itksgnekvl	tstnnssrv	akiispkhng dsvnhT-----
msa209368.2{147_CJB110}	tvttqslske	itksgnekvl	tstnnssrv	akiispkhng dsvnhT-----
msa209368.2{147_1169NT}	tvttqslske	itksgnekvl	tstnnssrv	akiispkhng dsvnhT-----
msa209368.2{147_H36B}	tvttqslske	itqsgnekvl	tstnnssrv	akiispkhng dsvnhT-----
msa209368.2{147_A909}	ysyysiiv.r	nnsirk.esp	hfykq...qs	s.dhit.t.r gfc.py-----
Consensus	-----	-----	-----	-----*****
	1201			1233
msa209368.2{147_COH1}	-----	-----	-----	---
msa209368.2{147_M732}	-----	-----	-----	---
msa209368.2{147_M781}	-----	-----	-----	---
msa209368.2{147_18RS21}	-----	-----	-----	---
msa209368.2{147_2603}	sdtratnglfv	gtlallsl	lylvpkktkn	nsk
msa209368.2{147_JM9130013}	-----	-----	-----	---
msa209368.2{147_090}	-----	-----	-----	---
msa209368.2{147_CJB110}	-----	-----	-----	---
msa209368.2{147_1169NT}	-----	-----	-----	---
msa209368.2{147_H36B}	-----	-----	-----	---
msa209368.2{147_A909}	-----	-----	-----	---
Consensus	*****	*****	*****	***

**Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)****SEQ ID NO. 4501****STRAIN 2603**

ATGAAAAAGATTAGAAAAAGTTTAGGACTTCTACTATGTTGCTTTTATAGGATTGGTACAA  
 TTAGCGTTTTTTTCGGTAGCCAGTGTAATGCTGATACCCCTAATCAACTAACAATCACA  
 CAGATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTATGGACTGTG  
 ACTGACAACTTAAAAGTTGATTATTGAGCCAAATGACAGATAGCGAATTGAACCAGAAG  
 TATAAGAGTATCTTGACTTCTCTACTGATACTAATGGTCAGACAAAGATAGCACTCCCA  
 AATGGTTTCGTACTTTGGTCGTCTTATAAGCTGATCAAAGCGTTTCAACAATAGTACCT  
 TTTTATATTGAATTACAGATGATAAGTTTATCAATCAATTACAGATAAATCCTAAGCGA  
 AAAGTTGAAACAGGCCGATTAAAACCTTATTAAATATACAAAAGAAGGAAAGATAAAGAAA  
 AGGCTATCCGGAGTAATTTTGTATTATACGATAACCAGAATCAGCCAGTTTCGCTTTAAA  
 AATGGACGATTACGACCGATCAAGATGGGATTACTTCATTAGTAAGTATGATAAGGGA  
 GAAATTGAGGTTGAAGGTTTATACCTGGTAAGTATATTTTCGAGAAGCAAAAGCACTA  
 ACGGTTTACCGTATATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAACACAG  
 GAAGTAGAGGTAGAAAACGAAAAGAACTCCTCCACCAACAATCCTAAACCATCACAA  
 CCGCTTTTTCGACATCTTTCTTCTAAAACAGGAATGATTATTGGTGGAGGACTGACA  
 ATTCTTGGTTGTATTATTTTGGGAATTTTGTATTCTTTTAAAGAAAACTAAAAATAGC  
 AAATCTGAAGAAACGATACAGTA

**SEQ ID NO. 4502****STRAIN 090**

GATACCCCTAATCAACTAACAATCACAC  
 AGATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTA  
 TGGACTGTGACTGACAACTTAAAAGTTGATTATTGAGCCAAATGACAGA  
 TAGCGAATTGAACCAGAGTATAAGAGTATCTTGACTTCTCTACTGATA  
 CTAATGGTCAGACAAAGATAGCACTCCCAAATGGTTTCGTACTTTGGTCGT  
 GCTTATAAAGCTGATCAAAGCGTTTCAACAATAGTACCTTTTATATTGA  
 ATTACAGATGATAAGTTTATCAATCAATTACAGATAAATCCTAAGCGAA  
 AAGTTGAAACAGGCCGATTAAAACCTTATTAAATATACAAAAGAAGGAAAG  
 ATAAAGAAAAGGCTATCAGGAGTAATTTGTATTATACGATAACAGAA  
 TCAGCCAGTTTCGCTTTAAAAATGGACGATTTCAGACCGATCAAGATGGGA  
 TTACTTCATTAGTAAGTATGATGATAAGGGAGAAATTGAGGTTGAAGGTTTA  
 TTACCTGGTAAGTATATTTTCGAGAAGCAAAAGCACTAACTGGTTACCG  
 TATATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAACACAGG  
 AAGTaGAGGTaGAAAACGAAAAGAACTCCTCCACCAACAATCCTAAA  
 CCAATCAACCG

**SEQ ID NO. 4503****STRAIN H36B**

GATACCCCTAATCAACTAACAATCACACAGA  
 TAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTATGG  
 ACTGTGACTGACAACTTAAAAGTTGATTATTGAGCCAAATGACAGATAG  
 CGAATTGAACCAGAGTATAAGAGTATCTTGACTTCTCTACTGATACTA  
 ATGGTCAGACAAAGATAGCACTCCCAAATGGTTTCGTACTTTGGTCGTGCT  
 TATAAAGCTGATCAAAGCGTTTCAACAATAGTACCTTTTATATTGAATT  
 ACCAGATGATAAGTTTATCAATCAATTACAGATAAATCCTAAGCGAAAAG  
 TTGAAAACAGGCCGATTAAAACCTTATTAAATATACAAAAGAAGGAAAGATA  
 AAGAAAAGGCTwTCCGGAGTAATTTGTATTATACGATAACAGAAATCA  
 CGCAGTTTCGCTTTAAAAATGGACGATTTCAGACCGATCAAGATGGGATTA  
 CTTTATTAGTAAGTATGATAAGGGAGAAATTGAGGTTGAAGGTTTATTA  
 CCTGGTAAGTATATTTTCGAGAAGCAAAAGCACTAACTGGTTACCGTAT  
 ATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAACACAGGAAG  
 TAGAGGTAGAAAACGAAAAGAACTCCTCCACCAACAATCCTAAACCA  
 TCACAACCGC

**SEQ ID NO. 4504****STRAIN 18RS21**

GATACCCCTAATCAACTAACAATCACACAG  
 ATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTATG  
 GACTGTGACTGACAACTTAAAAGTTGATTATTGAGCCAAATGACAGATA  
 GCGAATTGAACCAGAGTATAAGAGTATCTTGACTTCTCTACTGATACT  
 ATGGTCAGACAAAGATAGCACTCCCAAATGGTTTCGTACTTTGGTCGTGCT  
 TTATAAAGCTGATCAAAGCGTTTCAACAATAGTACCTTTTATATTGAAT  
 TACCAGATGATAAGTTTATCAATCAATTACAGATAAATCCTAAGCGAAAA  
 GTTGAAAACAGGCCGATTAAAACCTTATTAAATATACAAAAGAAGGAAAGAT  
 AAAGAAAGGCTATCCGGAGTAATTTGTATTATACGATAACAGAAATC  
 AGCCAGTTTCGCTTTAAAAATGGACGATTTCAGACCGATCAAGATGGGATT  
 ACTTCATTAGTAAGTATGATAAGGGAGAAATTGAGGTTGAAGGTTTATTA  
 ACCTGGTAAGTATATTTTCGAGAAGCAAAAGCACTAACTGGTTACCGTA  
 TATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAACACAGGAAG  
 GTAGAGGTAGAAAACGAAAAGAACTCCTCCACCAACAATCCTAAACCA  
 ATCAACACC

**SEQ ID NO. 4505****STRAIN CJB110**

GATACCCCTAATCAACTAACAATCACACA  
 GATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTAT  
 GGACTGTGACTGACAACTTAAAAGTTGATTATTGAGCCAAATGACAGAT  
 AGCGAATTGAACCAGAGTATAAGAGTATCTTGACTTCTCTACTGATACT  
 TAATGGTCAGACAAAGATAGCACTCCCAAATGGTTTCGTACTTTGGTCGTG  
 CTTATAAAGCTGATCAAAGCGTTTCAACAATAGTACCTTTTATATTGAA  
 TTACCAGATGATAAGTTTATCAATCAATTACAGATAAATCCTAAGCGAAA  
 AGTTGAAAACAGGCCGATTAAAACCTTATTAAATATACAAAAGAAGGAAAGGA



Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)

TAAAGAAAAGGCTaTCAGGAGTAATATTTGTATTATACGATAACCCAGAAAT  
 CAGCCAGTTTCGCTTTTAAAAATGGACGATTTCAGCCGATCAAGATGGGAT  
 TACTTCATTAGTAAGTATGATGATAAGGGAGAAATTTAGGTTGAAGGTTTAT  
 TACCTGGTAAGTATATTTTCGAGAAGCAAAAGCACTAACTGGTTaCCGT  
 ATATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAACACAGGA  
 AGTAGAGGTAGAAAACGAAAAAGAACTCCTCCACCAACAAATCCTAAAC  
 CATCACACC

SEQ ID NO. 4506

STRAIN 1169NT

GATACCCCTAATCAACTAACATCACACAG

ATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTATG  
 GACTGTGACTGACAACTTAAAGTTGATTTATTGAGCCAAATGACAGATA  
 GCGAATTGAACCAAGTATAAGAGTATCTTGACTTCTCCTACTGATACT  
 AATGGtCagaCAAAGATAGCACTCCCAATGGTTTCGTACTTTGGTCGTGC  
 TTATAAAGCTGATCAAGCGTTTCAACAATAGTACCTTTTATATGAAT  
 TACCAGATGATAAGTTATCAAATCAATTACAGATAAATCCTAAGCGAAAA  
 GTTGAACACAGGCCGATTAAAACTTATTAAATATACAAAGAGGAAAGAT  
 AAAGAAAAGGCTATCAGGAGTAATATTTGTATTATACGATAACCCAGAAATC  
 AGCCAGTTTCGCTTTTAAAAATGGACGATTTCAGCCGATCAAGATGGGAT  
 ACTTCATTAGTAAGTATGATGATAAGGAGAAATTTAGGTTGAAGGTTTAT  
 ACCTGGTAAGTATATTTTCGAGAAGCAAAAGCACTAACTGGTTACCGTA  
 TATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAACACAGGA  
 GTAGAGGTAGAAAACGAAAAAGAACTCCTCCACCAACAAATCCTAAACC  
 ATCACACC

PRETTY of: /biotmp/msa184750.2{\*} May 13, 2003 06:23 ..

	1		50
msa184750.2{150_090}	-----	-----	-----
msa184750.2{150_1169NT}	-----	-----	-----
msa184750.2{150_CJB110}	-----	-----	-----
msa184750.2{150_18RS21}	-----	-----	-----
msa184750.2{150_2603}	atgaaaaaga	ttagaaaaag	tttaggactt ctactatgtt gctttttagg
msa184750.2{150_H36B}	-----	-----	-----
Consensus	*****	*****	*****
	51		100
msa184750.2{150_090}	-----	-----	---GATACCC
msa184750.2{150_1169NT}	-----	-----	---GATACCC
msa184750.2{150_CJB110}	-----	-----	---GATACCC
msa184750.2{150_18RS21}	-----	-----	---GATACCC
msa184750.2{150_2603}	attggtacaa	ttagcgtttt	tttcggtagc cagtgtaaat gctGATACCC
msa184750.2{150_H36B}	-----	-----	---GATACCC
Consensus	*****	*****	*****
	101		150
msa184750.2{150_090}	CTAATCAACT	AACAATCACA	CAGATAGGAC TTCAGCCAAA TACTACAGAG
msa184750.2{150_1169NT}	CTAATCAACT	AACAATCACA	CAGATAGGAC TTCAGCCAAA TACTACAGAG
msa184750.2{150_CJB110}	CTAATCAACT	AACAATCACA	CAGATAGGAC TTCAGCCAAA TACTACAGAG
msa184750.2{150_18RS21}	CTAATCAACT	AACAATCACA	CAGATAGGAC TTCAGCCAAA TACTACAGAG
msa184750.2{150_2603}	CTAATCAACT	AACAATCACA	CAGATAGGAC TTCAGCCAAA TACTACAGAG
msa184750.2{150_H36B}	CTAATCAACT	AACAATCACA	CAGATAGGAC TTCAGCCAAA TACTACAGAG
Consensus	*****	*****	*****
	151		200
msa184750.2{150_090}	GAGGGGATTT	CTTATCGTTT	ATGGACTGTG ACTGACAACT TAAAAGTTGA
msa184750.2{150_1169NT}	GAGGGGATTT	CTTATCGTTT	ATGGACTGTG ACTGACAACT TAAAAGTTGA
msa184750.2{150_CJB110}	GAGGGGATTT	CTTATCGTTT	ATGGACTGTG ACTGACAACT TAAAAGTTGA
msa184750.2{150_18RS21}	GAGGGGATTT	CTTATCGTTT	ATGGACTGTG ACTGACAACT TAAAAGTTGA
msa184750.2{150_2603}	GAGGGGATTT	CTTATCGTTT	ATGGACTGTG ACTGACAACT TAAAAGTTGA
msa184750.2{150_H36B}	GAGGGGATTT	CTTATCGTTT	ATGGACTGTG ACTGACAACT TAAAAGTTGA
Consensus	*****	*****	*****
	201		250
msa184750.2{150_090}	TTTATTGAGC	CAAATGACAG	ATAGCGAATT GAACCAGAAG TATAAGAGTA
msa184750.2{150_1169NT}	TTTATTGAGC	CAAATGACAG	ATAGCGAATT GAACCAGAAG TATAAGAGTA
msa184750.2{150_CJB110}	TTTATTGAGC	CAAATGACAG	ATAGCGAATT GAACCAGAAG TATAAGAGTA
msa184750.2{150_18RS21}	TTTATTGAGC	CAAATGACAG	ATAGCGAATT GAACCAGAAG TATAAGAGTA
msa184750.2{150_2603}	TTTATTGAGC	CAAATGACAG	ATAGCGAATT GAACCAGAAG TATAAGAGTA
msa184750.2{150_H36B}	TTTATTGAGC	CAAATGACAG	ATAGCGAATT GAACCAGAAG TATAAGAGTA
Consensus	*****	*****	*****
	251		300
msa184750.2{150_090}	TCTTGACTTC	TCCTACTGAT	ACTAATGGTC AGACAAAGAT AGCACTCCCA
msa184750.2{150_1169NT}	TCTTGACTTC	TCCTACTGAT	ACTAATGGTC AGACAAAGAT AGCACTCCCA
msa184750.2{150_CJB110}	TCTTGACTTC	TCCTACTGAT	ACTAATGGTC AGACAAAGAT AGCACTCCCA
msa184750.2{150_18RS21}	TCTTGACTTC	TCCTACTGAT	ACTAATGGTC AGACAAAGAT AGCACTCCCA
msa184750.2{150_2603}	TCTTGACTTC	TCCTACTGAT	ACTAATGGTC AGACAAAGAT AGCACTCCCA
msa184750.2{150_H36B}	TCTTGACTTC	TCCTACTGAT	ACTAATGGTC AGACAAAGAT AGCACTCCCA
Consensus	*****	*****	*****
	301		350

Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)

msa184750.2{150_090}	AATGGTTCGT	ACTTTGGTTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
msa184750.2{150_1169NT}	AATGGTTCGT	ACTTTGGTTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
msa184750.2{150_CJB110}	AATGGTTCGT	ACTTTGGTTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
msa184750.2{150_18RS21}	AATGGTTCGT	ACTTTGGTTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
msa184750.2{150_2603}	AATGGTTCGT	ACTTTGGTTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
msa184750.2{150_H36B}	AATGGTTCGT	ACTTTGGTTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	351	400			
msa184750.2{150_1169NT}	AATAGTACCT	TTTTATATTG	AATTACCAGA	TGATAAGTTA	TCAAATCAAT
msa184750.2{150_CJB110}	AATAGTACCT	TTTTATATTG	AATTACCAGA	TGATAAGTTA	TCAAATCAAT
msa184750.2{150_18RS21}	AATAGTACCT	TTTTATATTG	AATTACCAGA	TGATAAGTTA	TCAAATCAAT
msa184750.2{150_2603}	AATAGTACCT	TTTTATATTG	AATTACCAGA	TGATAAGTTA	TCAAATCAAT
msa184750.2{150_H36B}	AATAGTACCT	TTTTATATTG	AATTACCAGA	TGATAAGTTA	TCAAATCAAT
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	401	450			
msa184750.2{150_1169NT}	TACAGATAAA	TCCTAAGCGA	AAAGTTGAAA	CAGGCCGATT	AAAACTTATT
msa184750.2{150_CJB110}	TACAGATAAA	TCCTAAGCGA	AAAGTTGAAA	CAGGCCGATT	AAAACTTATT
msa184750.2{150_18RS21}	TACAGATAAA	TCCTAAGCGA	AAAGTTGAAA	CAGGCCGATT	AAAACTTATT
msa184750.2{150_2603}	TACAGATAAA	TCCTAAGCGA	AAAGTTGAAA	CAGGCCGATT	AAAACTTATT
msa184750.2{150_H36B}	TACAGATAAA	TCCTAAGCGA	AAAGTTGAAA	CAGGCCGATT	AAAACTTATT
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	451	500			
msa184750.2{150_1169NT}	AAATATACAA	AAGAAGGAAA	GATAAAGAAA	AGGCTaTCaG	GAGTAATATT
msa184750.2{150_CJB110}	AAATATACAA	AAGAAGGAAA	GATAAAGAAA	AGGCTaTCaG	GAGTAATATT
msa184750.2{150_18RS21}	AAATATACAA	AAGAAGGAAA	GATAAAGAAA	AGGCTaTCcG	GAGTAATATT
msa184750.2{150_2603}	AAATATACAA	AAGAAGGAAA	GATAAAGAAA	AGGCTaTCcG	GAGTAATATT
msa184750.2{150_H36B}	AAATATACAA	AAGAAGGAAA	GATAAAGAAA	AGGCTwTCcG	GAGTAATATT
Consensus	*****	*****	*****	*****_--_*	*****
msa184750.2{150_090}	501	550			
msa184750.2{150_1169NT}	TGTATTATAC	GATAACCAGA	ATCAGCCAGT	TCGCTTTAAA	AATGGACGAT
msa184750.2{150_CJB110}	TGTATTATAC	GATAACCAGA	ATCAGCCAGT	TCGCTTTAAA	AATGGACGAT
msa184750.2{150_18RS21}	TGTATTATAC	GATAACCAGA	ATCAGCCAGT	TCGCTTTAAA	AATGGACGAT
msa184750.2{150_2603}	TGTATTATAC	GATAACCAGA	ATCAGCCAGT	TCGCTTTAAA	AATGGACGAT
msa184750.2{150_H36B}	TGTATTATAC	GATAACCAGA	ATCAGCCAGT	TCGCTTTAAA	AATGGACGAT
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	551	600			
msa184750.2{150_1169NT}	TTACGACCGA	TCAAGATGGG	ATTACTTCAT	TAGTAACTGA	TGATAAGGGA
msa184750.2{150_CJB110}	TTACGACCGA	TCAAGATGGG	ATTACTTCAT	TAGTAACTGA	TGATAAGGGA
msa184750.2{150_18RS21}	TTACGACCGA	TCAAGATGGG	ATTACTTCAT	TAGTAACTGA	TGATAAGGGA
msa184750.2{150_2603}	TTACGACCGA	TCAAGATGGG	ATTACTTCAT	TAGTAACTGA	TGATAAGGGA
msa184750.2{150_H36B}	TTACGACCGA	TCAAGATGGG	ATTACTTCAT	TAGTAACTGA	TGATAAGGGA
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	601	650			
msa184750.2{150_1169NT}	GAAATTGAGG	TTGAAGGTTT	ATTACCTGGT	AAGTATATTT	TTCGAGAAGC
msa184750.2{150_CJB110}	GAAATTGAGG	TTGAAGGTTT	ATTACCTGGT	AAGTATATTT	TTCGAGAAGC
msa184750.2{150_18RS21}	GAAATTGAGG	TTGAAGGTTT	ATTACCTGGT	AAGTATATTT	TTCGAGAAGC
msa184750.2{150_2603}	GAAATTGAGG	TTGAAGGTTT	ATTACCTGGT	AAGTATATTT	TTCGAGAAGC
msa184750.2{150_H36B}	GAAATTGAGG	TTGAAGGTTT	ATTACCTGGT	AAGTATATTT	TTCGAGAAGC
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	651	700			
msa184750.2{150_1169NT}	AAAAGCACTA	ACTGGTTACC	GTATATCTAT	GAAGGATGCT	GTAGTTGCTG
msa184750.2{150_CJB110}	AAAAGCACTA	ACTGGTTACC	GTATATCTAT	GAAGGATGCT	GTAGTTGCTG
msa184750.2{150_18RS21}	AAAAGCACTA	ACTGGTTACC	GTATATCTAT	GAAGGATGCT	GTAGTTGCTG
msa184750.2{150_2603}	AAAAGCACTA	ACTGGTTACC	GTATATCTAT	GAAGGATGCT	GTAGTTGCTG
msa184750.2{150_H36B}	AAAAGCACTA	ACTGGTTACC	GTATATCTAT	GAAGGATGCT	GTAGTTGCTG
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	701	750			
msa184750.2{150_1169NT}	TAGTTGCTAA	TAAAACACAG	GAAGTAGAGG	TAGAAAACGA	AAAAGAACT
msa184750.2{150_CJB110}	TAGTTGCTAA	TAAAACACAG	GAAGTAGAGG	TAGAAAACGA	AAAAGAACT
msa184750.2{150_18RS21}	TAGTTGCTAA	TAAAACACAG	GAAGTAGAGG	TAGAAAACGA	AAAAGAACT
msa184750.2{150_2603}	TAGTTGCTAA	TAAAACACAG	GAAGTAGAGG	TAGAAAACGA	AAAAGAACT
msa184750.2{150_H36B}	TAGTTGCTAA	TAAAACACAG	GAAGTAGAGG	TAGAAAACGA	AAAAGAACT
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	751	800			
msa184750.2{150_1169NT}	CCTCCACCAA	CAAATCCTAA	ACCATCACAA	CCg-----	-----
msa184750.2{150_1169NT}	CCTCCACCAA	CAAATCCTAA	ACCATCACAA	CC-----	-----

**Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)**

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msa184750.2{150_CJB110} CCTCCACCAA CAAATCCTAA ACCATCACAA CC-----
msa184750.2{150_18RS21} CCTCCACCAA CAAATCCTAA ACCATCACAA CC-----
msa184750.2{150_2603} CCTCCACCAA CAAATCCTAA ACCATCACAA CCgCtttttc cacaatcatt
msa184750.2{150_H36B} CCTCCACCAA CAAATCCTAA ACCATCACAA CCgC-----
Consensus *****

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801 850

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msa184750.2{150_090} -----
msa184750.2{150_1169NT} -----
msa184750.2{150_CJB110} -----
msa184750.2{150_18RS21} -----
msa184750.2{150_2603} tcttcctaaa acaggaatga ttattggtgg aggactgaca attccttggtt
msa184750.2{150_H36B} -----
Consensus *****

```

851 900

```

msa184750.2{150_090} -----
msa184750.2{150_1169NT} -----
msa184750.2{150_CJB110} -----
msa184750.2{150_18RS21} -----
msa184750.2{150_2603} gtattatttt gggaattttt tttatctttt taagaaaaaac taaaaatagc
msa184750.2{150_H36B} -----
Consensus *****

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901 924

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msa184750.2{150_090} -----
msa184750.2{150_1169NT} -----
msa184750.2{150_CJB110} -----
msa184750.2{150_18RS21} -----
msa184750.2{150_2603} aaatctgaaa gaaacgatac agta
msa184750.2{150_H36B} -----
Consensus *****

```

**SEQ ID NO. 4507****STRAIN 2603**

MKKIRKSLGGLLCCFLGLVQLAFFSVASVNADTPNQLTITQIGLQPNTEEGISYRLWTV  
 TDNLKVDLLSQMTDSELNQKYKSILTSPTDTNGQTKIALPNGSYFGRAYKADQSVSTIVP  
 FYIELPDDKLSNQLQINPKRKVETGRLKLIK YTKEGKIKKRLSGVIFVLVDNQNPQVRFK  
 NGRFTTDDGITSVLVTDKGEIEVEGLLPKYIFREAKALTGYRISMKDAVVAVVANKTQ  
 EVEVEKEKETPPPTNPKPSQPLFPQSFLPKTGMIGGGLTILGCI ILGILFIFLRKTKNS  
 KSERNDTV

**SEQ ID NO. 4508****STRAIN 090**

DTPNQLTITQIGLQPNTEEGISYRLWTVTDNLKVDLLSQMTDSELNQKYKSILTSPTDT  
 NGQTKIALPNGSYFGRAYKADQSVSTIVPFYIELPDDKLSNQLQINPKRKVETGRLKLIK  
 YTKEGKIKKRLSGVIFVLVDNQNPQVRFKNGRFTTDDGITSVLVTDKGEIEVEGLLPKG  
 YIFREAKALTGYRISMKDAVVAVVANKTQEVENEKETPPPTNPKPSQ

**SEQ ID NO. 4509****STRAIN H36B**

DTPNQLTITQIGLQPNTEEGISYRLWTVTDNLKVDLLSQMTDSELNQKYKSILTSPTDT  
 NGQTKIALPNGSYFGRAYKADQSVSTIVPFYIELPDDKLSNQLQINPKRKVETGRLKLIK  
 YTKEGKIKKRLSGVIFVLVDNQNPQVRFKNGRFTTDDGITSVLVTDKGEIEVEGLLPKG  
 YIFREAKALTGYRISMKDAVVAVVANKTQEVENEKETPPPTNPKPSQ

**SEQ ID NO. 4510****STRAIN 18RS21**

DTPNQLTITQIGLQPNTEEGISYRLWTVTDNLKVDLLSQMTDSELNQKYKSILTSPTDT  
 NGQTKIALPNGSYFGRAYKADQSVSTIVPFYIELPDDKLSNQLQINPKRKVETGRLKLIK  
 YTKEGKIKKRLSGVIFVLVDNQNPQVRFKNGRFTTDDGITSVLVTDKGEIEVEGLLPKG  
 YIFREAKALTGYRISMKDAVVAVVANKTQEVENEKETPPPTNPKPSQ

**SEQ ID NO. 4511****STRAIN 1169NT**

DTPNQLTITQIGLQPNTEEGISYRLWTVTDNLKVDLLSQMTDSELNQKYKSILTSPTDT  
 NGQTKIALPNGSYFGRAYKADQSVSTIVPFYIELPDDKLSNQLQINPKRKVETGRLKLIK  
 YTKEGKIKKRLSGVIFVLVDNQNPQVRFKNGRFTTDDGITSVLVTDKGEIEVEGLLPKG  
 YIFREAKALTGYRISMKDAVVAVVANKTQEVENEKETPPPTNPKPSQ

PRETTY of: /biotmp/msa184868.2{\*} May 13, 2003 06:25 ..

```

msa184868.2{150_090} 1 ----- 50
msa184868.2{150_2603} mkkirkslgl llccflglvq laffsvasvn -DTPNQLTIT QIGLQPNTE
msa184868.2{150_H36B} ----- -DTPNQLTIT QIGLQPNTE
msa184868.2{150_1169NT} ----- -DTPNQLTIT QIGLQPNTE
msa184868.2{150_18RS21} ----- -DTPNQLTIT QIGLQPNTE
Consensus *****

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51 100

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msa184868.2{150_090} EGISYRLWTV TDNLKVDLLS QMTDSELNQK YKSILTSPTD TNGQTKIALP

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**Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)**

```

msa184868.2{150_2603} EGISYRLWTV TDNLKVDLLS QMTDSELNQK YKSILTSPTD TNGQTKIALP
msa184868.2{150_H36B} EGISYRLWTV TDNLKVDLLS QMTDSELNQK YKSILTSPTD TNGQTKIALP
msa184868.2{150_1169NT} EGISYRLWTV TDNLKVDLLS QMTDSELNQK YKSILTSPTD TNGQTKIALP
msa184868.2{150_18RS21} EGISYRLWTV TDNLKVDLLS QMTDSELNQK YKSILTSPTD TNGQTKIALP
Consensus *****

101
msa184868.2{150_090} NGSYFGRAYK ADQSVSTIVP FYIELPDDKL SNQLQINPKR KVGTRGLKLI
msa184868.2{150_2603} NGSYFGRAYK ADQSVSTIVP FYIELPDDKL SNQLQINPKR KVGTRGLKLI
msa184868.2{150_H36B} NGSYFGRAYK ADQSVSTIVP FYIELPDDKL SNQLQINPKR KVGTRGLKLI
msa184868.2{150_1169NT} NGSYFGRAYK ADQSVSTIVP FYIELPDDKL SNQLQINPKR KVGTRGLKLI
msa184868.2{150_18RS21} NGSYFGRAYK ADQSVSTIVP FYIELPDDKL SNQLQINPKR KVGTRGLKLI
Consensus *****

151
msa184868.2{150_090} KYTKEGKIKK RLSGVIFVLY DNQNPVRFK NGRFTTDQDG ITSLVTDDKG
msa184868.2{150_2603} KYTKEGKIKK RLSGVIFVLY DNQNPVRFK NGRFTTDQDG ITSLVTDDKG
msa184868.2{150_H36B} KYTKEGKIKK RLSGVIFVLY DNQNPVRFK NGRFTTDQDG ITSLVTDDKG
msa184868.2{150_1169NT} KYTKEGKIKK RLSGVIFVLY DNQNPVRFK NGRFTTDQDG ITSLVTDDKG
msa184868.2{150_18RS21} KYTKEGKIKK RLSGVIFVLY DNQNPVRFK NGRFTTDQDG ITSLVTDDKG
Consensus *****

201
msa184868.2{150_090} EIEVEGLLPG KYIFREAKAL TGYRISMKDA VVAVVANKTQ EVEVENEKET
msa184868.2{150_2603} EIEVEGLLPG KYIFREAKAL TGYRISMKDA VVAVVANKTQ EVEVENEKET
msa184868.2{150_H36B} EIEVEGLLPG KYIFREAKAL TGYRISMKDA VVAVVANKTQ EVEVENEKET
msa184868.2{150_1169NT} EIEVEGLLPG KYIFREAKAL TGYRISMKDA VVAVVANKTQ EVEVENEKET
msa184868.2{150_18RS21} EIEVEGLLPG KYIFREAKAL TGYRISMKDA VVAVVANKTQ EVEVENEKET
Consensus *****

251
msa184868.2{150_090} PPPTNPKPSQ p-----
msa184868.2{150_2603} PPPTNPKPSQ plfpqsfllpk tgmigggt ilgciilgil fiflrktkns
msa184868.2{150_H36B} PPPTNPKPSQ p-----
msa184868.2{150_1169NT} PPPTNPKPSQ -----
msa184868.2{150_18RS21} PPPTNPKPSQ -----
Consensus *****

301
msa184868.2{150_090} -----
msa184868.2{150_2603} kserndtv
msa184868.2{150_H36B} -----
msa184868.2{150_1169NT} -----
msa184868.2{150_18RS21} -----
Consensus *****

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**Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)**

SEQ ID NO. 4601

STRAIN A909

TGACAAATATTTTACCCAACGTTGGTTTAGAGCAAGCAGGTGTAACATATTTACCTTT  
 CTCACCGAATAATATCAGTGAGGATTTAGAGATTATTGCGAGAAATGCTTTTCGTCCAGA  
 TAACATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTATCATTTTAAACGATATCATGA  
 ATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGTGTAGCTGGGGCAGATGGAAA  
 AACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAATATTACAGACACTTCTTTTCCT  
 AATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAATTACTTTGTGTTTGAAGCTGA  
 TGAATACGAACGTCATTTTATGCCGTACCATCCAGAATACTCAATTATTACCAATATTGA  
 TTTTGACCATCCTGATTATTTACAGGCCATAGAGGACGTATTTCAATGCCTTTAATGACTA  
 TGCTAAGCAAGTTCAAAAAGGTTTATTCATTTTGGAGAAGATCCAAAACCTTCATGAAAT  
 CACTTCTGAGGCACCAATATATTATTGGTTTGAAGATTCAAATGATTTTATAGCAAA  
 AGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGTTTCTATAACCAAGAAAGAAAT  
 TGGTCAGTTTTCATGTACCGATACGGTAAACATAATATCTTAAATGCAACTGCTGTTAT  
 TGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTAGCTGAGCATTGGAAGACATT  
 TTCAGGGGTAAAGCGTCGTTTACTGAGAAGATTATTGACGATACTGTCTATTATGATGA  
 CTTTGGCTCACCATCCTACTGAGATTATTGCGACATTAGATGCTGCTCGACAAAAATACCC  
 GTCAAAAGAAATTTAGCTAATTTTCCAACCGCATACGTTCACTCGTACGATAGCTCTTTT  
 AGACGAATTTGCCCATGCTTGGAGTCAAGCGGATAGCGTTTATCTCGCTCAAAATATATGG  
 TTCTGTCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGAAGATTAGCTGCTAAGATTGT  
 CAAACACTCAGATTAGTGACAGTCGAAAATGTCTCGCCTTTACTCAATCATGATAATGC  
 TGTCTATGTCCTTATGGGTGCTGGAGACATTCAAATGTATGAGCGCTCTTTTGAAGAATT  
 ATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4602

STRAIN 1169NT

AAAAGCAGGCTCTAGTGACGTTGACAAATATTATTTTACCCAACGTTGGTTTAGAGCAAGC  
 AGGTGTAACATATATTTACCTTTCTCACCAGAATAATATCAGTGAGGATTTAGAGATTATTGC  
 AGGAAATGCTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTA  
 TCATTTTAAACGATATCATGAATTTCTCGGAGATTATTATGCGTCAGTTCACTAGTCTAGG  
 TGTAGCTGGGGCAGATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAA  
 TATTACAGACACTTCTTTTCCCTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAA  
 TTACTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATA  
 CTCAAATTATACCAANTATGATTTTGACCATCCTGATTATTTTACAGGCCATAGAGGACGT  
 ATTCAATGCCCTTAAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCATTTATGGAGA  
 AGATCCAAAACCTTCATGAATTCACCTTCTGAGGCACCAATATATTATTATGGTTTGAAGA  
 TTCAAATGATTTTATAGCAAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGT  
 TTTCTATAACCAAGAAAGAAATTTGGTCAGTTTTCATGTACCGATACGGTAAACATAATAT  
 CTTAAATGCAACTGCTGTTTATGCTAACCCTTTACATAATGGGAATTGATATGGCATTAGT  
 AGCTGAGCATTTGAAGACATTTTTCAGGGGTAAAGCGTCGTTTACTGAGAAGATTATTGA  
 CGATACTGTCTATTATGATGACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGA  
 TGCTGCTCGACAAAAATACCCGTCAAAAGAAATTTAGCTAATTTTCCAACCGCATACGTT  
 CACTCGTACGATAGCTCTTTTACAGCAATTTGCCATGCCCTTGGTCAAGCGGATAGCGT  
 TTATCTCGCTCAAAATATGATGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGA  
 AGATTAGCTGCTAAGATTGTCAAACTCAGATTAGTGACAGTCGAAAATGTCTCGCC  
 TTACTCAATCATGATAATGCTGTCTATGTCCTTATGGGTGCTGGAGACATTCAAATGTA  
 TGAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4603

STRAIN 090

AAAGCAGGCTCTAGTGACGTTGACAAATATTATTTTACCCAACGTTGGTTTAGAGCAAGCA  
 GGTGTAACATATATTTACCTTTCTCACCAGAATAATATCAGTGAGGATTTAGAGATTATTGCA  
 GGAAATGCTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTAT  
 CATTTTAAACGATATCATGAATTTCTCGGAGATTATTATGCGTCAGTTCACTAGTCTAGGT  
 GTAGCTGGGGCAGATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAA  
 ATTACAGACACTTCTTTTCCCTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAAT  
 TACTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATA  
 TCAATTATTACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCCATAGAGGACGTA  
 TTCATGCTTTTAAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCATTTATGGAGAA  
 GATTCAAAACCTTCATGAAATCACCTCTAAGGCACCAATATATTATTATGGTTTGAAGAT  
 TCAATGATTTTATAGCAAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGT  
 TTCTATAACCAAGAAAGAAATTTGGTCAGTTTTCATGTACCGATACGGTAAACATAATAT  
 TTAATGCAACTGCTGTTTATGCTAACCCTTTACATAATGGGAATTGATATGGCATTAGTA  
 GCTGAGCATTTGAAGACATTTTTCAGGGGTAAACGTCGTTTACTGAGAAGATTATTGAC  
 GATACTGTCTATTATGATGACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGAT  
 GCTGCTCGACAAAAATACCCGTCAAAAGAAATTTAGCTAATTTTCCAACCGCATACGTT  
 ACTCGTACGATAGCTCTTTTACAGCATTTTGCCCATGCTTTGAGTCAAGCGGATAGCGTT  
 TATCTTGTCTCAAAATATGCTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGAA  
 GATTAGCTGCTAAGATTGTCAAACTCAGATTAGTGACAGTCGAAAATGTCTCGCCT  
 TTACTCAATCATGATAATGCTGTCTATGTCCTTATGGGTGCTGGAGACATTCAAATGTA  
 GAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4604

STRAIN H36B

AAAAGCAGGCTCTAGTGACGTTGACAAATATTATTTTACTCAACGTTGGTTTAGAGCAAGCAGGT  
 ATAACATATATTTACCTTTCTCACCAGAATAATATCAGTGAGGATTTAGAGATTATTGCAAGGA  
 AATGCTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTATCAT  
 TTTAAACGATATCATGAATTTCTCGGAGATTATTATGCGTCAGTTCACTAGTCTAGGTGTA  
 GCTGGGGCAGATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAATATT  
 ACAGACACTTCTTTTCCCTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAATTAC  
 TTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATACTCA  
 ATTATTACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCCATAGAGGACGTATTC  
 AATGCTTTTAAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCATTTATGGAGAAGAT

**Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)**

CCAAAACCTTCATGAAATCACTTCTGAGGCACCAATATATTATTATGGTTTGAAGATTCA  
AATGATTTTATAGCAAAAGATATCACTCGAACTGTTAATGGTTCTGACTTTAAGGTTTC  
TATAACCAAGAAGAAATTGGTCAGTTTACGTAACCATACGATACGGTAAACATAATATCTTA  
AATGCAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTAGCT  
GAGCAITTTGAAGACATTTTCAGGGGTAACCGTTCGTTTACTGAGAAAATTATTGACGAT  
ACTGTCAITTTATGATGACTTTTGTCTACCATCTTACTGAGATTATTGCGCATTAGATGCT  
GCTCGACAAAATACCCGTCAAAGAAATTTAGCTATTTTCCAACCGCATACGTTCACT  
CGTACGATAGCTCTTTTAGACGAATTTGCCCATGCCTTGAGTCAAGCGGATAGCGTTTAT  
CTCGCTCAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGAAGAT  
TTAGCTGCTAAGATTGTCAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCCTTTA  
CTCAATCATGATAATGCTGTCTATGCTTTATGGGTGCTGGAGACATTCAATTGTATGAG  
CGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4605

STRAIN 18RS21

AAAGCAGGCTCTAGTGACGTTGACAAATATTTTACCACCGTGGTTTAGAGCAAGCA  
GGTGTAACCTATATACCTTTCTCACCGAATAATATCAGTGAGGATTAGAGATTATTGCA  
GGAAATGCTTTTCGTCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTAT  
CATTTTAAACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGT  
GTAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAAT  
ATTACAGACACTTCTTTCTAATGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAAT  
TACTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATA  
TCAATTATTACCAATATTGATTTTGACCATCTGATTATTTTACAGGCTTAGAGGACGTA  
TTCAATGCTTTTAAATGACTATGCTAAGCAAGTTCAAAGAGTTTATTCAATTATGGAGAA  
GATCCAAAACCTTCATGAATCACTTCTGAGGCACCAATATATTTATGGTTTGAAGAT  
TCAAATGATTTTATAGCAAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGTT  
TTCTATAACCAAGAAGAAATTGGTCAGTTTTCATGTACAGCATACGGTAAACATAATATC  
TTAAATGCAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTA  
GCTGAGCAITTTGAAGACGTTTTCAGGGGTAAAGCGTCGTTTACTGAGAAGATTATTGAC  
GATACGTGCTATTATTTAGTACGTTTGTCTCACCATCCTACTGAGATTATTGCGCATTAGAT  
GCTGCTCGACAAAATACCCGTCAAAGAAATTTAGTAGCTATTTTCCAACCGCATACGTTT  
ACTCGTACGATAGCTCTTTTAGACGAATTTGCCCATGCCTTGAGTCAAGCGGATAGCGTT  
TATCTCGCTCAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGA  
AGTTTATAGCTGCTAAGATTGTCAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCCT  
TTACTCAATCATGATAATGCTGTCTATGCTTTTATGGGTGCTGGAGACATTCAATTGTAT  
GAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4606

STRAIN M732

AAAAGCAGGCTCTAGTGACGTTGACAAATATTTTACCACCGTGGTTTAGAGCAAGCAG  
GTGTAACCTATATACCTTTCTCACCGAATAATATCAGTGAGGATTAGAGATTATTGCA  
GAAATGCTTTTCGTCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTATC  
ATTTTAAACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGT  
TAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAATA  
TTACAGACACTTCTTTCTAATGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAAT  
ACTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATACT  
CAATTATTACCAATATTGATTTTGACCATCTGATTATTTTACAGGCTTAGAGGACGTTAT  
TCAATGCTTTTAAATGACTATGCTAAGCAAGTTCAAAGAGTTTATTCAATTATGGAGAA  
ATCCAAAACCTTCATGAATCACTTCTGAGGCACCAATATATTTATGGTTTGAAGAT  
CAAATGATTTTATAGCAAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGTT  
TTCTATAACCAAGAAGAAATTGGTCAGTTTTCATGTACAGCATACGGTAAACATAATATCT  
TAAATGCAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTAG  
CTGAGCAITTTGAAGACATTTTCAGGGGTAAAGCGTCGTTTACTGAGAAGATTATTGACG  
ATACGTGCTATTATTTAGTACGTTTGTCTCACCATCCTACTGAGATTATTGCGCATTAGATG  
CTGCTCGACAAAATACCCGTCAAAGAAATTTAGTAGCTATTTTCCAACCGCATACGTTTCA  
CTCGTACGATAGCTCTTTTAGACGAATTTGCCCATGCCTTGAGTCAAGCGGATAGCGTTT  
ATCTCGCTCAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGA  
AGTTTATAGCTGCTAAGATTGTCAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCCT  
TACTCAATCATGATAATGCTGTCTATGCTTTTATGGGTGCTGGAGACATTCAATTGTATG  
AGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4607

STRAIN M781

AAAGCAGGCTCTAGTGACGTTGACAAATATTTTACCACCGTGGTTTAGAGCAAGCAG  
GTGTAACCTATATACCTTTCTCACCGAATAATATCAGTGAGGATTAGAGATTATTGCA  
GAAATGCTTTTCGTCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTATC  
ATTTTAAACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGT  
GTAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAA  
TATTACAGACACTTCTTTCTAATGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAA  
TTACTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATA  
TCAATTATTACCAATATTGATTTTGACCATCTGATTATTTTACAGGCTTAGAGGACGT  
ATTCAATGCTTTTAAATGACTATGCTAAGCAAGTTCAAAGAGTTTATTCAATTATGGAGA  
AGATCCAAAACCTTCATGAATCACTTCTGAGGCACCAATATATTTATGGTTTGAAGA  
TTCAAATGATTTTATAGCAAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGT  
TTTCTATAACCAAGAAGAAATTGGTCAGTTTTCATGTACAGCATACGGTAAACATAATAT  
CTTAAATGCAACTGCTGTTTATGCTAACCTTTACATAATGGGAATTGATATGGCATTAGT  
AGCTGAGCAITTTGAAGACATTTTCAGGGGTAAAGCGTCGTTTACTGAGAAGATTATTGA  
CGATACTGTCAATATTAGTACGTTTGTCTCACCATCCTACTGAGATTATTGCGACATTAGA  
TGCTGCTCGACAAAATACCCGTCAAAGAAATTTAGTAGCTATTTTCCAACCGCATACGTT  
CACTCGTACGATAGCTCTTTTAGACGAATTTGCCCATGCCTTGAGTCAAGCGGATAGCGT  
TTATCTCGCTCAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGA  
AGATTAGCTGCTAAGATTGTCAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCC  
TTTACTCAATCATGATAATGCTGTCTATGCTTTTATGGGTGCTGGAGACATTCAATTGTAT

**Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)**

TGAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4608

STRAIN CJB110

AAAAAGCAGGCTCTAGTGACGTTGACAAATATATTTTACCCAACGTGGTTAGAGCAAGCA  
 GGTGTAACATAATACCTTTCTCACCAGAAATATATCAGTGAGGATTTAGAGATTATTGCA  
 GGAAATGCTTTTCTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTAT  
 CATTTTAAACGATATCATGAATTTCTCGGAGATTTATGCGTCAGTTCACTAGTCTAGGT  
 GTAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAAT  
 ATTACAGACACTTCTTTCTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAAT  
 TACTTTGTGTTGAAGCTGATGAATACGACGTCATTTTATGCCGTACCATCCAGAATAC  
 TCAATTATTACCAATATGATTGTTGACCATCCTGATTATTTTACAGGCCCTAGAGGACGTA  
 TTCAATGCTTTAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCAATTATGGAGAA  
 GATTCAAACTTTCATGAATCACTTCTAAGGCACCAATATATATTATGTTTGAAGAT  
 TCAAATGATTTTATAGCAAAAGACATCACTCGAAGCTTAAATGGTTCTGACTTTAAGGTT  
 TTCTATAACCAAGAGAAATGGTCAAGTTTTCATGTACAGCATACGGTAAACATAATATC  
 TTAATATCAACTGCTGTTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTA  
 GCTGAGGATTTGAAGACATTTTCAAGGGTAAAACGTCGTTTACTGAGAAGATTATTGAC  
 GATACTGTCAATTATGATGACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGAT  
 GCTGCTCGACAAAAATACCCGTCAAAAGAAATTGTAGCTATTTTCAACCCGCATACGTTT  
 ACTCGTACGATAGCTCTTTTAGACGATTTTGCCCATGCTTTGAGTCAAGCGGATAGCGTT  
 TATCTTGCTCAAAATATGTTGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGAA  
 GATTAGCTGCTAAGATTGTTCAAACTCAGATTAGTGACAGTCGAAAAATGTCGCGCT  
 TTACTCAATCATGATAATGCTGCTATGTCCTTATGGGTGCTGGAGACATTCAATTGTAT  
 GAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4609

STRAIN JM9130013 (reverse complement)

GTTCAAAAAGCAGGCTCTAGTGACGTTGACAAATATTTTACTCAACGTGGTTTGA  
 GCAAGCAGGTATACCTATATTAACCTTTCTCACCAGAAATATCAGTGAGGATTTAGAGAT  
 TATGTCAGGAAATGCTTTTCCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAA  
 GGGCTATCATTTTAAACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAG  
 TCTAGGTGATAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTT  
 AAAAAATATTACAGACACTTCTTTCTAATTGGAGATGGTACAGGACGTGGTTCTGCTAA  
 TGCTAATTACTTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCC  
 AGAATACCTCAATATATTACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCCCTAGA  
 GGAGCTATTCAATGCTTTTAAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCAATT  
 TGGAGAAGATCCAAACITTCATGAATCACTTCTGAGGCACCAATATATATTATGTTT  
 TGAAGATTCAATGATTTTATAGCAAAAGATATCACTCGAAGCTTAAATGGTTCTGACTT  
 TAAGGTTTCTTATAACCAAGAGAAATTTGGTCAGTTTCAAGTACAGCATACGGTAAACA  
 TAATATCTTAAATGCAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGC  
 ATTAGTAGCTCAGCATTTGAAGACATTTTCAAGGGTAAAACGTCGTTTACTGAGAAAT  
 TATTGACGATACCTGCTATTATTGATGACTTTGCTCACCATCCTACTGAGATTATTGCGAC  
 ATTAGATGCTGCTCGACAAAAATACCCGTCAAAAGAAATTGTAGCTATTTTCCAACCGCA  
 TACGTTCACTCGTACGATAGCTCTTTTAGACGAATTTGCCCATGCGTTGAGTCAAGCGGA  
 TAGCGTTTATCTCGCTCAAAATATGTTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAA  
 GGTAGAAGATTATAGCTGCTTAAGATTGTCAAACTCAGATTATTAGTGACAGTCGAAAAATG  
 CTCGCTTTACTCAATCATGATAATGCTGCTATGTCCTTATGGGTGCTGGAGACATTCA  
 ATTGTATGAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4610

STRAIN COH1 reverse complement

CAGGCTCTAGTGACGTTGACAAATATTTTACCCAACGTGGTTAGAGCAAGCAGGTGTAA  
 CTATATTACCTTTCTCACCAGAAATATATCAGTGAGGATTTAGAGATTATTGTCAGGAAATG  
 CTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTCATTTTAA  
 AACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGTGTAGCTG  
 GGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAATATTACAG  
 ACACCTCTTTCTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAATTACTTTG  
 TGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATACTCAATTA  
 TTACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCCCTAGAGGACGTAATCAATG  
 CCTTAAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCAATTATGGAGAAGATCCAA  
 AACITTCATGAATCACTTCTGAGGCACCAATATATATTATGTTTGAAGATTCAATG  
 ATTTTATAGCAAAAGACATCACTCGAAGCTTAAATGGTTCTGACTTTAAGGTTTCTATA  
 ACCAAGAAGAAATTTGGTCAGTTTTCATGTACAGCATACGGTAAACATAATATCTTAAATG  
 CAACTGCTGTTTATGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTAGCTGAGC  
 ATTTGAAGACATTTTCAAGGGTAAAACGTCGTTTACTGAGAAGATTATTGACGATACTG  
 TCATTATTGATGACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGATGCTGCTC  
 GACAAAAATACCCGTCAAAAGAAATTTAGCTATTTTCCAACCGCATACGTTCACTCGTA  
 CGATAGCTCTTTTAGACGAATTTGCCCATGCTTTGAGTCAAGCGGATAGCGTTTATCTCG  
 CTCAAATATATTGTTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGAAGATTG  
 CTGCTAAGATTGTCAAACTCAGATTATTAGTGACAGTCGAAAAATGTCGCGCTTTACTCA  
 ATCATGATAATGCTGCTATGTCCTTATGGGTGCTGGAGACATTCAATTGTATGAGCGCT  
 CTTTGAAGAATTAATAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4611

STRAIN 2603

atgtcaaaaacttatcattttattgggtattaaaggatccggaatgagtgccctagcactg  
 atgcttcacatacaaatgggacataacgtccaaggaagtgcggttgacaaatattattttacc  
 caacgtgggttagaggaagcaggtgtaactatattacctttctcaccgaataatcagc  
 gaggatttagagattattgcaggaatgcttttctgctccagataacaatgaagagttggct  
 tatgttattgaaagggtatcaattttaaagcagatacaggaatttctcgagagatttatg  
 cgtcagttcaactagtcaggtgtagctggggcacatggaaaaacctcaacgacaggttta  
 ttagctcatgttttaaaaaatattacagacacttctttcctaattggagatgggtacagga

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

cgtgggtctgctaattgctaattactttgtgtttgaagctgatgaatacgaacgtcatttt  
 atgccgtaccatccagaataactcaattattaccaatattgattttgaccatcctgattat  
 tttacaggcttagaggacgtattcaatgcctttaatgactatgctaagcaagttcaaaaa  
 ggtttattcatttatggagaagatccaaaacttcatgaaatcacttctgaggcaccaata  
 tattattatgggttttgaagattcaaatgattttatagcaaaagacatcactcgaactgtt  
 aatgggtctgacttttaagggtttctataaccaagaagaatttggtcagtttcatgtacca  
 gcatacggtaaaacataatattcttaaatgcaactgctgtttatgctaaccctttacataatg  
 ggaatttgatattggcatttagtagctgagcatttgaagacgttttcaggggtaagcgtcgt  
 ttactgagaagattattgacgatactgtcattattgatgactttgctcaccatcctact  
 gagattattgcgacatttagatgctgctcgacaaaaataccggtcaaaagaattttagct  
 attttccaacccgatacgttcaactcgtacgtagctcttttagacgaatttgcccatgcc  
 ttgagtcaagcgatagcgtttatctcgctcaaatatattggttctgctagagaagtagat  
 aatgggtgaggtgaaggtagaagatttagctgctaagattgtcacaactcagatttagtg  
 acagtcgaaaaatgtctcgcttactcaatcatgataatgctgtctatgtctttatgggt  
 gctggagacattcaattgtatgagcgtcttttgaagaattatttagtaacctaaactaaa  
 aatacacia

SEQ ID NO. 4612

STRAIN COH1 reverse complement

CAGGCTCTAGTGACGTTGACAAATATATTTTACCCCAACGTGGTATTAGAGCAAGCAGGTGTAA  
 CTATATTACTCTTTCTCACCGAATAATATCAGTGAGGATTATGAGATTATGCAGGAAATG  
 CTTTTCGTCAGATAACAAATGAAGATTGGCTTATGTTATTGAAAAGGCTATCATTTTA  
 AACGATATCATGAATTTCTCGGAGATTTATGCGTCAGTTCACTAGTCTAGGTGTAGCTG  
 GGGACATGGAAAAACCTCAACGACAGGTTTATAGCTCATGTTTAAAAAATATACAG  
 ACACCTCTTTCTTAATTGGAGATGGTACAGGACGTGGTCTGCTAATGCTAATTACTTTG  
 TGTTTGAAGCTGATGAATACGACGTCAATTTATGCGGTACCATCCAGAATACTCAATTA  
 TTACAATATTGATTTTGACCATCTGATTATTTACAGGCTTAGAGGACGTATTCAATG  
 CCTTTAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCATTTATGGAGAAGATCCAA  
 AACCTCATGAAATCACTTCTGAGGCACCAATATATTTATTTGTTTGAAGATTCAAATG  
 ATTTTATAGCAAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGTTTCTATA  
 ACCAAGAAGAAATTTGGTCAGTTTATGTAACGACATACGGTAACATAATATCTTAAATG  
 CACTGCTGTTTATGCTAACCCTTTACATAATGGGAATTGATATGGCATTAGTAGCTGAGC  
 ATTTGAAGACATTTTCAGGGGTAAGCGTCTGTTTACTGAGAAGATTATTGACGACTACTG  
 TCATTTATGATGACTTTGCTCACCATCTACTGAGATTATTGCGACATTAGATGCTGCTC  
 GACAAAAATACCCGTCAAAAGAAATTTGTAGCTATTTTCCAACCGCATACGTTCACTCGTA  
 CGATAGCTCTTTTAGACGAATTTGCCCATGCTTGAAGTCAAGCGGATAGCGTTTATCTCG  
 CTCAAATATATGTTTCTAGAGAAGTAGATAATGGTGAGGTGAAGTGAAGAAGATTTCAG  
 CTGCTAAGATTGTCAAACACTCAGATTATTAGTGACAGTCAAAAAATGCTCTCGCTTTACTCA  
 ATCATGATAATGCTGTCTATGCTCTTTATGGGTGCTGGAGACATTCAATTGTATGAGCGCT  
 CTTTGAAGAATTTATTAGCTAACCTAACCTAAAAATACACAA

PRETTY of: /biotmp/msa56524.2{\*} November 26, 2002 08:06 ..  
 PRETTY of: /biotmp/msa253045.2{\*} January 31, 2003 03:51 ..

	1				50
msa253045.2{157_090}	-----	-----	-----	-----	-----
msa253045.2{157_CJB110}	-----	-----	-----	-----	-----
msa253045.2{157_H36B}	-----	-----	-----	-----	-----
msa253045.2{157_JM9130013}	-----	-----	-----	-----	-----
msa253045.2{157_1169NT}	-----	-----	-----	-----	-----
msa253045.2{157_A909}	-----	-----	-----	-----	-----
msa253045.2{157_COH1}	-----	-----	-----	-----	-----
msa253045.2{157_M732}	-----	-----	-----	-----	-----
msa253045.2{157_M781}	-----	-----	-----	-----	-----
msa253045.2{157_18RS21}	-----	-----	-----	-----	-----
msa253045.2{157_2603}	atgtcaaaaa	cttatcattt	tattgggatt	aaaggatccg	gaatgagtcg
Consensus	*****	*****	*****	*****	*****
	51				100
msa253045.2{157_090}	-----	-----	-----	-aaagcaggc	tctagtgcg
msa253045.2{157_CJB110}	-----	-----	-----	-Aaaaagcaggc	tctagtgcg
msa253045.2{157_H36B}	-----	-----	-----	-Aaaaagcaggc	tctagtgcg
msa253045.2{157_JM9130013}	-----	-----	-----	-GttcaAaaaagcaggc	tctagtgcg
msa253045.2{157_1169NT}	-----	-----	-----	-Aaaaagcaggc	tctagtgcg
msa253045.2{157_A909}	-----	-----	-----	-----	-----
msa253045.2{157_COH1}	-----	-----	-----	-----caggc	tctagtgcg
msa253045.2{157_M732}	-----	-----	-----	-Aaaaagcaggc	tctagtgcg
msa253045.2{157_M781}	-----	-----	-----	-aaagcaggc	tctagtgcg
msa253045.2{157_18RS21}	-----	-----	-----	-aaagcaggc	tctagtgcg
msa253045.2{157_2603}	cctagcactg	atgcttcac	aaatGggacA	taacgtccaa	ggaagtgcg
Consensus	*****	*****	*****	*****	*****
	101				150
msa253045.2{157_090}	tTGACAAATA	TTATTTTACc	CAACGTGGTT	TAGAGCAAGC	AGGTgTAACT
msa253045.2{157_CJB110}	tTGACAAATA	TTATTTTACc	CAACGTGGTT	TAGAGCAAGC	AGGTgTAACT
msa253045.2{157_H36B}	tTGACAAATA	TTATTTTACt	CAACGTGGTT	TAGAGCAAGC	AGGTaTAACT
msa253045.2{157_JM9130013}	tTGACAAATA	TTATTTTACt	CAACGTGGTT	TAGAGCAAGC	AGGTaTAACT
msa253045.2{157_1169NT}	tTGACAAATA	TTATTTTACc	CAACGTGGTT	TAGAGCAAGC	AGGTgTAACT
msa253045.2{157_A909}	-TGACAAATA	TTATTTTACc	CAACGTGGTT	TAGAGCAAGC	AGGTgTAACT
msa253045.2{157_COH1}	tTGACAAATA	TTATTTTACc	CAACGTGGTT	TAGAGCAAGC	AGGTgTAACT
msa253045.2{157_M732}	tTGACAAATA	TTATTTTACc	CAACGTGGTT	TAGAGCAAGC	AGGTgTAACT
msa253045.2{157_M781}	tTGACAAATA	TTATTTTACc	CAACGTGGTT	TAGAGCAAGC	AGGTgTAACT
msa253045.2{157_18RS21}	tTGACAAATA	TTATTTTACc	CAACGTGGTT	TAGAGCAAGC	AGGTgTAACT



Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

msa253045.2{157_2603}	tTGACAAATA	TTATTTTAcc	CAACGTGGTT	TAGAGCAAGC	AGGTgTAACT
Consensus	*****	*****	*****	*****	*****
	151				200
msa253045.2{157_090}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_CJB110}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_H36B}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_JM9130013}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_1169NT}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_A909}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_COH1}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_M732}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_M781}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_18RS21}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_2603}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
Consensus	*****	*****	*****	*****	*****
	201				250
msa253045.2{157_090}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_CJB110}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_H36B}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_JM9130013}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_1169NT}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_A909}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_COH1}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_M732}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_M781}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_18RS21}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_2603}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
Consensus	*****	*****	*****	*****	*****
	251				300
msa253045.2{157_090}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_CJB110}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_H36B}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_JM9130013}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_1169NT}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_A909}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_COH1}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_M732}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_M781}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_18RS21}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_2603}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
Consensus	*****	*****	*****	*****	*****
	301				350
msa253045.2{157_090}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_CJB110}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_H36B}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_JM9130013}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_1169NT}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_A909}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_COH1}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_M732}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_M781}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_18RS21}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_2603}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
Consensus	*****	*****	*****	*****	*****
	351				400
msa253045.2{157_090}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_CJB110}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_H36B}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_JM9130013}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_1169NT}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_A909}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_COH1}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_M732}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_M781}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_18RS21}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_2603}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
Consensus	*****	*****	*****	*****	*****
	401				450
msa253045.2{157_090}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_CJB110}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_H36B}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_JM9130013}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_1169NT}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_A909}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_COH1}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_M732}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_M781}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

msa253045.2{157_18RS21}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_2603}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
Consensus	*****	*****	*****	*****	*****
	451				500
msa253045.2{157_090}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_CJB110}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_H36B}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_JM9130013}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_1169NT}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_A909}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_COH1}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_M732}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_M781}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_18RS21}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_2603}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
Consensus	*****	*****	*****	*****	*****
	501				550
msa253045.2{157_090}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_CJB110}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_H36B}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_JM9130013}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_1169NT}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_A909}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_COH1}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_M732}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_M781}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_18RS21}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_2603}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
Consensus	*****	*****	*****	*****	*****
	551				600
msa253045.2{157_090}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_CJB110}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_H36B}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_JM9130013}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_1169NT}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_A909}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_COH1}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_M732}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_M781}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_18RS21}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_2603}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
Consensus	*****	*****	*****	*****	*****
	601				650
msa253045.2{157_090}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTaA
msa253045.2{157_CJB110}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTaA
msa253045.2{157_H36B}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTgA
msa253045.2{157_JM9130013}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTgA
msa253045.2{157_1169NT}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTgA
msa253045.2{157_A909}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTgA
msa253045.2{157_COH1}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTgA
msa253045.2{157_M732}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTgA
msa253045.2{157_M781}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTgA
msa253045.2{157_18RS21}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTgA
msa253045.2{157_2603}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTgA
Consensus	*****	*****	*****	*****	*****
	651				700
msa253045.2{157_090}	GGCACCATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_CJB110}	GGCACCATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_H36B}	GGCACCATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_JM9130013}	GGCACCATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_1169NT}	GGCACCATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_A909}	GGCACCATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_COH1}	GGCACCATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_M732}	GGCACCATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_M781}	GGCACCATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_18RS21}	GGCACCATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_2603}	GGCACCATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
Consensus	*****	*****	*****	*****	*****
	701				750
msa253045.2{157_090}	AAGAcATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_CJB110}	AAGAcATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_H36B}	AAGAcATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_JM9130013}	AAGAcATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_1169NT}	AAGAcATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_A909}	AAGAcATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_COH1}	AAGAcATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_M732}	AAGAcATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

msa253045.2{157_M781}	AAGACATCAC	TCGAAC <b>TGTT</b>	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC	
msa253045.2{157_18RS21}	AAGACATCAC	TCGAAC <b>TGTT</b>	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC	
msa253045.2{157_2603}	AAGACATCAC	TCGAAC <b>TGTT</b>	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC	
Consensus	*****	*****	*****	*****	*****	
751						800
msa253045.2{157_090}	CAAGAAGAAA	TTGGTCAGTT	TCATGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_CJB110}	CAAGAAGAAA	TTGGTCAGTT	TCATGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_H36B}	CAAGAAGAAA	TTGGTCAGTT	TCAGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_JM9130013}	CAAGAAGAAA	TTGGTCAGTT	TCATGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_1169NT}	CAAGAAGAAA	TTGGTCAGTT	TCATGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_A909}	CAAGAAGAAA	TTGGTCAGTT	TCATGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_COH1}	CAAGAAGAAA	TTGGTCAGTT	TCATGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_M732}	CAAGAAGAAA	TTGGTCAGTT	TCATGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_M781}	CAAGAAGAAA	TTGGTCAGTT	TCATGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_18RS21}	CAAGAAGAAA	TTGGTCAGTT	TCATGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_2603}	CAAGAAGAAA	TTGGTCAGTT	TCATGTACCA	GCATACGGTA	AACATAATAT	
Consensus	*****	*****	*****	*****	*****	
801						850
msa253045.2{157_090}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_CJB110}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_H36B}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_JM9130013}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_1169NT}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_A909}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_COH1}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_M732}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_M781}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_18RS21}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_2603}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
Consensus	*****	*****	*****	*****	*****	
851						900
msa253045.2{157_090}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCGT	
msa253045.2{157_CJB110}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCGT	
msa253045.2{157_H36B}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCGT	
msa253045.2{157_JM9130013}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCGT	
msa253045.2{157_1169NT}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCGT	
msa253045.2{157_A909}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCGT	
msa253045.2{157_COH1}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCGT	
msa253045.2{157_M732}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCGT	
msa253045.2{157_M781}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCGT	
msa253045.2{157_18RS21}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACgT	TTTCAGGGGT	AAAaCGTCGT	
msa253045.2{157_2603}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACgT	TTTCAGGGGT	AAAaCGTCGT	
Consensus	*****	*****	*****	*****	*****	
901						950
msa253045.2{157_090}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_CJB110}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_H36B}	TTTACTGAGA	AaATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_JM9130013}	TTTACTGAGA	AaATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_1169NT}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_A909}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_COH1}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_M732}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_M781}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_18RS21}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_2603}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
Consensus	*****	*_*****	*****	*****	*****	
951						1000
msa253045.2{157_090}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_CJB110}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_H36B}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_JM9130013}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_1169NT}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_A909}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_COH1}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_M732}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_M781}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_18RS21}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_2603}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
Consensus	*****	*****	*****	*****	*****	
1001						1050
msa253045.2{157_090}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG	
msa253045.2{157_CJB110}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG	
msa253045.2{157_H36B}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG	
msa253045.2{157_JM9130013}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG	
msa253045.2{157_1169NT}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG	
msa253045.2{157_A909}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG	
msa253045.2{157_COH1}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG	

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

msa253045.2{157_M732}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG		
msa253045.2{157_M781}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG		
msa253045.2{157_18RS21}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG		
msa253045.2{157_2603}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG		
Consensus	*****	*****	*****	*****	*****		
msa253045.2{157_090}	1051	ATAGCTCTTT	TAGACGAAAT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT	1100
msa253045.2{157_CJB110}	ATAGCTCTTT	TAGACGAAAT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT		
msa253045.2{157_H36B}	ATAGCTCTTT	TAGACGAAAT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT		
msa253045.2{157_JM9130013}	ATAGCTCTTT	TAGACGAAAT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT		
msa253045.2{157_1169NT}	ATAGCTCTTT	TAGACGAAAT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT		
msa253045.2{157_A909}	ATAGCTCTTT	TAGACGAAAT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT		
msa253045.2{157_COH1}	ATAGCTCTTT	TAGACGAAAT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT		
msa253045.2{157_M732}	ATAGCTCTTT	TAGACGAAAT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT		
msa253045.2{157_M781}	ATAGCTCTTT	TAGACGAAAT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT		
msa253045.2{157_18RS21}	ATAGCTCTTT	TAGACGAAAT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT		
msa253045.2{157_2603}	ATAGCTCTTT	TAGACGAAAT	TGCCCATGCT	TTGAGTCAAG	CGGATAGCGT		
Consensus	*****	*****	*****	*****	*****		
msa253045.2{157_090}	1101	TTATCTtGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG	1150
msa253045.2{157_CJB110}	TTATCTtGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
msa253045.2{157_H36B}	TTATCTtGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
msa253045.2{157_JM9130013}	TTATCTtGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
msa253045.2{157_1169NT}	TTATCTtGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
msa253045.2{157_A909}	TTATCTtGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
msa253045.2{157_COH1}	TTATCTtGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
msa253045.2{157_M732}	TTATCTtGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
msa253045.2{157_M781}	TTATCTtGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
msa253045.2{157_18RS21}	TTATCTtGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
msa253045.2{157_2603}	TTATCTtGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
Consensus	*****	*****	*****	*****	*****		
msa253045.2{157_090}	1151	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG	1200
msa253045.2{157_CJB110}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
msa253045.2{157_H36B}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
msa253045.2{157_JM9130013}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
msa253045.2{157_1169NT}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
msa253045.2{157_A909}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
msa253045.2{157_COH1}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
msa253045.2{157_M732}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
msa253045.2{157_M781}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
msa253045.2{157_18RS21}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
msa253045.2{157_2603}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
Consensus	*****	*****	*****	*****	*****		
msa253045.2{157_090}	1201	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT	1250
msa253045.2{157_CJB110}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
msa253045.2{157_H36B}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
msa253045.2{157_JM9130013}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
msa253045.2{157_1169NT}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
msa253045.2{157_A909}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
msa253045.2{157_COH1}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
msa253045.2{157_M732}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
msa253045.2{157_M781}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
msa253045.2{157_18RS21}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
msa253045.2{157_2603}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
Consensus	*****	*****	*****	*****	*****		
msa253045.2{157_090}	1251	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT	1300
msa253045.2{157_CJB110}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
msa253045.2{157_H36B}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
msa253045.2{157_JM9130013}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
msa253045.2{157_1169NT}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
msa253045.2{157_A909}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
msa253045.2{157_COH1}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
msa253045.2{157_M732}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
msa253045.2{157_M781}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
msa253045.2{157_18RS21}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
msa253045.2{157_2603}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
Consensus	*****	*****	*****	*****	*****		
msa253045.2{157_090}	1301	TATTAGCTAA	CCTAACTAAA	AATACACAA			1329
msa253045.2{157_CJB110}	TATTAGCTAA	CCTAACTAAA	AATACACAA				
msa253045.2{157_H36B}	TATTAGCTAA	CCTAACTAAA	AATACACAA				
msa253045.2{157_JM9130013}	TATTAGCTAA	CCTAACTAAA	AATACACAA				
msa253045.2{157_1169NT}	TATTAGCTAA	CCTAACTAAA	AATACACAA				
msa253045.2{157_A909}	TATTAGCTAA	CCTAACTAAA	AATACACAA				

**Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)**

msa253045.2{157_COH1}	TATTAGCTAA	CCTAACTAAA	AATACACAA
msa253045.2{157_M732}	TATTAGCTAA	CCTAACTAAA	AATACACAA
msa253045.2{157_M781}	TATTAGCTAA	CCTAACTAAA	AATACACAA
msa253045.2{157_18RS21}	TATTAGCTAA	CCTAACTAAA	AATACACAA
msa253045.2{157_2603}	TATTAGCTAA	CCTAACTAAA	AATACACAA
Consensus	*****	*****	*****

**SEQ ID NO. 4613**  
**STRAIN A909 frame: 2**  
DKYYFTQRGLEQAGVTILPFPSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGYHFKRYHE  
FLGDGFMROFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANANYFVFEAD  
EYERHFMYPHYEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGEDPKLHEI  
TSEAPIYYYGFEEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNILNATAVI  
ANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEI IATLDAARQKYP  
SKEIVAI FQPHFTFTRTIALLDEFahalSQADSVYLAQIYGSAREVDNGEVKVEDLAAKIV  
KHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNQ

**SEQ ID NO. 4614**  
**STRAIN 1169NT frame: 2**  
KAGSSDVKYYFTQRGLEQAGVTILPFPSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY  
HFKRYHEFLGDGFMROFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN  
YFVFEADEYERHFMYPHYEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGE  
DPKLHEITSEAPIYYYGFEEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNIL  
NATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEI IATLD  
AARQKYPSEKEIVAI FQPHFTFTRTIALLDEFahalSQADSVYLAQIYGSAREVDNGEVKVE  
DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNQ

**SEQ ID NO. 4615**  
**STRAIN 090 FRAME:1**  
KAGSSDVKYYFTQRGLEQAGVTILPFPSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY  
HFKRYHEFLGDGFMROFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN  
YFVFEADEYERHFMYPHYEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGE  
DSKLHEITSEAPIYYYGFEEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNIL  
NATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEI IATLD  
AARQKYPSEKEIVAI FQPHFTFTRTIALLDEFahalSQADSVYLAQIYGSAREVDNGEVKVE  
DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNQ

**SEQ ID NO. 4616**  
**STRAIN H36B frame: 2**  
KAGSSDVKYYFTQRGLEQAGVTILPFPSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY  
HFKRYHEFLGDGFMROFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN  
YFVFEADEYERHFMYPHYEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGE  
DPKLHEITSEAPIYYYGFEEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNIL  
NATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEI IATLD  
AARQKYPSEKEIVAI FQPHFTFTRTIALLDEFahalSQADSVYLAQIYGSAREVDNGEVKVE  
DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNQ

**SEQ ID NO. 4617**  
**STRAIN 18RS21 frame: 1**  
KAGSSDVKYYFTQRGLEQAGVTILPFPSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY  
HFKRYHEFLGDGFMROFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN  
YFVFEADEYERHFMYPHYEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGE  
DPKLHEITSEAPIYYYGFEEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNIL  
NATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEI IATLD  
AARQKYPSEKEIVAI FQPHFTFTRTIALLDEFahalSQADSVYLAQIYGSAREVDNGEVKVE  
DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNQ

**SEQ ID NO. 4618**  
**STRAIN M732 frame: 2**  
KAGSSDVKYYFTQRGLEQAGVTILPFPSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY  
HFKRYHEFLGDGFMROFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN  
YFVFEADEYERHFMYPHYEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGE  
DPKLHEITSEAPIYYYGFEEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNIL  
NATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEI IATLD  
AARQKYPSEKEIVAI FQPHFTFTRTIALLDEFahalSQADSVYLAQIYGSAREVDNGEVKVE  
DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNQ

**SEQ ID NO. 4619**  
**STRAIN JM9130013 frame: 2**  
FKKAGSSDVKYYFTQRGLEQAGVTILPFPSPNNISEDLEIIAGNAFRPDNNEELAYVIEK  
GYHFKRYHEFLGDGFMROFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSAN  
ANYFVFEADEYERHFMYPHYEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIY  
GEDPKLHEITSEAPIYYYGFEEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKH  
NILNATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEI IAT  
LDAARQKYPSEKEIVAI FQPHFTFTRTIALLDEFahalSQADSVYLAQIYGSAREVDNGEVK  
VEDLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNQ

**SEQ ID NO. 4620**  
**STRAIN M781 frame: 1**  
KAGSSDVKYYFTQRGLEQAGVTILPFPSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY  
HFKRYHEFLGDGFMROFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

YFVFEADEYERHFMPYHPEYSIIITNIDFDHPDYFTGLEDFVNAFNDYAKQVQKGLFIYGE  
 DPKLHEITSEAPIYYYGFEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAKGKHN  
 LNATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDTVIIDFAHHPTTEIIATLD  
 AARQKYPSEKIVAI FQPHFTFTRTIALLDFAHALSQADSVYLAQIYGSAREVDNGEVKVE  
 DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ

SEQ ID NO. 4621

STRAIN CJB110 frame: 3

KAGSSDVKYYFTQRLGQAGVTILPFPSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY  
 HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLKNITDTSFLIGDGTGRGSANAN  
 YFVFEADEYERHFMPYHPEYSIIITNIDFDHPDYFTGLEDFVNAFNDYAKQVQKGLFIYGE  
 DSKLHEITSEAPIYYYGFEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAKGKHN  
 LNATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDTVIIDFAHHPTTEIIATLD  
 AARQKYPSEKIVAI FQPHFTFTRTIALLDFAHALSQADSVYLAQIYGSAREVDNGEVKVE  
 DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ

SEQ ID NO. 4622

STRAIN 2603 frame: 1

MSKTYHFIGIKGSGMSALALMLHQMGNHVQGSVDVKYYFTQRLGQAGVTILPFPSPNNIS  
 EDLEIIAGNAFRPDNNEELAYVIEKGYQFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGL  
 LAHVLKNITDTSFLIGDGTGRGSANANYFVFEADEYERHFMPYHPEYSIIITNIDFDHPDY  
 FTGLEDFVNAFNDYAKQVQKGLFIYGEDPKLHEITSEAPIYYYGFEDSNDFIAKDITRTV  
 NGSDFKVFYNQEEIGQFHVPAKGKHNILNATAVIANLYIMGIDMALVAEHLKTFSGVKRR  
 FTEKIIDTVIIDFAHHPTTEIIATLDAARQKYPSEKIVAI FQPHFTFTRTIALLDFAHA  
 LSQADSVYLAQIYGSAREVDNGEVKVEDLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMG  
 AGDIQLYERSFEELLANLTKNTQ

SEQ ID NO. 4623

STRAIN COH1 frame: 3

GSSDVKYYFTQRLGQAGVTILPFPSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGYHF  
 KRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLKNITDTSFLIGDGTGRGSANANYF  
 VFEADEYERHFMPYHPEYSIIITNIDFDHPDYFTGLEDFVNAFNDYAKQVQKGLFIYGEDP  
 KLHEITSEAPIYYYGFEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAKGKHNILN  
 ATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDTVIIDFAHHPTTEIIATLDAAR  
 QKYPSEKIVAI FQPHFTFTRTIALLDFAHALSQADSVYLAQIYGSAREVDNGEVKVEDL  
 AAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ

PRETTY of: /biotmp/msa56635.2{\*} November 26, 2002 08:08 ..

	1		50
msa253220.2{157_090}	-----	-----kag	ssdvDKYYFT QRGLEQAGvT
msa253220.2{157_CJB110}	-----	-----kag	ssdvDKYYFT QRGLEQAGvT
msa253220.2{157_1169NT}	-----	-----kag	ssdvDKYYFT QRGLEQAGvT
msa253220.2{157_18RS21}	-----	-----kag	ssdvDKYYFT QRGLEQAGvT
msa253220.2{157_M732}	-----	-----kag	ssdvDKYYFT QRGLEQAGvT
msa253220.2{157_M781}	-----	-----kag	ssdvDKYYFT QRGLEQAGvT
msa253220.2{157_COH1}	-----	-----g	ssdvDKYYFT QRGLEQAGvT
msa253220.2{157_H36B}	-----	-----kag	ssdvDKYYFT QRGLEQAGiT
msa253220.2{157_JM9130013}	-----	-----fkkag	ssdvDKYYFT QRGLEQAGiT
msa253220.2{157_2603}	msktyhfigi ksgsgmsalal mlhqmghnvq	gsdvDKYYFT	QRLGQAGvT
msa253220.2{157_A909}	-----	-----DKYYFT	QRLGQAGvT
Consensus	*****	*****	*****
	51		100
msa253220.2{157_090}	ILPFPSPNNIS	EDLEIIAGNA FRPDNNEELA	YVIEKGYhFK RYHEFLGDFM
msa253220.2{157_CJB110}	ILPFPSPNNIS	EDLEIIAGNA FRPDNNEELA	YVIEKGYhFK RYHEFLGDFM
msa253220.2{157_1169NT}	ILPFPSPNNIS	EDLEIIAGNA FRPDNNEELA	YVIEKGYhFK RYHEFLGDFM
msa253220.2{157_18RS21}	ILPFPSPNNIS	EDLEIIAGNA FRPDNNEELA	YVIEKGYhFK RYHEFLGDFM
msa253220.2{157_M732}	ILPFPSPNNIS	EDLEIIAGNA FRPDNNEELA	YVIEKGYhFK RYHEFLGDFM
msa253220.2{157_M781}	ILPFPSPNNIS	EDLEIIAGNA FRPDNNEELA	YVIEKGYhFK RYHEFLGDFM
msa253220.2{157_COH1}	ILPFPSPNNIS	EDLEIIAGNA FRPDNNEELA	YVIEKGYhFK RYHEFLGDFM
msa253220.2{157_H36B}	ILPFPSPNNIS	EDLEIIAGNA FRPDNNEELA	YVIEKGYhFK RYHEFLGDFM
msa253220.2{157_JM9130013}	ILPFPSPNNIS	EDLEIIAGNA FRPDNNEELA	YVIEKGYhFK RYHEFLGDFM
msa253220.2{157_2603}	ILPFPSPNNIS	EDLEIIAGNA FRPDNNEELA	YVIEKGYqFK RYHEFLGDFM
msa253220.2{157_A909}	ILPFPSPNNIS	EDLEIIAGNA FRPDNNEELA	YVIEKGYhFK RYHEFLGDFM
Consensus	*****	*****	*****
	101		150
msa253220.2{157_090}	RQFTSLGVAG	AHGKTSTTGL LAHVLKNITD	TSFLIGDGTG RGSANANYFV
msa253220.2{157_CJB110}	RQFTSLGVAG	AHGKTSTTGL LAHVLKNITD	TSFLIGDGTG RGSANANYFV
msa253220.2{157_1169NT}	RQFTSLGVAG	AHGKTSTTGL LAHVLKNITD	TSFLIGDGTG RGSANANYFV
msa253220.2{157_18RS21}	RQFTSLGVAG	AHGKTSTTGL LAHVLKNITD	TSFLIGDGTG RGSANANYFV
msa253220.2{157_M732}	RQFTSLGVAG	AHGKTSTTGL LAHVLKNITD	TSFLIGDGTG RGSANANYFV
msa253220.2{157_M781}	RQFTSLGVAG	AHGKTSTTGL LAHVLKNITD	TSFLIGDGTG RGSANANYFV
msa253220.2{157_COH1}	RQFTSLGVAG	AHGKTSTTGL LAHVLKNITD	TSFLIGDGTG RGSANANYFV
msa253220.2{157_H36B}	RQFTSLGVAG	AHGKTSTTGL LAHVLKNITD	TSFLIGDGTG RGSANANYFV
msa253220.2{157_JM9130013}	RQFTSLGVAG	AHGKTSTTGL LAHVLKNITD	TSFLIGDGTG RGSANANYFV
msa253220.2{157_2603}	RQFTSLGVAG	AHGKTSTTGL LAHVLKNITD	TSFLIGDGTG RGSANANYFV
msa253220.2{157_A909}	RQFTSLGVAG	AHGKTSTTGL LAHVLKNITD	TSFLIGDGTG RGSANANYFV
Consensus	*****	*****	*****
	151		200
msa253220.2{157_090}	FEADEYERHF	MPYHPEYSII TNIDFDHPDY	FTGLEDFVNA FNDYAKQVQK

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

msa253220.2{157_CJB110}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_1169NT}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_18RS21}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_M732}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_M781}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_COH1}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_H36B}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_JM9130013}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_2603}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_A909}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
Consensus	*****	*****	*****	*****	*****
msa253220.2{157_090}	GLFIYGEDsK	LHEITskAPI	YYYGFEDSND	FIKADITRTV	NGSDFKVFYN
msa253220.2{157_CJB110}	GLFIYGEDsK	LHEITskAPI	YYYGFEDSND	FIKADITRTV	NGSDFKVFYN
msa253220.2{157_1169NT}	GLFIYGEDpK	LHEITseAPI	YYYGFEDSND	FIKADITRTV	NGSDFKVFYN
msa253220.2{157_18RS21}	GLFIYGEDpK	LHEITseAPI	YYYGFEDSND	FIKADITRTV	NGSDFKVFYN
msa253220.2{157_M732}	GLFIYGEDpK	LHEITseAPI	YYYGFEDSND	FIKADITRTV	NGSDFKVFYN
msa253220.2{157_M781}	GLFIYGEDpK	LHEITseAPI	YYYGFEDSND	FIKADITRTV	NGSDFKVFYN
msa253220.2{157_COH1}	GLFIYGEDpK	LHEITseAPI	YYYGFEDSND	FIKADITRTV	NGSDFKVFYN
msa253220.2{157_H36B}	GLFIYGEDpK	LHEITseAPI	YYYGFEDSND	FIKADITRTV	NGSDFKVFYN
msa253220.2{157_JM9130013}	GLFIYGEDpK	LHEITseAPI	YYYGFEDSND	FIKADITRTV	NGSDFKVFYN
msa253220.2{157_2603}	GLFIYGEDpK	LHEITseAPI	YYYGFEDSND	FIKADITRTV	NGSDFKVFYN
msa253220.2{157_A909}	GLFIYGEDpK	LHEITseAPI	YYYGFEDSND	FIKADITRTV	NGSDFKVFYN
Consensus	*****	*****	*****	*****	*****
msa253220.2{157_090}	QEEIGQFHVP	AYGKHNLNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_CJB110}	QEEIGQFHVP	AYGKHNLNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_1169NT}	QEEIGQFHVP	AYGKHNLNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_18RS21}	QEEIGQFHVP	AYGKHNLNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_M732}	QEEIGQFHVP	AYGKHNLNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_M781}	QEEIGQFHVP	AYGKHNLNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_COH1}	QEEIGQFHVP	AYGKHNLNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_H36B}	QEEIGQFHVP	AYGKHNLNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_JM9130013}	QEEIGQFHVP	AYGKHNLNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_2603}	QEEIGQFHVP	AYGKHNLNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_A909}	QEEIGQFHVP	AYGKHNLNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
Consensus	*****	*****	*****	*****	*****
msa253220.2{157_090}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_CJB110}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_1169NT}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_18RS21}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_M732}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_M781}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_COH1}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_H36B}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_JM9130013}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_2603}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_A909}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
Consensus	*****	*****	*****	*****	*****
msa253220.2{157_090}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_CJB110}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_1169NT}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_18RS21}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_M732}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_M781}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_COH1}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_H36B}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_JM9130013}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_2603}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_A909}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
Consensus	*****	*****	*****	*****	*****
msa253220.2{157_090}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_CJB110}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_1169NT}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_18RS21}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_M732}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_M781}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_COH1}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_H36B}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_JM9130013}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_2603}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_A909}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
Consensus	*****	*****	*****	*****	*****

**Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)****SEQ ID NO. 4701****STRAIN A909**

TATTTTTTAAACAACAAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA  
 ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA  
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACITTTAAAGAT  
 TATAAAGGTAAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC  
 AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG  
 TCAATCAAGCTAAATCAAATTTCTCAGACGAGGATACCTGCTAAAAAAGAA  
 GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCAITGATTATAAAGA  
 AAACACAGAAGATAAAGAAAAA

**SEQ ID NO. 4702****STRAIN H36B**

TATTTTTTAAACAACAAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA  
 ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA  
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACITTTAAAGAT  
 TATAAAGGTAAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC  
 AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG  
 TCAATCAAGCTAAATCAAATTTCTCAGACGAGGATACCTGCTAAAAAAGAA  
 GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCAITGATTATAAAGA  
 AAACACAGAAGATAAAGAAAAA

**SEQ ID NO. 4703****STRAIN 18RS21**

TATTTTTTAAACAACAAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA  
 ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA  
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACITTTAAAGAT  
 TATAAAGGTAAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC  
 AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG  
 TCAATCAAGCTAAATCAAATTTCTCAGACGAGGATACCTGCTAAAAAAGAA  
 GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCAITGATTATAAAGA  
 AAACACAGAAGATAAAGAAAAA

**SEQ ID NO. 4704****STRAIN M732**

TATTTTTTAAACAACAAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA  
 ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA  
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACITTTAAAGAT  
 TATAAAGGTAAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC  
 AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG  
 TCAATCAAGCTAAATCAAATTTCTCAGACGAGGATACCTGCTAAAAAAGAA  
 GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCAITGATTATAAAGA  
 AAACACAGAAGATAAAGAAAAA

**SEQ ID NO. 4705****STRAIN COH1**

TATTTTTTAAACAACAAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA  
 ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA  
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACITTTAAAGAT  
 TATAAAGGTAAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC  
 AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG  
 TCAATCAAGCTAAATCAAATTTCTCAGACGAGGATACCTGCTAAAAAAGAA  
 GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCAITGATTATAAAGA  
 AAACACAGAAGATAAAGAAAAA

**SEQ ID NO. 4706****STRAIN M781**

TATTTTTTAAACAACAAAAAAGGAAAAGAGC  
 TAAGGAAAAATGCAGAAAAATTTCTATGGAGAATATAAAGAAAATCCAGAA  
 GAATATCATCAAATAGCTAAAGATAAAGCAAGTGAATATTCAAATTTAGC  
 TGTGATACITTTAAAGATTATAAAGGTAAATTTGAATCAGGTGAATTGA  
 CAACAGAGGATATCGTCTCAGCCGTTAAGGAAAAAAGCGGAGAAGTAGTT  
 GACTTTGCTAATGATTTTGTCAATCAAGCTAAATCAAATTTCTCAGACGA  
 GGATACCTGCTAAAAAAGAGATAAGGCTCCTGAAACAAAAGTAGAAGATA  
 TTGTCAITGATTATAAAGAAAACACAGAAGATAAAGAAAAA

**SEQ ID NO. 4707****STRAIN 2603**

tatTTTTTAAACAACAAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA  
 attctatggagaatataaagaaaatccagaagaatcatcaaataagcta  
 aagataaagcaagtgaaattcaaatTTAGCTGTTGATACITTTAAAGAT  
 tataaaggtaaatTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC  
 agccgTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG  
 tcaatcaagctaaatcaaaattctcagacgaggatactgctaaaaaagaa  
 gataaggctcctgaacaaaagtagaagatattgtcattgattataaaga  
 aaacacagaagataaagaaaaa

**SEQ ID NO. 4708****STRAIN 090**

TATTTTTTAAACAACAAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA  
 ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA  
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACITTTAAAGAT



Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)

TATAAAGGTAAATTGAATCAGGTGAATTGACACAGAGGATATCGTCTC  
 AGCCGTTAAGGAAAAAGCGGAGAGTAGTTGACTTTGCTAATGATTTTG  
 TCAATCAAGCTAAATCAAAATTTCTCAGACGAGGATCTGCTAAAAAGAA  
 GATAAGGCTCTGAAACAAAAAGTAGAAGATATTGTCATTGATTATAAAGA  
 AAACACAGAAGATAAGAAAA

SEQ ID NO. 4709

STRAIN CJB110

TATTTTAAACAACAAAAAGGAAAAGAGCTAAGGAAA  
 ATGCAGAAAAATTTCTATGGAGAATATAAGAAAAATCCAGAAGATATCAT  
 CAAATAGCTAAAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATAC  
 TTTTAAAGATTATAAAGGTAAATTTGAATCAGGTGAATTGACACAGAGG  
 ATATCGTCTCAGCCGTAAAGGAAAAAGCGGAGAAGTAGTTGACTTTGCT  
 AATGATTTTGTCAATCAAGCTAAATCAAAATTTCTCAGACGAGGATACTGC  
 TAAAAAGAAGATAAGGCTCTGAAACAAAAGTAGAAGATATTGTCATTG  
 ATTATAAGAAAAACAGAAGATAAAGAAAA

SEQ ID NO. 4710

STRAIN 1169NT

TATTTTAAACAACAAAAAGGAAAAGAGCTAAGGAAA  
 AATGCAGAAAAATTTCTATGGAGAATATAAGAAAAATCCAGAAGATATCAT  
 TCAATAGCTAAAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATA  
 CTTTTAAAGATTATAAAGGTAAATTTGAATCAGGTGAATTGACACAGAG  
 GATATCGTCTCAGCCGTAAAGGAAAAAGCGGAGAAGTAGTTGACTTTGCT  
 TAATGATTTTGTCAATCAAGCTAAATCAAAATTTCTCAGATGAGGATACTGC  
 CTAAAAAGAAAAATAAGGCTCTGAAACAAAAGTAGAAGATATTGTCATT  
 GATTATAAGAAAAACAGAAGATAAAGAAAA

SEQ ID NO. 4711

STRAIN JM9130013

TATTTTAAACAACAAAAAGGAAAAGAGCTAAGGAAA  
 ATGCAGAAAAATTTCTATGGAGAATATAAGAAAAATCCAGAAGATATCAT  
 CAAATAGCTAAAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATAC  
 TTTTAAAGATTATAAAGGTAAATTTGAATCAGGTGAATTGACACAGAGG  
 ATATCGTCTCAGCCGTAAAGGAAAAAGCGGAGAAGTAGTTGACTTTGCT  
 AATGATTTTGTCAATCAAGCTAAATCAAAATTTCTCAGACGAGGATACTGC  
 TAAAAAGAAGATAAGGCTCTGAAACAAAAGTAGAAGATATTGTCATTG  
 ATTATAAGAAAAACAGAAGATAAAGAAAA

PRETTY of: /biotmp/msa68511.2{\*} January 22, 2003 05:47 ..

	1	50
msa68511.2{164_090}	TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA	
msa68511.2{164_18RS21}	TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA	
msa68511.2{164_2603}	TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA	
msa68511.2{164_A909}	TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA	
msa68511.2{164_CJB110}	TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA	
msa68511.2{164_COH1}	TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA	
msa68511.2{164_H36B}	TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA	
msa68511.2{164_JM9130013}	TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA	
msa68511.2{164_M732}	TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA	
msa68511.2{164_M781}	TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA	
msa68511.2{164_1169NT}	TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA	
Consensus	*****	*****
	51	100
msa68511.2{164_090}	ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA	
msa68511.2{164_18RS21}	ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA	
msa68511.2{164_2603}	ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA	
msa68511.2{164_A909}	ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA	
msa68511.2{164_CJB110}	ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA	
msa68511.2{164_COH1}	ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA	
msa68511.2{164_H36B}	ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA	
msa68511.2{164_JM9130013}	ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA	
msa68511.2{164_M732}	ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA	
msa68511.2{164_M781}	ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA	
msa68511.2{164_1169NT}	ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA	
Consensus	*****	*****
	101	150
msa68511.2{164_090}	AAGATAAAGC AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT	
msa68511.2{164_18RS21}	AAGATAAAGC AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT	
msa68511.2{164_2603}	AAGATAAAGC AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT	
msa68511.2{164_A909}	AAGATAAAGC AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT	
msa68511.2{164_CJB110}	AAGATAAAGC AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT	
msa68511.2{164_COH1}	AAGATAAAGC AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT	
msa68511.2{164_H36B}	AAGATAAAGC AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT	
msa68511.2{164_JM9130013}	AAGATAAAGC AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT	
msa68511.2{164_M732}	AAGATAAAGC AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT	
msa68511.2{164_M781}	AAGATAAAGC AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT	
msa68511.2{164_1169NT}	AAGATAAAGC AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT	
Consensus	*****	*****

Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)

	151		200
msa68511.2{164_090}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_18RS21}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_2603}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_A909}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_CJB110}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_COH1}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_H36B}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_JM9130013}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_M732}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_M781}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_1169NT}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
Consensus	*****	*****	*****
	201		250
msa68511.2{164_090}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_18RS21}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_2603}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_A909}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_CJB110}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_COH1}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_H36B}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_JM9130013}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_M732}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_M781}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_1169NT}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
Consensus	*****	*****	*****
	251		300
msa68511.2{164_090}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_18RS21}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_2603}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_A909}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_CJB110}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_COH1}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_H36B}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_JM9130013}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_M732}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_M781}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_1169NT}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
Consensus	*****	*****	*****
	301		350
msa68511.2{164_090}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_18RS21}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_2603}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_A909}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_CJB110}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_COH1}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_H36B}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_JM9130013}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_M732}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_M781}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_1169NT}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
Consensus	*****	*****	*****
	351		372
msa68511.2{164_090}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_18RS21}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_2603}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_A909}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_CJB110}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_COH1}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_H36B}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_JM9130013}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_M732}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_M781}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_1169NT}	AAACACAGAA	GATAAAGAAA	AA
Consensus	*****	*****	**

SEQ ID NO. 4712

STRAIN 2603

YFLITTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSLNLAVDTFKDYKGFESGEL  
 TTEDIVSAVKEKSGEVDFDFVNFQAKSKFSDEDTAKKEDKAPETKVEDIVIDYKENTE  
 DKEK

SEQ ID NO. 4713

STRAIN A909 frame: 1

YFLITTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSLNLAVDTFKDYKGFESGEL  
 TTEDIVSAVKEKSGEVDFDFVNFQAKSKFSDEDTAKKEDKAPETKVEDIVIDYKENTE  
 DKEK

SEQ ID NO. 4714

Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)

STRAIN H36B frame: 1  
 YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL  
 TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDDETAKKEDKAPETKVEDIVIDYKENTE  
 DKEK

SEQ ID NO. 4715  
 STRAIN 18RS21 frame: 1  
 YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL  
 TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDDETAKKEDKAPETKVEDIVIDYKENTE  
 DKEK

SEQ ID NO. 4716  
 STRAIN M732 frame: 1  
 YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL  
 TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDDETAKKEDKAPETKVEDIVIDYKENTE  
 DKEK

SEQ ID NO. 4717  
 STRAIN COH1 frame: 1  
 YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL  
 TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDDETAKKEDKAPETKVEDIVIDYKENTE  
 DKEK

SEQ ID NO. 4718  
 STRAIN M781 frame: 1  
 YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL  
 TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDDETAKKEDKAPETKVEDIVIDYKENTE  
 DKEK

SEQ ID NO. 4719  
 STRAIN 090 frame: 1  
 YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL  
 TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDDETAKKEDKAPETKVEDIVIDYKENTE  
 DKEK

SEQ ID NO. 4720  
 STRAIN CJB110 frame: 1  
 YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL  
 TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDDETAKKEDKAPETKVEDIVIDYKENTE  
 DKEK

SEQ ID NO. 4721  
 STRAIN 1169NT frame: 1  
 YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL  
 TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDDETAKKENKAPETKVEDIVIDYKENTE  
 DKEK

SEQ ID NO. 4722  
 STRAIN JM9130013 frame: 1  
 YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL  
 TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSDDETAKKEDKAPETKVEDIVIDYKENTE  
 DKEK

PRETTY of: /biotmp/msa68746.2(\*) January 22, 2003 05:54 ..

	1		50
msa68746.2{164_090}	YFLTTKKGKE	LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_1169NT}	YFLTTKKGKE	LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_18RS21}	YFLTTKKGKE	LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_2603}	YFLTTKKGKE	LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_A909}	YFLTTKKGKE	LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_CJB110}	YFLTTKKGKE	LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_COH1}	YFLTTKKGKE	LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_H36B}	YFLTTKKGKE	LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_JM9130013}	YFLTTKKGKE	LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_M732}	YFLTTKKGKE	LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_M781}	YFLTTKKGKE	LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
Consensus	*****	*****	*****
	51		100
msa68746.2{164_090}	YKGFESGEL	TTEDIVSAVK EKSSEVVVDF NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_1169NT}	YKGFESGEL	TTEDIVSAVK EKSSEVVVDF NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_18RS21}	YKGFESGEL	TTEDIVSAVK EKSSEVVVDF NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_2603}	YKGFESGEL	TTEDIVSAVK EKSSEVVVDF NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_A909}	YKGFESGEL	TTEDIVSAVK EKSSEVVVDF NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_CJB110}	YKGFESGEL	TTEDIVSAVK EKSSEVVVDF NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_COH1}	YKGFESGEL	TTEDIVSAVK EKSSEVVVDF NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_H36B}	YKGFESGEL	TTEDIVSAVK EKSSEVVVDF NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_JM9130013}	YKGFESGEL	TTEDIVSAVK EKSSEVVVDF NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_M732}	YKGFESGEL	TTEDIVSAVK EKSSEVVVDF NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_M781}	YKGFESGEL	TTEDIVSAVK EKSSEVVVDF NDFVNQAKSK FSDEDTAKKE	

**Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)**

```

Consensus *****
msa68746.2{164_090} 101 dKAPETKVED IVIDYKENTE DKEK 124
msa68746.2{164_1159NT} nKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_18RS21} dKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_2603} dKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_A909} dKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_CJB110} dKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_COH1} dKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_H36B} dKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_JM9130013} dKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_M732} dKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_M781} dKAPETKVED IVIDYKENTE DKEK
Consensus -*****

```

Table 48: Comparative Sequences relating to SAG1474

SEQ ID NO: 4801

STRAIN 2603

aatagtactgagacaagtgccttcagtagttcctactacaaatactatcgt  
tcaaactaatgacagtaaatcctaccgcaaaatttggatcagaatcaggac  
aatctgttaataaggtcaagtaaaaccagataattctcgccgcttacaaca  
gttgacacgcctcatcatatttcagctccagatgctttaaaacaactca  
atcaagtcctgtcgttgagagtacttctactaagttaactgaagagactt  
acaaacaaaaagatgggtcaagatttagccaacatgggtgagaagtggtcaa  
gttactagttaggaactcgttaatatggcatacagataatttctgctaaaga  
aaaccatctttaaatgcagtcattactactagacgccaagaagctattg  
aagaggttagaaaacttaagataccaatcagccgtttttagggtgtccc  
ttggtagtcaaggggttagggcacagtattaaagggtggtaaaccaataa  
tggcttgatctatgcagatggaaaaattagcacatttgacagtatgctatg  
tcaaaaaataaaagatttaggatttattatttttaggacaaacgaacttt  
ccagagtattgggtggcgtaataataacagatttctaaattatcgggtctaac  
gcataatccttgggatcttgcctcataatgctgggtgctcttctgggtgaa  
gtgcagcagccattgctagcggaatgacgccaattgctagcggtagtgat  
gctgggtgggtctatccgtattccatctcttggacgggttggtaggttt  
aaaaccaacaagaggattgggtgagtaaatgaaaagccagattcgtatagta  
cagcagttcattttccattactaagtcattagagacgcagaaaactta  
ttaacttatctaaagaaaagcgatcaaacgctagtatcagttaatgattt  
aaaatctttaccaattgcttatactttgaaatcaccaatgggaacagaag  
ttagtaagatgctaaaaacgctatttaggacaacgctcacattcttaaga  
aaacaaggattcaagtaaacagagatagacttaccatttgatggttagagc  
attaatgctgattattcaacctgggtattggcatgggaggagcttttt  
caacaattgaaaaagacttaaaaaaacatgggttttactaaagaagacgtt  
gatcctattacttgggcagttcatgtttttatcaaaatcagataaaggc  
tgaacttaagaaatctattatggaagcccaaaaacataggatgattatc  
gtaaggcaatggagaagcttcacaagcaatttccatcttcttatcgcca  
acgacgcgaagtttagccctctaaatacagatccatagttaacagagga  
agataaaaagagcgatttataatattggaacttgagccaagaagaagaa  
ttgctctctttaatcgccagtgaggagcctatgttgcttagaacaccttt  
acacaaattgctaatatgacaggactcccagctatcagtatcccagctta  
cttatctgagtcgtgttaccatagggacgagtgtaatggcaggtgcaa  
actatgatgggtatttaattaaatttgcaacttctttgaaaaacatcat  
ggttttaatgttaaatggcaagaataatagataaagaagtgaaccatc  
tactggcctaataacagcctaactccctctttaaagctcattcatcat  
tagtaaaattagaagaaaattcacagttactcaagtatctatctctaaa  
aatggatgaaatcgtctgttaaaaataaacatccgtaattggcatatca  
aaaagca

SEQ ID NO: 4802

STRAIN 090

AATAGTACTGAGACAAGTGCCTTCAGTAGTTCCTACTACAA  
ATACTATCGTTCAAACCTAATGACAGTAATCCTACCGCAAAATTTGTATCA  
GAATCAGGACAATCTGTAATAGGTCAAGTAAAACAGATAATTTCTCGGC  
GCTTACAACAGTTGACACGCCTCATCATATTTAGCTCCAGATGCTTTAA  
AAACAACCTCAATCAAGTCTGTGCTGAGAGTACTTCTACTAAGTTAACT  
GAAGAGACTTACAACAAAAAGATGGTAAAGATTTAGCCAACATGGTGAG  
AAGTGGTCAAGTTACTAGTGAGGAACCTCGTTAATATGGCATACGATATTA  
TTGCTAAAGAAAAACCCATCTTTAAATGCACTCATTTACTACTAGACGCCAA  
GAAGCTTATTGAAGAGGCTAGAAAACTTAAAGATACCAATCAGCCGTTT  
AGGTGTTTCCCTTTGTTAGTCAAGGGGTTAGGGCACAGTATTAAAGGTGGTG  
AAACCAATAATGGCTTGATCTATGCAGATGGAAAAATTAGCACATTTGAC  
AGTAGCTATGTCAAAAAATATAAAGATTTAGGATTTATTATTTTAGGACA  
AACGAACCTTCCAGAGTATGGGTGGCGTAATAAACAAGATTCTAAATTTAT  
ACGGTCTAACGCATAATCCTTGGGATCTTGCTCATAATGCTGGTGGCTCT  
TCTGGTGGAAAGTGCAGCAGCCATTGCTAGCGGAATGACGCCAATTGCTAG  
CGGTAGTGATGCTGGTGGTTCTATCCGTATTCCATCTTCTTGGACGGGCT  
TGGTAGGTTTAAACCAACAAGAGGATTGGTGAGTAATGAAAGCCAGAT  
TCGTATAGTACAGCAGTTCAATTTCCATTAACTAAGTCATCTAGAGACGC  
AGAAACATTATTAACCTTATCTAAAGAAAAGCGATCAACCGCTAGTATCAG  
TTAATGATTTAAATCTTTACCAATTGCTTATACTTTGAAATCACCAATG  
GGAACAGAAGTTAGTCAAGATGCTAAAAACGCTATTATGGACAACGTCAC  
ATTCTTAAGAAAAACAAGGATTCAAAGTAACAGAGATAGACTTACCAATTG  
ATGGTAGAGCATTAAATGCGTGATTATTCAACCTTGGCTATTGGCATGGGA  
GGAGCTTTTCAACAATTGAAAAAGACTTAAAAAATCATGGTTTACTAA  
AGAAGACGTTGATCCTATTACTTGGGCAGTTCAATGTTATTTATCAAAAT  
CAGATAAGGCTGAACCTTAAGAAATCTATTATGGAAGCCCAAAACATATG  
GATGATTATCGTAAGGCAATGGAGAAGCTTCACAAGCAATTTCTCATTTT  
CTTATCGCCAACGACCGCAAGTTTAGCCCTCTAAATACAGATCCATATG  
TAACAGAGGAAGATAAAGAGCGATTATAATATGGAACCTTGAAGCAA  
GAAGAAGAATTGCTCTCTTTAATCGCCAGTGGGAGCCTATGTTGCGTAG  
AACACCTTTTACACAAATGCTAATATGACAGGACTCCAGCTATCAGTA  
TCCCCGACTTACTTATCTGAGTCTGGTTTACCCATAGGGACGATGTTAATG  
GCAGGTGCAAACTATGATATGGTATTAATTAATTTGCAACTTTCTTTGA  
AAAACATCATGGTTTAAATGTTAAATGGCAAGAATAATAGATAAAGAAG  
TGAAACCATCTACTGGCCTAATACAGCCTACTAATCCCTCTTTAAAGCT  
CATTCATCATAGTAAATTTAGAAGAAAATTCACAAGTTACTCAAGTATC  
TATCTCTAAAAATGGATGAAATCGTCTGTTAAAAATAAACCATCCGTAA  
TGGCATATCAAAAAGCA

SEQ ID NO: 4803

Table 48: Comparative Sequences relating to SAG1474

## STRAIN A909

TACTACAAATACTATCGTTCAAACCTAATGACAGTAATCCTACCGCAAAAT  
 TTGTATCAGAATCAGGACAATCTGTAATAGGTCAAGTAAACAGATAAT  
 TCTGCGGCGCTTACAACAGTTGACACGCTCATCATATTTAGCTCCAGA  
 TGCTTTAAAAACAACCTCAATCAAGTCCTGTCTGTTGAGAGTACTTCTACTA  
 AGTTAATCGAAGAGACTTACAACAAAAAGATGGTCAAGATTAGCCAAC  
 ATGGTGAGAAAGTGGTCAAGTTACTAGTGAGGAACTCGTTAATATGGCATA  
 CGATATTATTGCTAAAGAAAACCCATCTTTAAATGCAGTCATTACTACTA  
 GACGCCAAGAAGCTATTGAAGAGGCTAGAAAACTTAAAGATACCAATCAG  
 CCGTTTTTAGGTGTTCCCTTGTAGTCAAGGGGTTAGGGCAGATATTAA  
 AGGTGGTGAACCAATAATGGCTTGATCTATGCAGATGGAAAAATTAGCA  
 CATTTGACAGTAGCTATGTCAAAAAATATAAGATTAGGATTATATTATT  
 TTAGGACAAACGAACCTTCCAGAGTATGGGTGGCGTAATATAACAGATTC  
 TAAATTATACGGTCTAACGCATAATCCTTGGGATCTTGCTCATAATGCTG  
 TGGCTCTTCTGGTGAAGTGACAGCCATTGCTAGCGGAATGACGCCA  
 ATTGCTAGCGGTAGTGATGCTGGTGGTTCTATCCGTATTCATCTTCTTG  
 GACGGGCTTGGTAGGTTTAAAAACCAACAGAGGATTGGTGAGTAATGAAA  
 AGCCAGATTCTATAGTACAGCAGTTTCTTTCCATTAACTAAGTCATCT  
 AGAGACCGAGAAACATTATTAACCTTATCTAAAGAAAAGCGATCAACGCT  
 AGTATCAGTTAATGATTAAAAATCTTTACCAATTGCTTATACCTTTGAAAT  
 CACCAATGGGAACAGAAAGTTAGTCAAGATGCTAAAAACGCTATTATGGAC  
 AAGTCACaTTCTTAAGAAAACAAGGATTCAAGTAACAGAGATAGACTT  
 ACCAATTGATGGTAGAGCATTATGCGTGATTATCAACCTTGGCTATTG  
 GCATGGGAGGAGCTTTTTCAACAATTGAAAAAGACTTAAAAAACATGGT  
 TTTACTAAAGAAGAGCTTGATCCTATTACTTGGGCAGTTTCATGTTATTTA  
 TCAAAATTCAGATAAGGCTGAACCTTAAGAAATCTATTATGGAAGCCCAAA  
 AACATATGGATGATTATCGTAAGGCAATGGAGAAGCTTCACAAGCAATTT  
 CCTATTTTCTTATCGCCAACGACCGCAAGTTTAGCCCTCTAATAACAGA  
 TCCATATGTaACAGAGGAAGATAAAAGAGCGATTATATATGGAAGAACT  
 TGAGCCAAAGAAGAAAGAAATGCTCTCTTTAATCGCCAGTGGGAGCCATG  
 TTGCGTAGAACACCTTTTACACAAATTGCTAATATGACAGGACTCCCAGC  
 TATCAGTATCCGACTTACTTATCTGAGTCTGGTTTACCCATAGGGACGA  
 TGTTAATGGCAGGTGCAAACTATGATATGTTAATTAAATTTGCAACT  
 TTCTTTGAAAAACATCATGGTTTTAATGTTAAATGGCAAAGAAATAATAGA  
 TAAAGAAGTGAAACCATCTACTGGCCCTAATACAGCTCTAATCTCCCTCT  
 TTAAAGCTCATTTCATCTAGTAAATTTAGAAGAAAATTCAAGGTTACT  
 CAAGTATCTATCTCTAAAAAATGGATGAAATCGTCTGTTAAAAATAAACC  
 ATCCGTAATGCGATATCAAAAAGCA

SEQ ID NO: 4804

## STRAIN COH1

AATAGTACTGAGACAAGTGCTTCAGTAGCTCCTACTACAAAT  
 ACTATCGTTCAAACCTAATGACAGTAATCCTACCGCAAAATTTGCATCAGA  
 ATCAGGCACAATCTGTAATAGGTCAAGTAAACAGCTAATCTGCGGCGC  
 TTACAACAGTTGACACGCTCATATTTAGCTCCAGATGCTTTAAAAACA  
 ACTCAATCAAGTCCTGTCTGTTGAGAGTCTTCTACTAAGTTAACTGAAGA  
 GACATACAAACAAAAAGATGGTCAAGATTAGCCAACTGGTGAGAAAGTG  
 GTCAGGTTACTAGTGAGGAACCTCGTCAATATGGCATACGATATTATCGCT  
 AAAGAAAACCCATCTTTAAATGAGTCATTACTACTAGACGCCAAGAAGC  
 CATTGAAGAGGCTAGAAAACTTAAAGATACTAATCAGCCGTTTTTAGGTG  
 TTCCCTTGTAGTCAAGGGGTTAGGGCAGATATTAAAGGTGGTGAACCC  
 AATAATGGCTTGATCTATGCAGATGGAAAAATTAGCACATTTGACAGTAG  
 CTATGTCAAAAAATATAAGATTAGGATTATTATTTTAGGACAAACGA  
 ATTTTCCAGATATGGGTGGCGTAATATAACAGACTCTAAATATATACGGT  
 CCAACGCATAATCCTTGAATCTTGTCTATAACGCTGGTGGCTCTTCTGG  
 TGGAAAGTGACAGCAGCTATTGCTAGCGGAATGACGCCAATTGCTAGCGGCA  
 GTGATGCTGGTGGTTCTATCCGTATTCATCTTCTGGACGGGCTTAGTA  
 GGTTTAAACCAACAGAGGATTGGTGAGTAATGAAAAGCCAGATTGCTA  
 TAGTACAGCAGTTTCTTTCCATTAACTAAGTCATCTAGAGACGAGAAA  
 CATTGTTAACTTACCTAAAGAAAAGCGATCAACGCTAGTATCAGTTAAT  
 GATTTAAATCTTTACCAATTGCTTATACTTTGAAATCACCATTGGGAAC  
 AGAAGTTAGTCAAGATGCTAAAAATGCTATTATGGACAACGTCACATTTCT  
 TAAGAAAACAAGGATTCAAAGTGACAGAGATAGATTACCAATTGATGGT  
 AGAGCATTAATGCGTGATTATTCAACCTTGGCTATTGGCATGGGAGGAGC  
 TTTTTCAACAATTGAAAAAGACTTAAAAAACATGGTTTTACTTAAAGAAG  
 ACGTTGATCCCATTACTTGGGCAGTTTATGTTATTATCAAAATTCAGAT  
 AAGGCTGAACCTTAAGAAATCTATTGTGAAGCCCAAAACATATGGATGA  
 TTATCGTTAAGGCAATGGAGAAGCTTCACAAGCAATTTCTATTTTCTTAT  
 CGCCAACGACCGCAAGTTTAGCCCTCTAATAACAGATCCATATGTAACA  
 GAGAAAGATAAAAGAGCGATTATATAATATGAAAACTTGAGCCAAGAAGA  
 AAGAATTGCTCTTTAATCGCCAGTGGGAGCCTATGTTGCGTAGAACAC  
 CTTTACACCAATTGCTAATATGACAGGACTCCCAGCTATCAGTATCCCG  
 ACTTACTTATCTGAGTCTGGTTTACCCATAGGGACGATGTTAATGGCAGG  
 TGCAAACTATGATATGGTATTAAATTAATTTGCAACTTTCTTTGAAAAAC  
 ATCATGGTTTTAATGTTAATGGCAAAGAATAATAGATAAAGAAGTGAAA  
 CCATCTGCTGACCTAATACAGCCTACTAATCTCCCTCTTTAAAGCTCATT  
 ATCATTAGTAAATTTAGAAGAAAATTCAAGGTTACTCAAGTATCTATCT  
 CTAAAAAATGGATGAAATCGTCTGTTAAAAATAAACCATCCGTAATGGCA  
 TATCAAAAGCA

SEQ ID NO: 4805

## STRAIN M732

TCAGTAGCTCCTACTACAAATACTATCGTTCAAACCTAATGACAGTAATCC

Table 48: Comparative Sequences relating to SAG1474

TACCGCAAAATTGTCATCAGAATCAGGACAACTCTGTAATAGGTCAAGTAA  
 AACCGAGCTAATCTGCGGCGCTTACAACAGTTGACACGCTCATATTTCA  
 GCTCCAGATGCTTTAAAAACAACCTCAATCAAGTCCTGTGCTTGAGAGTCC  
 TTCTACTAAGTTAACTGAAGAGACATACAAACAAAAAGATGGTCAAGATT  
 TAGCCAACATGGTGAGAAAGTGGTCAAGTTACTAGTGAGGAACCTGCTCAAT  
 ATGGCATACGATATTATCGCTAAAGAAAAACCATCTTTAAATGCAGTCAT  
 TACTACTAGACGCCAAGAGCCATTGAAGAGGCTAGAAAACTTAAAGATA  
 CTAATCAGCCGTTTCTAGGTGTTCCCTGTGTAGTCAAGGGGTAGGGCAC  
 AGTATTAAAGGTGGTGAAACCAATTAATGGCTTGATCTATGCAGATGGAAA  
 AATTAGCACATTGACAGTAGCTATGTCAAAAAATATAAAGATTAGGAT  
 TTATTATTTTAGGACAAACGAATTTCCAGAGTATGGGTGGCGTAATATA  
 ACAGACTCTAAATTATACGCTCAACGCATTAATCCTTGGGATCTTGTCTCA  
 TAACGCTGGTGGCTCTTCTGGTGGAGGTGACAGCAGTATGTAGCGGAA  
 TGACGCCAATTGCTAGCGGCAGTGATGCTGGTGGTCTATCCGTATTTCCA  
 TCTTCTTGGACGGGCTTAGTAGGTTTAAACCAACAAGAGGATTGGTGAG  
 TAATGAAAAGCCAGATTCTGTATAGTACAGCAGTTTCTTTCCATTAACTA  
 AGTCATCTAGAGACGCAGAAACATTGTTAACTTACTTAAAGAAAAGCGAT  
 CAAACGCTAGTATCAGTTAATGATTTAAAACTTTTACCAATTGCTTATAC  
 TTTGAAATCACCATTGGGAACAGAAGTTAGTCAAGATGCTAAAAATGCTA  
 TTATGGACAACGCTCACATTCTTAAGAAAAACAGGATTCAAAGTGACAGAG  
 ATAGATTTACCAATTGATGGTAGAGCATTAAATGCGTGATTATTCAACCTT  
 GGCTATTGGCATGGGAGGAGCTTTTCAACAATTGAAAAAGACTTAAAAA  
 AACATGGTTTCTTAAAGAAAGACGTTGATCCCATTTACTGGGCGAGTTTCA  
 GTTATTTATCAAAATTCAGATAAGGCTGAACCTTAAGAAATCTATTGTGGA  
 AGCCCAAAACATATGGATGATTATCGTAAGCAATGGAGAAGCTTCCACA  
 AGCAATTTCTTATTTCTTATCGCCAACGACCGCAAGTTTGGCCCTCTA  
 AATACAGATCCATATGTTACAGAGAAAGATAAAAGAGCGATTATATAAT  
 GGAAACCTTGAGCCAGAAGAAAGAAATGTCTCTTTAATCGCCAGTGGG  
 AGCTTATGTTGCGTAGAACACCTTTTACACCAATTGCTAATATGACAGGA  
 CTCCCGCTATCAGTATCCGACTTACTTATCTGAGTCTGGTTTACCCAT  
 AGGGACGATGTTAATGGCAGGTGCAACTATGATATGGTATTAAATTAAT  
 TTGCAACTTTCTTTGAAAACATCATGGTTTAAATGTTAAATGGCAAGA  
 ATAATAGATAAAGAAAGTGAAACCATCTGCTGACCTAATACAGCCTACTAA  
 CTCCTCTTTAAAGCTCATTCATCATTAGTAAATTTAGAAGAAAATTCAC  
 AAGTTACTCAAGTATCTATCTCTAAAAAATGGATGAAATCGTCTGTAA  
 AATAAACCATCCGTAATGGCATATCAAAAAGCA

SEQ ID NO: 4806

STRAIN 18RS21

AATAGTACTGAGACAAGTGCTTCAGTAGTTCCTACTACAAATACTATCGT  
 TCAAACTAATGACAGTAATCCTACCGCAAAATTTGTATCAGAATCAGGAC  
 AATCTGTAATAGGTCAAGTAAACAGATAAATCTGCGGCGCTTACAACA  
 GTTGACAGCCTCATCATATTTAGCTCCAGATGCTTTAAAAACAACCTCA  
 ATCAAGTCTGTCTGTGAGAGTACTTCTACTAAGTTAACTGAAGAGACTT  
 ACAACAAAAAGATGGTCAAGATTTAGCCACATGGTGAGAAGTGGTCAA  
 GTTACTAGTGAGGAACCTGTTAATATGGCATACGATATTATTGCTAAAGA  
 AAACCCATCTTTAAATGCAGTCATTACTACTAGACGCCAAGAGCTATTG  
 AAGAGGCTAGAAAACTTAAAGATACCAATCAGCCGTTTGTAGGTGTTCC  
 TTGTAGTCAAGGGTTAGGGCACAGTATTAAAGGTGGTGAAACCAATAA  
 TGGCTTGATCTATGCAGATGGAAAAATTAGCACATTGACAGTAGCTATG  
 TCAAAAAATATAAAGATTAGGATTTATTTATTTTAGGACAAACGAACCTT  
 CCAGAGTATGGGTGGCGTAAATATAACAGATTCTAAATTATACGGTCTAAC  
 GCATAATCTTGGGATCTTGTCTATAATGCTGGTGGCTCTTCTGGTGGAA  
 GTGCAGCAGCCATTGCTAGCGGAATGACGCCAATTGCTAGCGGTAGTGAT  
 GCTGGTGGTCTATCCGTATTCATCTTCTTGGACGGGCTTGGTAGGTTT  
 AAAACCAACAGAGGATTTGGTGAGTAATGAAAAGCCAGATTCTGTATAGTA  
 CAGCAGTTCAATTTCCATTAACTAAGTCATCTAGAGACGCAGAAACATTA  
 TTAACCTATCTAAAGAAAAGCGATCAACCGCTAGTATCAGTTAATGATTT  
 AAAATCTTTACCAATTGCTTATCTTTGAAATCACCATTGGGAACAGAAG  
 TTAGTCAAGATGCTAAAAACGCTATTATGGACACAGTCACATTCTTAAGA  
 AAACAAGGATTCAAAGTAACAGAGATAGACTTACCAATTGATGGTAGAGC  
 ATTAATGCGTGATTATTCAACCTTGGCTATTGGCATGGGAGGAGCTTTT  
 CAACAATTGAAAAAGACTTAAAAAACATGGTTTACTAAAGAAAGCGTT  
 GATCCTATTACTTGGGCAGTTTATGTTATTTATCAAAATTCAGATAAGGC  
 TGAACCTTAAGAAATCTATTATGGAAGCCAAAAACATATGGATGATTATC  
 GTAAGGCAATGGAGAAGCTTCAACAAGCAATTTCTATTCTTCTATCGCCA  
 ACGACCGCAAGTTTAGCCCTCTAAATACAGATCCATATGTAACAGAGGA  
 AGATAAAGAGCGATTATAATATGGAACCTTGAGCCAAGAAAGAA  
 TTGCTCTCTTTAATCGCCAGTGGGAGCCTATGTTGCGTAGAACACCTTTT  
 ACACAAATTTGCTAATATGACAGGACTCCAGCTATCAGTATCCGACTTA  
 CTTATCTGAGTCTGGTTTACCCATAGGGACGATGTTAATGGCAGGTGCAA  
 ACTATGATATGGTATTAAATTAATTTGCAACTTTCTTTGAAAACATCAT  
 GGTTTAATGTTAAATGGCAAGAAATAATAGATAAAGAAAGTGAACCATC  
 TACTGGCCTAATACAGCCTACTAACTCCCTCTTTAAAGCTCATTCATCAT  
 TAGTAAATTTAGAAGAAAATTCACAAGTTACTCAAGTATCTATCTTAA  
 AATGGATGAAATCGTCTGTAAAAAATAAACCATCCGTAATGGCATATCA  
 AAAAGCA

SEQ ID NO: 4807

STRAIN M781

TGCTTCAGTAGCTCTACTACAAATACTATCGTTCAAACCTAATGACAGTA  
 ATCTTACCGCAAAATTTGCATCAGAATCAGGACAACTCTGTAATAGGTCAA  
 GTAAACAGCTAATTTCTGCGGCGCTTACAACAGTTGACACGCTCATAT

Table 48: Comparative Sequences relating to SAG1474

TTCAGCTCCAGATGCTTTAAAAACAACCTCAATCAAGTCCTGTCGTTGAGA  
 GTCCTTCTACTAAGTTAACTGAAGAGACATACAAACAAAAGATGGTCAA  
 GATTAGCCAAACATGGTGAGAAGTGGTCAAGTTACTAGTGAGGAATCGT  
 CAATATGGCATAACGATATTATCGCTAAAGAAAACCCATCTTTAAATGCAG  
 TCATTTACTACTAGACGCCAAGAAGCCATTGAAGAGGCTAGAAAACTTAAA  
 GATACTAATCAGCCGTTTCTAGGTGTTCCCTTGTGTAGTCAAGGGGTTAGG  
 GCACAGTATTAAGGTGGTGAAACCAATAATGGCTTGATCTATGCAGATG  
 GAAAAATTAGCACATTTGACAGTAGCTATGTCAAAAAATATAAAGATTTA  
 GGATTTATTATTTTAGGACAAACGAATTTCCAGAGTATGGGTGGCGTAA  
 TATAACAGACTCTAAATTATACGGTCCAACGCATAATCCTTGGAACTCTTG  
 CTCATAACGCTGGTGGCTCTTCTGGTGGAAAGTGCAGCAGCTATTTGCTAGC  
 GGAATGACGCCCAATTGCTAGCGGCAGTGATGCTGGTGGTTCTATCCGTAT  
 TCCATCTTCTTGGACGGGCTTAGTAGGTTTAAAACCAACAGAGGATTGG  
 TGAGTAATGAAAAGCCAGATTCTGTATAGTACAGCAGTTCAITTTCCATTA  
 ACTAAGTCATCTAGAGACGCAGAAAACATTGTTAACTTACCTAAAGAAAAG  
 CGATCAACGCTAGTATCAGTTAATGATTTAAAACTTTACCAATTTGCTT  
 ATACTTTGAAATCACCAATGGGAACAGAATAGTCAAGATGCTAAAAAT  
 GCTATTATGGACAACGCTCACATTTCTAAGAGAACAAGGATTCAAAGTGAC  
 AGAGATAGATTACCAATTTGATGGTAGAGCATTAATGCGTGATTTATCAA  
 CCTTGGCTATTGGCATGGGAGGAGCTTTTCAACAATTGAAAAGAGCTTA  
 AAAAAACATGGTTTTACTAAAGAAAGCGTTGATCCCATTTACTTGGGCAGT  
 TCACTGTATTATCAAAATTCAGATAAGGCTGAACCTTAAGAAATCTATTG  
 TGGAAGCCCAAAACATATGGATGATTATCGTAAGGCAATGGAGAAGCTT  
 CACAAGCAATTTCTTATTTCTTATCGCCAACGACCGCAAGTTTAGCCCC  
 TCTAAATACAGATCCATATGTAAACAGAGAAAGATAAAAGAGCGATTATA  
 ATATGGAAAACCTTGAGCCAGAAGAAAGAAATGCTCTCTTAAATCGCCAG  
 TGGAGCGCTATGTTGGGTAGAACACCTTTTACACCAATTTGCTAATAAGAC  
 AGGACTCCCAGCTATCAGTATCCCGACTTACTTATCTGAGTCTGGTTTAC  
 CCATAGGGACGATGTTAATGGCAGGTGCAAACTATGATATGGTATTAAAT  
 AAATTTGCAACTTTCTTTGAAAAACATCATGGTTTAAATGTTAAATGGCA  
 AAGAATATAGATAAAGAGTGAACCATCTGCTGACCTAATACAGCCTA  
 CTAATCCCTCTTTAAAGCTCATTCATCATTAGTAAATTTAGAAGAAAT  
 TCACAAGTTACTCAAGTATCTATCTCTAAAAAATGGATGAAATCGTCTGT  
 TAAAAATAAACCATCCGTAAATGGCATATCAAAAAGCA

SEQ ID NO: 4810

STRAIN CJB110

TAGTTCTTACTACAAATACTATCGTTCAAACCTAATGACAGTAATCCTACC  
 GCAAAATTTGTATCAGAAATCAGGACAATCTGTAATAGGTCAAGTAAACCC  
 AGATAATTTCTGCGCGCTTACAACAGTTGACACGCTCATCATATTTTCAG  
 CTCAGATGCTTTAAAAACAACCTCAATCAAGTCCTGTCTGTTGAGAGTACT  
 TCTACTAAGTTAACTGAAGAGACTTACAAAACAAAAGATGGTAAAGATTT  
 AGCCAACATGGTGAGAAGTGGTCAAGTTACTAGTGAGGAACCTCGTTAATA  
 TGGCATACGATATTATGCTAAAGAAAACCCATCTTTAAATGCAGTCATT  
 ACTACTAGACGCGCAAGAAGCTATTGAAGAGGCTAGAAAACCTTAAAGATAC  
 CAATCAGCCGTTTTAGGTGTTCCCTTGTGTAGTCAAGGGGTTAGGGCACA  
 GTATTAAAGGTGGTGAACCAATAATGGCTTGATCTATGCAGATGGAAAA  
 ATTAGCACATTTGACAGTAGCTATGTCAAAAAATATAAAGATTAGGATT  
 TATTATTTTAGGACAAACGAATTTCCAGAGTATGGGTGGCGTAAATATAA  
 CAGATTCTAAATTTATACGGTCTAACGCATAATCCTTGGGATCTTGCTCAT  
 AATGCTGGTGGCTCTTCTGGTGAAGTGCAGCAGCCATTGCTAGCGGAAT  
 GAGCCCAATTTGCTAGCGGTAGTGTGCTGGTGGTTCTATCCGTATTCCAT  
 CTTCTTGGACGGGCTTGGTAGGTTTAAAACCAACAGAGGATTGGTGAGT  
 CATGAAAGCCAGATTCGTATAGTACAGCAGTTCAITTTCCATTAACATAA  
 GTCATCTAGAGACGCAGAAAACATTATTAACCTTATCTAAGAAAAGCGATC  
 AAACGCTAGTATCAGTTAATGATTTAAATCTTTACCAATTGCTTATACT  
 TTGAAATCACCATGGGAACAGAAGTTAGTCAAGATGCTAAAAACGCTAT  
 TAGGACAAACGTCACATTCTTAAGAAAACAGGATTCAAAGTAACAGAGA  
 TAGACTTACCAATTGATGGTAGAGCATTAATGCGGTGATTATTCAACCTTG  
 GCTATTGGCATGGGAGGAGCTTTTCAACAATTGAAAAAGACTTAAAAAA  
 AcATGGTTTTACTAAAGAAGACGTTGATCTCTATTACTTGGGCAGTTCATG  
 TTATTTATCAAAATTCAGATAAGGCTGAACCTTAAGAAATCTATTATGGAA  
 GCCCAAAACATATGGATGATTATCGTAAGGCAATGGAGAAGCTTCACAA  
 GCAATTTCTATTTCTTATCGCCAACGACCGCAAGTTTAGCCCCCTTAA  
 ATACAGATCCATATGTAACAGAGGAAGATAAAAGAGCGATTATAATATG  
 GAAAACCTTGAGCCAAGAAGAAAGAAATGCTCTCTTAAATCGCCAGTGGGA  
 GCCTATGTTGGGTAGAACACCTTTTACACAAATTGCTAATATGACAGGAC  
 TCCAGCTATCAGTATCCCGACTTACTTATCTGAGTCTGGTTTACCCATA  
 gGGACgATGTTAATGGCAGGTGCAAACTATGATATGGTATTAAATTAAT  
 TGGAACTTTCTTTGAAAAACATCATGGTTTAAATGTTAAATGGCAAGAA  
 TAATAGATAAAGAGTGAACCATCTACTGGCCTAATACAGCCTACTAAC  
 TCCCTCTTTAAAGCTCATTCATCATTAGTAAATTTAGAAGAAAATTCACA  
 AGTTACTCAAGTATCTATCTCTAAAAAATGGATGAAATCGTCTGTTAAAA  
 ATAAACCATCCGTAAATGGCATATCAAAAAGCA

SEQ ID NO: 4811

STRAIN 1169NT

AATAGTACTGAGACAAGTGCTTCAGTAGCTCTACTACAAATACTATCGT  
 TCAAACCTAATGACAGTAATCCTACCGCAAAATTTGCATCAGAAATCAGGAC  
 AATCTGTAATATGTCAAGTAAACAGAGATAATTTCTGCGGCGCTTACACAA  
 GTTGACAGCGCTCATATTTAGCTCCAGATGATTAAAAACCAACTCAATC  
 AAGTCTGTGCTTGAGAGTACTTCTACTAAGTTAACTGAAGAGACATACA  
 AACAAAAAGATGGTCAAGATTAGCCACATGGTGAGAAGTGGTCAAGTT



Table 48: Comparative Sequences relating to SAG1474

ACTAGTGAGGAACTCGTCAATATGGCATACGATATTATTGCTAAAGAAAA  
 CCCCTCTTTAAATGCAGTCATTACTACTAGACGCCAAGAAGCCATTGAAG  
 AGGCTAGAAAACCTTAAAGATACTAATCAGCCATTTTGGTGTTCCTTGG  
 TTAGTCAAGGGGTTAGGGCACAGTATTAAAGGTGGTGAAACCAATAATGG  
 CTTGATCTATGCAGATGGAAAAATAGCACATTGACAGTAGCTATGTCA  
 AAAATATAAAGATTAGGATTTATTTTATAGGACAAACGAACCTTTCCA  
 GAGTATGGGTGGCGTAATATAACAGATTCTAATTATACGGTCCAACGCA  
 TAACCTCGGAATCTTGCTCATAATGCTGGTGGCTCTTCTGGTGGAAAGTG  
 CAGCAGCCATTGCTAGCGGATGACGCCAATTGCTAGCGGTAGTGATGCT  
 GGTGGTCTATCCGTATTCATCTTCTTGGACGGGCTTGGTAGGTTTAAA  
 ACCAACAGAGGATTGGTGAATTAAGAACCCAGATTTCGTATAGTACAG  
 CAGTTTCATTTTCCATTAACTAAGTCACTAGAGACGCAGAAACATTATTA  
 ACTTATCTAAAGAAAGCGATCAAAACGCTAGTATCAGTTAATGATTTAAA  
 ATCTTTACCAATTGCTTATACTTTGAAATCACCAATGGGAACAGAAGTTA  
 GTCAGAGTGTAAAAACGCTATTATGGACAAAGTCACTTCTTAAGAAAA  
 CAAGGATTCAAAGTAACAGAGATAGACTTACCAATTGATGGTAGAGCATT  
 AATGCGTGAATTATTAACCTTGGCTATTGGCATGGGAGGAGCTTTTCAA  
 CAATTGAAAAAGACTTAAAAAACATGGTTTACTAAAGAAGACGTTGAT  
 CCTATTACTTGGGCAGTTTATGTTATTTATCAAAATTGAGTAAGGCTGA  
 CCTTAAGAAATCTATTATGGAGGCCAAAAACATATGGATGATTATCGTA  
 AGGCAATGGAGAGCTTCAACAGCAATTTCCTATTTCTTATCGCCAAAG  
 ACCGCAAGTTTAGCCCTCTAAATACAGATCCATATGTAACAGAGGAAGA  
 TAAAGAGCGATTATTAATATGGAAACCTTGAGCCAAGAAAGAAAGATTG  
 CTCCTTTAATCGCCAGTGGGAGCCTATGTTGCGTAGAACACCTTTTACA  
 CAAATTGCTAATATGACAGGACTCCAGCTATCAGTATCCGACTTACTT  
 ATCTGAGTCTGGTTTACCCTAGGAGCAGATGTTAATGGCAGGTGCAAACT  
 ATGATATGGTATTAATTAATTTGCAACTTTCTTTGAAAAACATCATGGT  
 TTTAATGTTAAATGGCAAGAAATATAGATAAAGAAGTGAACCATCTAC  
 TGGCCTAATACAGCCTACTAATCCCTCTTTAAAGCTCATTCATCATTAG  
 TAAATTTAGAGAAAAATTCACAGTTACTCAAGTATCTATCTCTAAAAAA  
 TGGATGAAATCGTCTGTTAAAAATAAACCATCCGTAATGGCATATCAAAA  
 AGCA

SEQ ID NO: 4812

STRAIN JM9130013

TTTCAGTAGTCTCTACTACAAATACTATCGTTCAAACCTAATGACAGTAATC  
 CTACCGCAAAATTTTCATCAGAAATCAGGACAATCTGTAATAGGTCAAGTA  
 AAACCAGCTAATCTGTGGCGCTTACAAAGTTGACACGCTCATATTTTC  
 AGCTCCAGATGCTTTAAAAACAACCTCAATCAAGTCTGTGCTGAGAGTC  
 CTTCTACTAAGTTAACTGAAGAGACATACAAACAAAAAGATGGTCAAGAG  
 TTAGCCAACATGGTGAGAGTGGTCAAGTTACTAGTGAGGAACTCGTCAA  
 TATGGCATACGATATTATTGCTAAAGAAACCCATCTTTAAATGCAGTCA  
 TTACTACTAGACGCCAAGAAGCTATTGAAGAGGCTAGAAAACTTAAAGAT  
 ACCAATCAGCCGTTTTCAGTGTTCCTTGTAGTCAAGGGGTTAGGGCA  
 CAGTATTAAAGGTGGTGAAACCAATAATGGCTTGATCTATGCAGGTGGAA  
 AAATTAGCACATTTGACAGTAGCTATGTCAAAAAATATAAGATTTAGGA  
 TTTATTATTTTAGGACAAACGAACCTTCCAGAGTATGGATGGCGCAATAT  
 AACAGATTCTAAATTATACGGTCCAACGCATAACCTTGGAACTCTTGCTC  
 ATAATGCTGGTGGCTCTTCTGGTGGAGTGACAGCAGTTATGCTAGCGGG  
 ATGACGCCAATGCTAGCGGTAGTGATGCTGGTGGTTCTATCGTATTTCC  
 ATCTTCTTGGACGGGCTTGGTAGGTTTAAACCAACAGAGGATTGGTGA  
 GTAATGAAAAGCCAGATTCTGTATAGTACAGCAGTTCAATTTCCATTAACCT  
 AAGTCATCTAGAGACGCAGAAACATTATTAACCTTATCTAAAGAAAGCGA  
 TCAAAACGCTAGTATCAGTTAATGATTTAAATCTTTTACCAATTTGCTTATA  
 CTTTGAATACCAATGGGAACAGAAAGTTAGTCAAGATGCTAAAAATGCT  
 ATTTAGGACACGTCATATTCTTAAGAAACCAAGGATTCAAAGTGACAGA  
 GATAGACTTACCAATTGATGGTAGAGCATTAAATGCGTGATTATTAACCT  
 TGGCTATTGGTATGGGAGGAGCTTTTCAACAATTGAAAAAGACTTAAAA  
 AAACATGGTTTACTAAAGAAAGACGTTGATCCCATTACTTGGGGAGTTCA  
 TGTATTATTATCAAAATTCAGATAAGGCTGAACCTTAAGAAATCTATTATGG  
 AAGCCCAAAACATATGGATGATTATCGTAAGGCAATGGAGAAGCTTCAC  
 AAGCAATTTCTATTTTCTTATCGCCAACGACCGCAAGTTTAGCCCTCT  
 AAATACAGATCCATATGTAACAGAGGAAGATAAAAGAGCGATTATAATA  
 TGGAAAACTTGAGCCAAGAGAAAGAAATGCTCTCTTAAATCGCCAGTGG  
 GAGCCTATGTTGCGTAGAACACCTTTTACACAAATGCTAATATGACAGG  
 ACTCCAGCTATCAGTATCCGACTTACTTATCTGAGTCTGGTTTACCCA  
 TAGGACGATGTTAATGGCAGGTGCAAACTATGATATGGTATTAAATAAA  
 TTTGCAACTTTCTTTGAAAAATATCATGGTTTAAATGTTAAATGGCAAG  
 AATAATAGATAAAGAGTGAACCATCTACTGGCCTAATACAGCCTACTA  
 ACTCCCTCTTTAAAGCTCATTCATCATTAGTAAATTTAGAAGAAATTC  
 CAAGTTACTCAAGTATCTATCTCTTAAAAATGGATGAAATCGTCTGTTAA  
 AAATAAACCATCCGTAATGGCATAT

SEQ ID NO: 4813

STRAIN H36B

CTTCAGTAGTCTCTACTACAAATACTATCGTTCAAACCTAATGACAGTAAT  
 CCTACCGCAAAATTTTCATCAGAAATCAGGACAATCTGTAATAGGTCAAGT  
 AAAACAGCTAATCTGTGGCGCTTACAAAGTTGACACGCTCATATTTTC  
 CAGTCCAGATGCTTTAAAAACAACCTCAATCAAGTCTGTGCTGAGAGT  
 CTTCTACTAAGTTAACTGAAGAGACATACAAACAAAAAGATGGTCAAGA  
 TTTAGCCACATGGTGAGAGTGGTCAAGTTACTAGTGAGGAACCTCGTCA  
 ATATGGCATACGATACTATTGCTAAAGAAACCCATCTTTAAATGCAGTC  
 ATTACTACTAGACGCCAAGAAGCTATTGAAGAGGCTAGAAAACTTAAAGA

Table 48: Comparative Sequences relating to SAG1474

TACCAATCAGCCGTTTTTAGGTGTTCCCTTGTAGTCAAGGGGTTAGGGC  
ACAGTATTAAAGGTGGTGAACCAATAATGGCTTGATCTATGCAGGTGGA  
AAAATTAGCACATTTGACAGTAGCTATGTCAAAAAATATAAGATTTAGG  
ATTTATTATTTTAGGACAAACGAACCTTCCAGAGTATGGATGGCGCAATA  
TAACAGATTCTAAATTATACGGTCCAACGCATAACCTTGGAACTTTGCT  
CATAATGCTGGTGGCTCTTCTGGTGAAGTGACAGCAGTTATGCTAGCGG  
GATGACGCCAATTGCTAGCGGTAGTGATGCTGGTGGTTCTATCCGTATTC  
CATCTTCTTGGACGGGCTTGGTAGGTTTAAACCAACAAGAGGATTGGTG  
AGTAATGAAAAGCCAGATTTCGTATAGTACAGCAGTTCAATTTCCATTAAAC  
TAAGTCATCTAGAGACGCGAGAAACATTATTAACCTTATCTAAAGAAAAGCG  
ATCAAACGCTAGTATCAGTTAATGATTAAATCTTTACCAATTCGTATAT  
ACTTTGAATCACCAATGGGAACAGAAAGTTAGTCAAGATGCTAAAAATGC  
TATTATGGACAACGTCATATTCTTAAGAAAACAAGGATTCAAAGTGACAG  
AGATAGACTTACCAATTGATGGTAGAGCATTAAATGCGTGATTATTCACCC  
TTGGCTATTGGTATGGGAGGAGCTTTTCAACAATTGAAAAGAGCTTAA  
AAAACATGGTTTTACTAAAGAAGACGTTGATCCCATTACTTGGGCAGTTTC  
ATGTTATTATTAATAATTCAGATAAGGCTGAACCTTAAGAAATCTATTATG  
GAAGCCCCAAAAACATATGGATGATTATCGTAAGGCAATGGAGAAGCTTCA  
CAAGCAATTTCCATTCTTCTATCGCCAACGACCGCAAGTTTAGCCCCCTC  
TAAATACAGATCCATATGTAACAGAGGAAGATAAAAGAGCGATTATTAAT  
ATGGAAAACCTTGAGCCAAGAAGAAAGAAATTGCTCTCTTAAATCGCCAGTG  
GGAGCCTATGTTCCGTAGAACACCTTTTACACAAATGCTAATATGACAG  
GACTCCCCAGCTATCAGTATCCCGACTTACTTATCTGAGTCTGGTTTACCC  
ATAGGGACGATGTTAATGGCAGGTGCAAACTATGATATGTTAATTAATAA  
ATTTGCAACTTTCTTTGAAAAATATCATGGTTTAAATGTTAAATGGCAAA  
GAATAATAGATAAAGAGTGAACCATCTATGGCCCTAATACAGCCCTACT  
AACTCCCTCTTTAAAGCTCAITTCATCATAGTAAATTTAGAAGAAAATTC  
ACAAGTTACTCAAGTATCTATCTCTAAAAAATGGATGAAATCGTCTGTTA  
AAAAATAA

PRETTY of: /biotcmp/msa71927.2{\*} January 22, 2003 07:23 ..

	1		50
msa71927.2{173_18RS21}	aatagtactg agacaagtgc ttcagtagtt ccTACTACAA ATACTATCGT		
msa71927.2{173_2603}	aatagtactg agacaagtgc ttcagtagtt ccTACTACAA ATACTATCGT		
msa71927.2{173_A909}	-----	-----	---TACTACAA ATACTATCGT
msa71927.2{173_090}	aatagtactg agacaagtgc ttcagtagtt ccTACTACAA ATACTATCGT		
msa71927.2{173_CJB110}	-----	-----tagtt	ccTACTACAA ATACTATCGT
msa71927.2{173_COH1}	aatagtactg agacaagtgc ttcagtagct ccTACTACAA ATACTATCGT		
msa71927.2{173_M781}	-----tgc	ttcagtagct	ccTACTACAA ATACTATCGT
msa71927.2{173_M732}	-----	-tcagtagct	ccTACTACAA ATACTATCGT
msa71927.2{173_H36B}	-----c	ttcagtagtt	ccTACTACAA ATACTATCGT
msa71927.2{173_JM9130013}	-----	ttcagtagct	ccTACTACAA ATACTATCGT
msa71927.2{173_1169NT}	aatagtactg agacaagtgc ttcagtagct ccTACTACAA ATACTATCGT		
Consensus	-----	-----	--***** *****

  

	51		100
msa71927.2{173_18RS21}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTgtATCA GAATCAGGAC		
msa71927.2{173_2603}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTgtATCA GAATCAGGAC		
msa71927.2{173_A909}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTgtATCA GAATCAGGAC		
msa71927.2{173_090}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTgtATCA GAATCAGGAC		
msa71927.2{173_CJB110}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTgtATCA GAATCAGGAC		
msa71927.2{173_COH1}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTgcATCA GAATCAGGAC		
msa71927.2{173_M781}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTgcATCA GAATCAGGAC		
msa71927.2{173_M732}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTgcATCA GAATCAGGAC		
msa71927.2{173_H36B}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTtcATCA GAATCAGGAC		
msa71927.2{173_JM9130013}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTtcATCA GAATCAGGAC		
msa71927.2{173_1169NT}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTgcATCA GAATCAGGAC		
Consensus	*****	*****	*****_--****

  

	101		150
msa71927.2{173_18RS21}	AATCTGTAAT AgGTCAAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA		
msa71927.2{173_2603}	AATCTGTAAT AgGTCAAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA		
msa71927.2{173_A909}	AATCTGTAAT AgGTCAAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA		
msa71927.2{173_090}	AATCTGTAAT AgGTCAAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA		
msa71927.2{173_CJB110}	AATCTGTAAT AgGTCAAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA		
msa71927.2{173_COH1}	AATCTGTAAT AgGTCAAGTA AAACCAGcTA ATTCTGcGGC GCTTACAACA		
msa71927.2{173_M781}	AATCTGTAAT AgGTCAAGTA AAACCAGcTA ATTCTGcGGC GCTTACAACA		
msa71927.2{173_M732}	AATCTGTAAT AgGTCAAGTA AAACCAGcTA ATTCTGcGGC GCTTACAACA		
msa71927.2{173_JM9130013}	AATCTGTAAT AgGTCAAGTA AAACCAGcTA ATTCTGtGGC GCTTACAACA		
msa71927.2{173_1169NT}	AATCTGTAAT AtGTCAAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA		
Consensus	*****	*_*****	*****_--****

  

	151		200
msa71927.2{173_18RS21}	GTTGACACGC CtcacTCATAT TTCAGTCCA GATGcTTTAA AAACAACCTCA		
msa71927.2{173_2603}	GTTGACACGC CtcacTCATAT TTCAGTCCA GATGcTTTAA AAACAACCTCA		
msa71927.2{173_A909}	GTTGACACGC CtcacTCATAT TTCAGTCCA GATGcTTTAA AAACAACCTCA		
msa71927.2{173_090}	GTTGACACGC CtcacTCATAT TTCAGTCCA GATGcTTTAA AAACAACCTCA		
msa71927.2{173_CJB110}	GTTGACACGC CtcacTCATAT TTCAGTCCA GATGcTTTAA AAACAACCTCA		
msa71927.2{173_COH1}	GTTGACACGC C...TCATAT TTCAGTCCA GATGcTTTAA AAACAACCTCA		
msa71927.2{173_M781}	GTTGACACGC C...TCATAT TTCAGTCCA GATGcTTTAA AAACAACCTCA		
msa71927.2{173_M732}	GTTGACACGC C...TCATAT TTCAGTCCA GATGcTTTAA AAACAACCTCA		

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_H36B}	GTTCACACGC	C...TCATAT	TTCAGCTCCA	GATGcTTTAA	AAACAACCTCA
msa71927.2{173_JM9130013}	GTTCACACGC	C...TCATAT	TTCAGCTCCA	GATGcTTTAA	AAACAACCTCA
msa71927.2{173_1169NT}	GTTCACACGC	C...TCATAT	TTCAGCTCCA	GATGaTTTAA	AAACAACCTCA
Consensus	*****	*-*****	*****	****-*****	*****
201					
msa71927.2{173_18RS21}	ATCAAGTCCT	GTCGTTGAGA	GtAcTTCTAC	TAAGTTAACT	GAAGAGAcT
msa71927.2{173_2603}	ATCAAGTCCT	GTCGTTGAGA	GtAcTTCTAC	TAAGTTAACT	GAAGAGAcT
msa71927.2{173_A909}	ATCAAGTCCT	GTCGTTGAGA	GtAcTTCTAC	TAAGTTAACT	GAAGAGAcT
msa71927.2{173_090}	ATCAAGTCCT	GTCGTTGAGA	GtAcTTCTAC	TAAGTTAACT	GAAGAGAcT
msa71927.2{173_CJB110}	ATCAAGTCCT	GTCGTTGAGA	GtAcTTCTAC	TAAGTTAACT	GAAGAGAcT
msa71927.2{173_COH1}	ATCAAGTCCT	GTCGTTGAGA	GtAcTTCTAC	TAAGTTAACT	GAAGAGAcT
msa71927.2{173_M781}	ATCAAGTCCT	GTCGTTGAGA	GtAcTTCTAC	TAAGTTAACT	GAAGAGAcT
msa71927.2{173_M732}	ATCAAGTCCT	GTCGTTGAGA	GtAcTTCTAC	TAAGTTAACT	GAAGAGAcT
msa71927.2{173_H36B}	ATCAAGTCCT	GTCGTTGAGA	GtAcTTCTAC	TAAGTTAACT	GAAGAGAcT
msa71927.2{173_JM9130013}	ATCAAGTCCT	GTCGTTGAGA	GtAcTTCTAC	TAAGTTAACT	GAAGAGAcT
msa71927.2{173_1169NT}	ATCAAGTCCT	GTCGTTGAGA	GtAcTTCTAC	TAAGTTAACT	GAAGAGAcT
Consensus	*****	*****	***-*****	*****	*****
251					
msa71927.2{173_18RS21}	ACAAACAAAA	AGATGGTcAA	GAtTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_2603}	ACAAACAAAA	AGATGGTcAA	GAtTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_A909}	ACAAACAAAA	AGATGGTcAA	GAtTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_090}	ACAAACAAAA	AGATGGTcAA	GAtTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_CJB110}	ACAAACAAAA	AGATGGTcAA	GAtTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_COH1}	ACAAACAAAA	AGATGGTcAA	GAtTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_M781}	ACAAACAAAA	AGATGGTcAA	GAtTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_M732}	ACAAACAAAA	AGATGGTcAA	GAtTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_H36B}	ACAAACAAAA	AGATGGTcAA	GAtTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_JM9130013}	ACAAACAAAA	AGATGGTcAA	GAtTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_1169NT}	ACAAACAAAA	AGATGGTcAA	GAtTTAGCCA	ACATGGTGAG	AAGTGGTCAA
Consensus	*****	*****	**-*****	*****	*****
301					
msa71927.2{173_18RS21}	GTTACTAGTG	AGGAACTCGT	tAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_2603}	GTTACTAGTG	AGGAACTCGT	tAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_A909}	GTTACTAGTG	AGGAACTCGT	tAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_090}	GTTACTAGTG	AGGAACTCGT	tAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_CJB110}	GTTACTAGTG	AGGAACTCGT	tAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_COH1}	GTTACTAGTG	AGGAACTCGT	tAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_M781}	GTTACTAGTG	AGGAACTCGT	tAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_M732}	GTTACTAGTG	AGGAACTCGT	tAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_H36B}	GTTACTAGTG	AGGAACTCGT	tAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_JM9130013}	GTTACTAGTG	AGGAACTCGT	tAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_1169NT}	GTTACTAGTG	AGGAACTCGT	tAATATGGCA	TACGATATTA	TtGCTAAAGA
Consensus	*****	*****	..*****	*****	*-*****
351					
msa71927.2{173_18RS21}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_2603}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_A909}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_090}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_CJB110}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_COH1}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_M781}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_M732}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_H36B}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_JM9130013}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_1169NT}	AAACCCtTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCcATTG
Consensus	*****-***	*****	*****	*****	*****-****
401					
msa71927.2{173_18RS21}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_2603}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_A909}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_090}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_CJB110}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_COH1}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_M781}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_M732}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_H36B}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_JM9130013}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_1169NT}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCaTTTTT	AGGTGTTCCC
Consensus	*****	*****	*****-****	*****-****	*****
451					
msa71927.2{173_18RS21}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_2603}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_A909}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_090}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_CJB110}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_COH1}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_M781}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_M732}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_H36B}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_JM9130013}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_1169NT}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_2603}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_A909}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_090}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_CJB110}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_COH1}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_M781}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_M732}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_H36B}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_JM9130013}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_1169NT}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAACTTT
msa71927.2{173_2603}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAACTTT
msa71927.2{173_A909}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAACTTT
msa71927.2{173_090}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAACTTT
msa71927.2{173_CJB110}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAACTTT
msa71927.2{173_COH1}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAACTTT
msa71927.2{173_M781}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAACTTT
msa71927.2{173_M732}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAACTTT
msa71927.2{173_H36B}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAACTTT
msa71927.2{173_JM9130013}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAACTTT
msa71927.2{173_1169NT}	TCAAAAAATA	TAAAGATTTA	GGATTTATTA	TTTTAGGACA	AACGAACTTT
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	CCAGAGTATG	GgTGGCGtAA	TATAACAGAT	TCTAAATTAT	ACGGTCTcAAC
msa71927.2{173_2603}	CCAGAGTATG	GgTGGCGtAA	TATAACAGAT	TCTAAATTAT	ACGGTCTcAAC
msa71927.2{173_A909}	CCAGAGTATG	GgTGGCGtAA	TATAACAGAT	TCTAAATTAT	ACGGTCTcAAC
msa71927.2{173_090}	CCAGAGTATG	GgTGGCGtAA	TATAACAGAT	TCTAAATTAT	ACGGTCTcAAC
msa71927.2{173_CJB110}	CCAGAGTATG	GgTGGCGtAA	TATAACAGAT	TCTAAATTAT	ACGGTCTcAAC
msa71927.2{173_COH1}	CCAGAGTATG	GgTGGCGtAA	TATAACAGAT	TCTAAATTAT	ACGGTCTcAAC
msa71927.2{173_M781}	CCAGAGTATG	GgTGGCGtAA	TATAACAGAT	TCTAAATTAT	ACGGTCTcAAC
msa71927.2{173_M732}	CCAGAGTATG	GgTGGCGtAA	TATAACAGAT	TCTAAATTAT	ACGGTCTcAAC
msa71927.2{173_H36B}	CCAGAGTATG	GgTGGCGtAA	TATAACAGAT	TCTAAATTAT	ACGGTCTcAAC
msa71927.2{173_JM9130013}	CCAGAGTATG	GgTGGCGtAA	TATAACAGAT	TCTAAATTAT	ACGGTCTcAAC
msa71927.2{173_1169NT}	CCAGAGTATG	GgTGGCGtAA	TATAACAGAT	TCTAAATTAT	ACGGTCTcAAC
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	GCATAAatCCT	tGGgATCtTTG	CTCATAAatGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_2603}	GCATAAatCCT	tGGgATCtTTG	CTCATAAatGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_A909}	GCATAAatCCT	tGGgATCtTTG	CTCATAAatGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_090}	GCATAAatCCT	tGGgATCtTTG	CTCATAAatGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_CJB110}	GCATAAatCCT	tGGgATCtTTG	CTCATAAatGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_COH1}	GCATAAatCCT	tGGgATCtTTG	CTCATAAatGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_M781}	GCATAAatCCT	tGGgATCtTTG	CTCATAAatGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_M732}	GCATAAatCCT	tGGgATCtTTG	CTCATAAatGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_H36B}	GCATAAatCCT	tGGgATCtTTG	CTCATAAatGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_JM9130013}	GCATAAatCCT	tGGgATCtTTG	CTCATAAatGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_1169NT}	GCATAAatCCT	tGGgATCtTTG	CTCATAAatGC	TGGTGGCTCT	TCTGGTGGAA
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_2603}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_A909}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_090}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_CJB110}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_COH1}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_M781}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_M732}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_H36B}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_JM9130013}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_1169NT}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_2603}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_A909}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_090}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_CJB110}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_COH1}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_M781}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TaGTAGGTTT
msa71927.2{173_M732}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TaGTAGGTTT
msa71927.2{173_H36B}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_JM9130013}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_1169NT}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
Consensus	*****	*****	*****	*****	*_*****
801	850				
msa71927.2{173_18RS21}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_2603}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_A909}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_090}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_CJB110}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_COH1}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_M781}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_M732}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_H36B}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_JM9130013}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_1169NT}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
Consensus	*****	*****	*****	*****	*****
851	900				
msa71927.2{173_18RS21}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_2603}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_A909}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_090}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_CJB110}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_COH1}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTg
msa71927.2{173_M781}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTg
msa71927.2{173_M732}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTg
msa71927.2{173_H36B}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_JM9130013}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_1169NT}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
Consensus	*****	*****	*****	*****	*****
901	950				
msa71927.2{173_18RS21}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTt
msa71927.2{173_2603}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTt
msa71927.2{173_A909}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTt
msa71927.2{173_090}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTt
msa71927.2{173_CJB110}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTt
msa71927.2{173_COH1}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTt
msa71927.2{173_M781}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTt
msa71927.2{173_M732}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTt
msa71927.2{173_H36B}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTt
msa71927.2{173_JM9130013}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTt
msa71927.2{173_1169NT}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTt
Consensus	*****	*****	*****	*****	*****
951	1000				
msa71927.2{173_18RS21}	AAAATCTTTA	CCAATTGCTT	ATACITTGAA	ATCACCAGTG	GGAACAGAAG
msa71927.2{173_2603}	AAAATCTTTA	CCAATTGCTT	ATACITTGAA	ATCACCAGTG	GGAACAGAAG
msa71927.2{173_A909}	AAAATCTTTA	CCAATTGCTT	ATACITTGAA	ATCACCAGTG	GGAACAGAAG
msa71927.2{173_090}	AAAATCTTTA	CCAATTGCTT	ATACITTGAA	ATCACCAGTG	GGAACAGAAG
msa71927.2{173_CJB110}	AAAATCTTTA	CCAATTGCTT	ATACITTGAA	ATCACCAGTG	GGAACAGAAG
msa71927.2{173_COH1}	AAAATCTTTA	CCAATTGCTT	ATACITTGAA	ATCACCAGTG	GGAACAGAAG
msa71927.2{173_M781}	AAAATCTTTA	CCAATTGCTT	ATACITTGAA	ATCACCAGTG	GGAACAGAAG
msa71927.2{173_M732}	AAAATCTTTA	CCAATTGCTT	ATACITTGAA	ATCACCAGTG	GGAACAGAAG
msa71927.2{173_H36B}	AAAATCTTTA	CCAATTGCTT	ATACITTGAA	ATCACCAGTG	GGAACAGAAG
msa71927.2{173_JM9130013}	AAAATCTTTA	CCAATTGCTT	ATACITTGAA	ATCACCAGTG	GGAACAGAAG
msa71927.2{173_1169NT}	AAAATCTTTA	CCAATTGCTT	ATACITTGAA	ATCACCAGTG	GGAACAGAAG
Consensus	*****	*****	*****	*****	*****
1001	1050				
msa71927.2{173_18RS21}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_2603}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_A909}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_090}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_CJB110}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_COH1}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_M781}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_M732}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_H36B}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_JM9130013}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_1169NT}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
Consensus	*****	*****	*****	*****	*****
1051	1100				
msa71927.2{173_18RS21}	aaACAAGGAT	TCAAAGTaAc	AGAGATAGAc	TTACCAATTG	ATGGTAGAGC
msa71927.2{173_2603}	aaACAAGGAT	TCAAAGTaAc	AGAGATAGAc	TTACCAATTG	ATGGTAGAGC
msa71927.2{173_A909}	aaACAAGGAT	TCAAAGTaAc	AGAGATAGAc	TTACCAATTG	ATGGTAGAGC
msa71927.2{173_090}	aaACAAGGAT	TCAAAGTaAc	AGAGATAGAc	TTACCAATTG	ATGGTAGAGC
msa71927.2{173_CJB110}	aaACAAGGAT	TCAAAGTaAc	AGAGATAGAc	TTACCAATTG	ATGGTAGAGC

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_COH1}	aAACAAGGAT	TCAAAGTgAC	AGAGATAGAT	TTACCAATTG	ATGGTAGAGC		
msa71927.2{173_M781}	gAACAAGGAT	TCAAAGTgAC	AGAGATAGAT	TTACCAATTG	ATGGTAGAGC		
msa71927.2{173_M732}	aAACAAGGAT	TCAAAGTgAC	AGAGATAGAT	TTACCAATTG	ATGGTAGAGC		
msa71927.2{173_H36B}	aAACAAGGAT	TCAAAGTgAC	AGAGATAGAC	TTACCAATTG	ATGGTAGAGC		
msa71927.2{173_JM9130013}	aAACAAGGAT	TCAAAGTgAC	AGAGATAGAC	TTACCAATTG	ATGGTAGAGC		
msa71927.2{173_1169NT}	aAACAAGGAT	TCAAAGTgAAC	AGAGATAGAC	TTACCAATTG	ATGGTAGAGC		
Consensus	*****	*****_*	*****_*	*****	*****		
msa71927.2{173_18RS21}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_2603}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_A909}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_090}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_CJB110}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_COH1}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_M781}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_M732}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_H36B}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_JM9130013}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_1169NT}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
Consensus	1101	*****	*****	*****	1150	*****	*****
msa71927.2{173_18RS21}	1151	CAACAATTGA	AAAAGACITTA	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_2603}	1151	CAACAATTGA	AAAAGACITTA	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_A909}	1151	CAACAATTGA	AAAAGACITTA	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_090}	1151	CAACAATTGA	AAAAGACITTA	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_CJB110}	1151	CAACAATTGA	AAAAGACITTA	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_COH1}	1151	CAACAATTGA	AAAAGACITTA	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_M781}	1151	CAACAATTGA	AAAAGACITTA	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_M732}	1151	CAACAATTGA	AAAAGACITTA	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_H36B}	1151	CAACAATTGA	AAAAGACITTA	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_JM9130013}	1151	CAACAATTGA	AAAAGACITTA	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_1169NT}	1151	CAACAATTGA	AAAAGACITTA	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
Consensus	1151	*****	*****	*****	1200	*****	*****
msa71927.2{173_18RS21}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_2603}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_A909}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_090}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_CJB110}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_COH1}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_M781}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_M732}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_H36B}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_JM9130013}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_1169NT}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
Consensus	1201	*****	*****_*	*****	1250	*****	*****
msa71927.2{173_18RS21}	1251	TGAACCTTAAG	AAATCTATTa	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_2603}	1251	TGAACCTTAAG	AAATCTATTa	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_A909}	1251	TGAACCTTAAG	AAATCTATTa	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_090}	1251	TGAACCTTAAG	AAATCTATTa	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_CJB110}	1251	TGAACCTTAAG	AAATCTATTa	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_COH1}	1251	TGAACCTTAAG	AAATCTATTg	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_M781}	1251	TGAACCTTAAG	AAATCTATTg	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_M732}	1251	TGAACCTTAAG	AAATCTATTg	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_H36B}	1251	TGAACCTTAAG	AAATCTATTa	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_JM9130013}	1251	TGAACCTTAAG	AAATCTATTa	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_1169NT}	1251	TGAACCTTAAG	AAATCTATTa	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
Consensus	1251	*****	*****_*	*****	1300	*****	*****
msa71927.2{173_18RS21}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_2603}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_A909}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_090}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_CJB110}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_COH1}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_M781}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_M732}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_H36B}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_JM9130013}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_1169NT}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
Consensus	1301	*****	*****	*****	1350	*****	*****
msa71927.2{173_18RS21}	1351	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	1400	GATCCATATG	TaACAGAGgA
msa71927.2{173_2603}	1351	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	1400	GATCCATATG	TaACAGAGgA
msa71927.2{173_A909}	1351	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	1400	GATCCATATG	TaACAGAGgA
msa71927.2{173_090}	1351	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	1400	GATCCATATG	TaACAGAGgA

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_CJB110}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCCATATG	TaACAGAGgA
msa71927.2{173_COH1}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCCATATG	TaACAGAGaA
msa71927.2{173_M781}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCCATATG	TaACAGAGaA
msa71927.2{173_M732}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCCATATG	TtACAGAGaA
msa71927.2{173_H36B}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCCATATG	TaACAGAGgA
msa71927.2{173_JM9130013}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCCATATG	TaACAGAGgA
msa71927.2{173_1169NT}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCCATATG	TaACAGAGgA
Consensus	*****	*****	*****	*****	*-*****
1401	AGATAAAAGA	GCGATTTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_18RS21}	AGATAAAAGA	GCGATTTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_2603}	AGATAAAAGA	GCGATTTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_A909}	AGATAAAAGA	GCGATTTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_090}	AGATAAAAGA	GCGATTTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_CJB110}	AGATAAAAGA	GCGATTTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_COH1}	AGATAAAAGA	GCGATTTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_M781}	AGATAAAAGA	GCGATTTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_M732}	AGATAAAAGA	GCGATTTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_H36B}	AGATAAAAGA	GCGATTTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_JM9130013}	AGATAAAAGA	GCGATTTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_1169NT}	AGATAAAAGA	GCGATTTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
Consensus	*****	*****	*****	*****	*****
1451	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_18RS21}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_2603}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_A909}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_090}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_CJB110}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_COH1}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_M781}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_M732}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_H36B}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_JM9130013}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_1169NT}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
Consensus	*****	*****	*****	*****	*****
1501	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_18RS21}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_2603}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_A909}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_090}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_CJB110}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_COH1}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_M781}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_M732}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_H36B}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_JM9130013}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_1169NT}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
Consensus	*****	*****	*****	*****	*****
1551	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_18RS21}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_2603}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_A909}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_090}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_CJB110}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_COH1}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_M781}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_M732}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_H36B}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_JM9130013}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_1169NT}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
Consensus	*****	*****	*****	*****	*****
1601	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_18RS21}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_2603}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_A909}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_090}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_CJB110}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_COH1}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_M781}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_M732}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_H36B}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_JM9130013}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_1169NT}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
Consensus	*****	*****	*****	*****	*****
1651	GGTTTTAATG	TAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAACCATC
msa71927.2{173_18RS21}	GGTTTTAATG	TAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAACCATC
msa71927.2{173_2603}	GGTTTTAATG	TAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAACCATC
msa71927.2{173_A909}	GGTTTTAATG	TAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAACCATC

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_090}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_CJB110}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_COH1}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_M781}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_M732}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_H36B}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_JM9130013}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_1169NT}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
Consensus	*****	*****	*****	*****	*****

1701

msa71927.2{173\_18RS21}

msa71927.2{173\_2603}

msa71927.2{173\_A909}

msa71927.2{173\_090}

msa71927.2{173\_CJB110}

msa71927.2{173\_COH1}

msa71927.2{173\_M781}

msa71927.2{173\_M732}

msa71927.2{173\_H36B}

msa71927.2{173\_JM9130013}

msa71927.2{173\_1169NT}

Consensus

TaCTGgCCTA

TaCTGgCCTA

TaCTGgCCTA

TaCTGgCCTA

TaCTGgCCTA

TgCTGaCCTA

TgCTGaCCTA

TgCTGaCCTA

TaCTGgCCTA

TaCTGgCCTA

TaCTGgCCTA

\*-\*\*\*\*

ATACAGCCTA

ATACAGCCTA

ATACAGCCTA

ATACAGCCTA

ATACAGCCTA

ATACAGCCTA

ATACAGCCTA

ATACAGCCTA

ATACAGCCTA

ATACAGCCTA

ATACAGCCTA

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CTAACTCCCT

CTAACTCCCT

CTAACTCCCT

CTAACTCCCT

CTAACTCCCT

CTAACTCCCT

CTAACTCCCT

CTAACTCCCT

CTAACTCCCT

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CTTTAAAGCT

CTTTAAAGCT

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1751

msa71927.2{173\_18RS21}

msa71927.2{173\_2603}

msa71927.2{173\_A909}

msa71927.2{173\_090}

msa71927.2{173\_CJB110}

msa71927.2{173\_COH1}

msa71927.2{173\_M781}

msa71927.2{173\_M732}

msa71927.2{173\_H36B}

msa71927.2{173\_JM9130013}

msa71927.2{173\_1169NT}

Consensus

TAGTAAATTT

TAGTAAATTT

TAGTAAATTT

TAGTAAATTT

TAGTAAATTT

TAGTAAATTT

TAGTAAATTT

TAGTAAATTT

TAGTAAATTT

TAGTAAATTT

TAGTAAATTT

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AGAAGAAAAT

AGAAGAAAAT

AGAAGAAAAT

AGAAGAAAAT

AGAAGAAAAT

AGAAGAAAAT

AGAAGAAAAT

AGAAGAAAAT

AGAAGAAAAT

AGAAGAAAAT

AGAAGAAAAT

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TCACAAGTTA

TCACAAGTTA

TCACAAGTTA

TCACAAGTTA

TCACAAGTTA

TCACAAGTTA

TCACAAGTTA

TCACAAGTTA

TCACAAGTTA

TCACAAGTTA

TCACAAGTTA

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CTCAAGTATC

CTCAAGTATC

CTCAAGTATC

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CTCAAGTATC

CTCAAGTATC

CTCAAGTATC

CTCAAGTATC

CTCAAGTATC

CTCAAGTATC

CTCAAGTATC

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TATCTCTAAA

TATCTCTAAA

TATCTCTAAA

TATCTCTAAA

TATCTCTAAA

TATCTCTAAA

TATCTCTAAA

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TATCTCTAAA

TATCTCTAAA

TATCTCTAAA

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1801

msa71927.2{173\_18RS21}

msa71927.2{173\_2603}

msa71927.2{173\_A909}

msa71927.2{173\_090}

msa71927.2{173\_CJB110}

msa71927.2{173\_COH1}

msa71927.2{173\_M781}

msa71927.2{173\_M732}

msa71927.2{173\_H36B}

msa71927.2{173\_JM9130013}

msa71927.2{173\_1169NT}

Consensus

AAATGGATGA

AAATGGATGA

AAATGGATGA

AAATGGATGA

AAATGGATGA

AAATGGATGA

AAATGGATGA

AAATGGATGA

AAATGGATGA

AAATGGATGA

AAATGGATGA

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AATCGTCTGT

AATCGTCTGT

AATCGTCTGT

AATCGTCTGT

AATCGTCTGT

AATCGTCTGT

AATCGTCTGT

AATCGTCTGT

AATCGTCTGT

AATCGTCTGT

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TAAAAATAAA

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ccatccgtaa

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ccatccgtaa

ccatccgtaa

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ccatccgtaa

ccatccgtaa

ccatccgtaa

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tggcatatca

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1851

msa71927.2{173\_18RS21}

msa71927.2{173\_2603}

msa71927.2{173\_A909}

msa71927.2{173\_090}

msa71927.2{173\_CJB110}

msa71927.2{173\_COH1}

msa71927.2{173\_M781}

msa71927.2{173\_M732}

msa71927.2{173\_H36B}

msa71927.2{173\_JM9130013}

msa71927.2{173\_1169NT}

Consensus

aaaagca

aaaagca

aaaagca

aaaagca

aaaagca

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aaaagca

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aaaagca

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SEQ ID NO: 4814

STRAIN 2603 frame: 1

NSTETSASVVPITNTIVQINDSNPTAKFVSESGQSVIGQVKPDNSAALTIVDTPHHISAP

DALKTTQSSPVVESTSTKLTEETYKQKQDLANMVRSGQVTSEELVNMAYDI IAKENPS

LNAVITTRRQEAIEBARKLKDTNQPLGVPLLVKGLGHSI KGETNNGLIYADGKISTFD

SSYVVKYKDLGFIILGQTNFPEYGWRNITDSKLYGLTHNPWDLAHNAGGSSGCSAAAIAS

GMPPIASGSDAGGSIRIPSSWTGLVGLKPTRGLVSNKPKDSYSTAVHPLTKSSRDAETL

LTYLKKSDQTLVSVNDLKSPLIATYTLKSPMGTEVSQDAKNALMDNVTFLRKQGFVKTEID

LPIDGRALMRDYSFLAIGMGGAFFSTIEKDLKKGFTKEDVDPITWAVHVIYQNSDKAELK

KSIMEAQKHMDYRKAMEKLHKQFPFIPLSPITASLAPLNTDPYVTEEDKRAIYNMENLSQ

EERIALFNRRQWEPMLRRTPFTQIANMTGLPAISIPYLSSEGLPIGTMLMAGANYDMVLI

KFATFFEKHHGFNVKQRIIDKEVKPSTGLIQPTNSLFAHSSLVNLENSQVTQVSISK

KWMKSSVKNKPSVMAYQKA

SEQ ID NO: 4815

STRAIN\_090 frame: 1

NSTETSASVVPITNTIVQINDSNPTAKFVSESGQSVIGQVKPDNSAALTIVDTPHHISAP



Table 48: Comparative Sequences relating to SAG1474

DALKTTQSSPVVESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAFYDIIAKENPS  
 LNAVITTRRQEAIEEARKLKDTNQPFLLVGLVPLLVKGLGHSIKGGETNNGLIYADGKISTFD  
 SSVYKVKYKDLGFIILGQTNFPEYGWRNITDSKLYGLTHNPWDLAHNAGSSGGSSAAAIAS  
 GMTPIASGSDAGGSIRIPSSWTGLVGLKPTRGLVSNKPDYSYTAHVHPLTKSSRDAETL  
 LTYLKKSDQTLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVTEID  
 LPIDGRALMRDYSTLAIGMGGAFFSTIEKDLKKGHFTKEDVDPITWAVHVIYQNSDKAELK  
 KSIMEAQKHMDYRKAMEKLHKQFPFIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQ  
 EERIALFNRQWEPMLRRTPTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLI  
 KFATFFEKHHGFFNVKQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVSISSK  
 KMKSSVKNKPSVMAYQKA

## SEQ ID NO: 4816

STRAIN A909 frame: 2

TTNTIVQTNDSNPTAKFVSESGQSVIGQVKPDNSAALTVDTPHISAPDALKTTQSSPV  
 VESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAFYDIIAKENPSLNAVITTRRQEA  
 AIEEARKLKDTNQPFLLVGLVPLLVKGLGHSIKGGETNNGLIYADGKISTFDSSSVYKVKYKDLG  
 FIIILGQTNFPEYGWRNITDSKLYGLTHNPWDLAHNAGSSGGSSAAAIASGMTPIASGSDA  
 GGSIRIPSSWTGLVGLKPTRGLVSNKPDYSYTAHVHPLTKSSRDAETLLTYLKKSDQTL  
 VSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVTEIDLPIDGRALMRD  
 YSTLAIGMGGAFFSTIEKDLKKGHFTKEDVDPITWAVHVIYQNSDKAELKKSIMEAQKHMD  
 DYRKAMEKLHKQFPFIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQEERIALFNRQW  
 EPMRLRTPPTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIKFATFFEKHHG  
 FNVKQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVSISSKMKSSVKNKPSV  
 MAYQKA

## SEQ ID NO: 4817

STRAIN COH1 frame: 1

NSTETSASVAPTNTIVQTNDSNPTAKFVSESGQSVIGQVKPANSAAALTVDTPHISAPD  
 ALKTTQSSPVVESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAFYDIIAKENPSL  
 NAVITTRRQEAIEEARKLKDTNQPFLLVGLVPLLVKGLGHSIKGGETNNGLIYADGKISTFD  
 SSVYKVKYKDLGFIILGQTNFPEYGWRNITDSKLYGPTHNPWDLAHNAGSSGGSSAAAIASG  
 MTPIASGSDAGGSIRIPSSWTGLVGLKPTRGLVSNKPDYSYTAHVHPLTKSSRDAETLL  
 TYLKKSDQTLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVTEIDLP  
 PIDGRALMRDYSTLAIGMGGAFFSTIEKDLKKGHFTKEDVDPITWAVHVIYQNSDKAELK  
 KSIMEAQKHMDYRKAMEKLHKQFPFIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQ  
 EERIALFNRQWEPMLRRTPTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIK  
 FATFFEKHHGFFNVKQRIIDKEVKPSADLIQPTNSLFKAHSSLVNLEENSQVTQVSISSK  
 WMKSSVKNKPSVMAYQKA

## SEQ ID NO: 4818

STRAIN M732 frame: 1

SVAPTNTIVQTNDSNPTAKFVSESGQSVIGQVKPANSAAALTVDTPHISAPDALKTTQSS  
 SPVVESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAFYDIIAKENPSLNAVITTR  
 RQEAIEEARKLKDTNQPFLLVGLVPLLVKGLGHSIKGGETNNGLIYADGKISTFDSSSVYKVKYK  
 DLGFIILGQTNFPEYGWRNITDSKLYGPTHNPWDLAHNAGSSGGSSAAAIASGMTPIASG  
 SDAGGSIRIPSSWTGLVGLKPTRGLVSNKPDYSYTAHVHPLTKSSRDAETLLTYLKKSD  
 QTLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVTEIDLPIDGRAL  
 MRDYSTLAIGMGGAFFSTIEKDLKKGHFTKEDVDPITWAVHVIYQNSDKAELKKSIVEAQK  
 HMDYRKAMEKLHKQFPFIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQEERIALFN  
 RQWEPMLRRTPTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIKFATFEK  
 HHGFFNVKQRIIDKEVKPSADLIQPTNSLFKAHSSLVNLEENSQVTQVSISSKMKSSSVK  
 NKPSVMAYQKA

## SEQ ID NO: 4819

STRAIN 18RS21 frame: 1

NSTETSASVAPTNTIVQTNDSNPTAKFVSESGQSVIGQVKPDNSAALTVDTPHISAPD  
 DALKTTQSSPVVESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAFYDIIAKENPS  
 LNAVITTRRQEAIEEARKLKDTNQPFLLVGLVPLLVKGLGHSIKGGETNNGLIYADGKISTFD  
 SSVYKVKYKDLGFIILGQTNFPEYGWRNITDSKLYGLTHNPWDLAHNAGSSGGSSAAAIAS  
 GMTPIASGSDAGGSIRIPSSWTGLVGLKPTRGLVSNKPDYSYTAHVHPLTKSSRDAETL  
 LTYLKKSDQTLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVTEIDLP  
 PIDGRALMRDYSTLAIGMGGAFFSTIEKDLKKGHFTKEDVDPITWAVHVIYQNSDKAELK  
 KSIMEAQKHMDYRKAMEKLHKQFPFIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQ  
 EERIALFNRQWEPMLRRTPTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLI  
 KFATFFEKHHGFFNVKQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVSISSK  
 KMKSSVKNKPSVMAYQKA

## SEQ ID NO: 4820

STRAIN M781 frame: 2

ASVAPTNTIVQTNDSNPTAKFVSESGQSVIGQVKPANSAAALTVDTPHISAPDALKTTQ  
 SSPVVESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAFYDIIAKENPSLNAVITTR  
 RQEAIEEARKLKDTNQPFLLVGLVPLLVKGLGHSIKGGETNNGLIYADGKISTFDSSSVYKVKYK  
 KDLGFIILGQTNFPEYGWRNITDSKLYGPTHNPWDLAHNAGSSGGSSAAAIASGMTPIAS  
 GSDAGGSIRIPSSWTGLVGLKPTRGLVSNKPDYSYTAHVHPLTKSSRDAETLLTYLKKSD  
 QTLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVTEIDLPIDGRA  
 LMRDYSTLAIGMGGAFFSTIEKDLKKGHFTKEDVDPITWAVHVIYQNSDKAELKKSIVEAQ  
 KHMDYRKAMEKLHKQFPFIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQEERIALF  
 NRQWEPMLRRTPTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIKFATFFE  
 KHHGFFNVKQRIIDKEVKPSADLIQPTNSLFKAHSSLVNLEENSQVTQVSISSKMKSSSV  
 KNKPSVMAYQKA

## SEQ ID NO: 4821

STRAIN CJB110 frame: 3

Table 48: Comparative Sequences relating to SAG1474

VPTTNTIVQTNDSNPTAKFVSESGQSVIGQVKPDNSAALTVDTPHHISAPDALKTTQSS  
 PVVESTSTKLTEETKYKQDGLANMVRSGQVTSEELVNMAVDIIAKENPSLNAVITTRR  
 QEAIIEARKLKDTNQPFGLVPLLVKGLGHSIKGGETNNGLIYADGKIISTFDSYVKKYK  
 LGFIILGQTNFPPEYGWRNITDSKLYGLTHNPWDLAHNAGSSGSSAAAIASGMTPIASG  
 DAGGSIRIPSSWTGLVGLKPTRGLVSHKPDYSYSTAVHFPPLTKSSRDAETLLTYLKKSDQ  
 TLVSVNDLKSPLIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVKVTEIDLPIDGRAL  
 RDYSTLAIGMGGAFTIEKDLKKGFTKEDVDPIWAVHVIYQNSDKAELKKSIMAQKH  
 MDDYRKAMEKLHKQFPFIPLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQEBRIALFNR  
 QWEPMLRRTPTFTQIANMTGLPAISIPTYLSSEGLPIGTMLMAGANYDMVLIKFATPFEEKH  
 HGFNVKQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVVSISKKWMKSSVK  
 KPSPMAYQKA

## SEQ ID NO: 4822

STRAIN 1169NT frame: 1

NSTETSASVAPTNTNTIVQTNDSNPTAKFSESGQSVIGQVKPDNSAALTVDTPHHISAPD  
 DLKTTQSSPVVESTSTKLTEETKYKQDGLANMVRSGQVTSEELVNMAVDIIAKENPSL  
 NAVITTRRQEAIIEARKLKDTNQPFGLVPLLVKGLGHSIKGGETNNGLIYADGKIISTFDS  
 SYVKKYKDLGFIILGQTNFPPEYGWRNITDSKLYGPTHNPRLAHNAGSSGSSAAAIASG  
 MTPIASGDAGGSIRIPSSWTGLVGLKPTRGLVSHKPDYSYSTAVHFPPLTKSSRDAETLL  
 TYLKKSDQTLVSVNDLKSPLIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVKVTEIDL  
 PIDGRALMRDYSTLAIGMGGAFTIEKDLKKGFTKEDVDPIWAVHVIYQNSDKAELKK  
 SIMAQKHMDYRKAMEKLHKQFPFIPLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQE  
 ERIALFNRQWEPMLRRTPTFTQIANMTGLPAISIPTYLSSEGLPIGTMLMAGANYDMVLIK  
 FATPFEEKHGFNVKQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVVSISKK  
 WMKSSVKKPSPMAYQKA

## SEQ ID NO: 4823

STRAIN JM9130013 frame: 2

SVAPTNTNTIVQTNDSNPTAKFSESGQSVIGQVKPANSVALTTVDTPHHISAPDALKTTQSS  
 SPVVESTSTKLTEETKYKQDGLANMVRSGQVTSEELVNMAVDIIAKENPSLNAVITTR  
 QEAIIEARKLKDTNQPFGLVPLLVKGLGHSIKGGETNNGLIYAGGKIISTFDSYVKKYK  
 DLGFIILGQTNFPPEYGWRNITDSKLYGPTHNPWDLAHNAGSSGSSAAAIASGMTPIASG  
 SDAGGSIRIPSSWTGLVGLKPTRGLVSHKPDYSYSTAVHFPPLTKSSRDAETLLTYLKKSD  
 QTLVSVNDLKSPLIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVKVTEIDLPIDGRAL  
 MRDYSTLAIGMGGAFTIEKDLKKGFTKEDVDPIWAVHVIYQNSDKAELKKSIMAQKH  
 HMDYRKAMEKLHKQFPFIPLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQEBRIALFN  
 RQWEPMLRRTPTFTQIANMTGLPAISIPTYLSSEGLPIGTMLMAGANYDMVLIKFATPFEEK  
 YHGFNVKQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVVSISKKWMKSSVK  
 NKPSVMAY

## SEQ ID NO: 4824

STRAIN H36B frame: 3

SVVPTTNTIVQTNDSNPTAKFSESGQSVIGQVKPANSVALTTVDTPHHISAPDALKTTQSS  
 SPVVESTSTKLTEETKYKQDGLANMVRSGQVTSEELVNMAVDIIAKENPSLNAVITTR  
 QEAIIEARKLKDTNQPFGLVPLLVKGLGHSIKGGETNNGLIYAGGKIISTFDSYVKKYK  
 DLGFIILGQTNFPPEYGWRNITDSKLYGPTHNPWDLAHNAGSSGSSAAAIASGMTPIASG  
 SDAGGSIRIPSSWTGLVGLKPTRGLVSHKPDYSYSTAVHFPPLTKSSRDAETLLTYLKKSD  
 QTLVSVNDLKSPLIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVKVTEIDLPIDGRAL  
 MRDYSTLAIGMGGAFTIEKDLKKGFTKEDVDPIWAVHVIYQNSDKAELKKSIMAQKH  
 HMDYRKAMEKLHKQFPFIPLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQEBRIALFN  
 RQWEPMLRRTPTFTQIANMTGLPAISIPTYLSSEGLPIGTMLMAGANYDMVLIKFATPFEEK  
 YHGFNVKQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVVSISKKWMKSSVK  
 NK

PRETTY of: /biotmp/msa72034.2{\*} January 22, 2003 07:25 ..

	1		50
msa72034.2{173_090}	nstetsasvv	pTTNTIVQTN DSNPTAKFvS	ESGQSVigQV KpDnSaALTT
msa72034.2{173_18RS21}	nstetsasvv	pTTNTIVQTN DSNPTAKFvS	ESGQSVigQV KpDnSaALTT
msa72034.2{173_2603}	nstetsasvv	pTTNTIVQTN DSNPTAKFvS	ESGQSVigQV KpDnSaALTT
msa72034.2{173_A909}	-----	-TTNTIVQTN DSNPTAKFvS	ESGQSVigQV KpDnSaALTT
msa72034.2{173_CJB110}	-----	pTTNTIVQTN DSNPTAKFvS	ESGQSVigQV KpDnSaALTT
msa72034.2{173_COH1}	nstetsasva	pTTNTIVQTN DSNPTAKFaS	ESGQSVigQV KPaNSaALTT
msa72034.2{173_M732}	-----	-sva pTTNTIVQTN DSNPTAKFaS	ESGQSVigQV KPaNSaALTT
msa72034.2{173_M781}	-----	-asva pTTNTIVQTN DSNPTAKFaS	ESGQSVigQV KPaNSaALTT
msa72034.2{173_1169NT}	nstetsasva	pTTNTIVQTN DSNPTAKFaS	ESGQSVicQV KpDnSaALTT
msa72034.2{173_H36B}	-----	-svv pTTNTIVQTN DSNPTAKFaS	ESGQSVigQV KPaNSvALTT
msa72034.2{173_JM9130013}	-----	-sva pTTNTIVQTN DSNPTAKFaS	ESGQSVigQV KPaNSvALTT
Consensus	-----	-*****	*****

  

	51		100
msa72034.2{173_090}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGk dLANMVRSGQ
msa72034.2{173_18RS21}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_2603}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_A909}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_CJB110}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGk dLANMVRSGQ
msa72034.2{173_COH1}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_M732}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_M781}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_1169NT}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_H36B}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_JM9130013}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ

Table 48: Comparative Sequences relating to SAG1474

Consensus	***--*****	*-*****	*****	*****	*****	*****
msa72034.2{173_090}	101	150				
msa72034.2{173_18RS21}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
msa72034.2{173_2603}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
msa72034.2{173_A909}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
msa72034.2{173_CJB110}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
msa72034.2{173_COH1}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
msa72034.2{173_M732}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
msa72034.2{173_M781}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
msa72034.2{173_1169NT}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
msa72034.2{173_H36B}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
msa72034.2{173_JM9130013}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
Consensus	*****	*****	*****	*****	*****	*****
msa72034.2{173_090}	151	200				
msa72034.2{173_18RS21}	LLVKGLGHSI	KGGETNNGLI	YADGKISTFD	SSYVKKYKDL	GFIILGQTNF	
msa72034.2{173_2603}	LLVKGLGHSI	KGGETNNGLI	YADGKISTFD	SSYVKKYKDL	GFIILGQTNF	
msa72034.2{173_A909}	LLVKGLGHSI	KGGETNNGLI	YADGKISTFD	SSYVKKYKDL	GFIILGQTNF	
msa72034.2{173_CJB110}	LLVKGLGHSI	KGGETNNGLI	YADGKISTFD	SSYVKKYKDL	GFIILGQTNF	
msa72034.2{173_COH1}	LLVKGLGHSI	KGGETNNGLI	YADGKISTFD	SSYVKKYKDL	GFIILGQTNF	
msa72034.2{173_M732}	LLVKGLGHSI	KGGETNNGLI	YADGKISTFD	SSYVKKYKDL	GFIILGQTNF	
msa72034.2{173_M781}	LLVKGLGHSI	KGGETNNGLI	YADGKISTFD	SSYVKKYKDL	GFIILGQTNF	
msa72034.2{173_1169NT}	LLVKGLGHSI	KGGETNNGLI	YADGKISTFD	SSYVKKYKDL	GFIILGQTNF	
msa72034.2{173_H36B}	LLVKGLGHSI	KGGETNNGLI	YADGKISTFD	SSYVKKYKDL	GFIILGQTNF	
msa72034.2{173_JM9130013}	LLVKGLGHSI	KGGETNNGLI	YADGKISTFD	SSYVKKYKDL	GFIILGQTNF	
Consensus	*****	*****	*****	*****	*****	*****
msa72034.2{173_090}	201	250				
msa72034.2{173_18RS21}	PEYGWRNITD	SKLYGLTHNP	wdLAHNAGGS	SGGSAaAIAS	GMPPIASGSD	
msa72034.2{173_2603}	PEYGWRNITD	SKLYGLTHNP	wdLAHNAGGS	SGGSAaAIAS	GMPPIASGSD	
msa72034.2{173_A909}	PEYGWRNITD	SKLYGLTHNP	wdLAHNAGGS	SGGSAaAIAS	GMPPIASGSD	
msa72034.2{173_CJB110}	PEYGWRNITD	SKLYGLTHNP	wdLAHNAGGS	SGGSAaAIAS	GMPPIASGSD	
msa72034.2{173_COH1}	PEYGWRNITD	SKLYGpTHNP	wnLAHNAGGS	SGGSAaAIAS	GMPPIASGSD	
msa72034.2{173_M732}	PEYGWRNITD	SKLYGxTHNP	wdLAHNAGGS	SGGSAaAIAS	GMPPIASGSD	
msa72034.2{173_M781}	PEYGWRNITD	SKLYGpTHNP	wnLAHNAGGS	SGGSAaAIAS	GMPPIASGSD	
msa72034.2{173_1169NT}	PEYGWRNITD	SKLYGpTHNP	rnLAHNAGGS	SGGSAaAIAS	GMPPIASGSD	
msa72034.2{173_H36B}	PEYGWRNITD	SKLYGpTHNP	wnLAHNAGGS	SGGSAaAIAS	GMPPIASGSD	
msa72034.2{173_JM9130013}	PEYGWRNITD	SKLYGpTHNP	wnLAHNAGGS	SGGSAaAIAS	GMPPIASGSD	
Consensus	*****	*****	*****	*****	*****	*****
msa72034.2{173_090}	251	300				
msa72034.2{173_18RS21}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPd	SYSTAVHFPL	TKSSRDAETL	
msa72034.2{173_2603}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPd	SYSTAVHFPL	TKSSRDAETL	
msa72034.2{173_A909}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPd	SYSTAVHFPL	TKSSRDAETL	
msa72034.2{173_CJB110}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPd	SYSTAVHFPL	TKSSRDAETL	
msa72034.2{173_COH1}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPd	SYSTAVHFPL	TKSSRDAETL	
msa72034.2{173_M732}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPd	SYSTAVHFPL	TKSSRDAETL	
msa72034.2{173_M781}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPd	SYSTAVHFPL	TKSSRDAETL	
msa72034.2{173_1169NT}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPd	SYSTAVHFPL	TKSSRDAETL	
msa72034.2{173_H36B}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPd	SYSTAVHFPL	TKSSRDAETL	
msa72034.2{173_JM9130013}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPd	SYSTAVHFPL	TKSSRDAETL	
Consensus	*****	*****	*****	*****	*****	*****
msa72034.2{173_090}	301	350				
msa72034.2{173_18RS21}	LTYLKKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR	
msa72034.2{173_2603}	LTYLKKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR	
msa72034.2{173_A909}	LTYLKKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR	
msa72034.2{173_CJB110}	LTYLKKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR	
msa72034.2{173_COH1}	LTYLKKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR	
msa72034.2{173_M732}	LTYLKKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR	
msa72034.2{173_M781}	LTYLKKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR	
msa72034.2{173_1169NT}	LTYLKKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR	
msa72034.2{173_H36B}	LTYLKKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR	
msa72034.2{173_JM9130013}	LTYLKKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR	
Consensus	*****	*****	*****	*****	*****	*****
msa72034.2{173_090}	351	400				
msa72034.2{173_18RS21}	kQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV	
msa72034.2{173_2603}	kQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV	
msa72034.2{173_A909}	kQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV	
msa72034.2{173_CJB110}	kQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV	
msa72034.2{173_COH1}	kQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV	
msa72034.2{173_M732}	kQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV	
msa72034.2{173_M781}	kQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV	
msa72034.2{173_1169NT}	kQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV	
msa72034.2{173_H36B}	kQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV	
msa72034.2{173_JM9130013}	kQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV	

Table 48: Comparative Sequences relating to SAG1474

msa72034.2{173_JM9130013}	kQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFSTIEKDL	KKHGFTKEDV
Consensus	*****	*****	*****	*****	*****
	401				450
msa72034.2{173_090}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_18RS21}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_2603}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_A909}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_CJB110}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_COH1}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_M732}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_M781}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_1169NT}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_H36B}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_JM9130013}	DPITWgVHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
Consensus	*****	*****	*****	*****	*****
	451				500
msa72034.2{173_090}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_18RS21}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_2603}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_A909}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_CJB110}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_COH1}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_M732}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_M781}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_1169NT}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_H36B}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
msa72034.2{173_JM9130013}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EERIALFNRO	WEPMLRRTPF
Consensus	*****	*****	*****	*****	*****
	501				550
msa72034.2{173_090}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_18RS21}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_2603}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_A909}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_CJB110}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_COH1}	TpIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_M732}	TpIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_M781}	TpIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_1169NT}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_H36B}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_JM9130013}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
Consensus	*..*****	*****	*****	*****	*****_*
	551				600
msa72034.2{173_090}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_18RS21}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_2603}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_A909}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_CJB110}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_COH1}	GFNVKQRII	DKEVKPSadL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_M732}	GFNVKQRII	DKEVKPSadL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_M781}	GFNVKQRII	DKEVKPSadL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_1169NT}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_H36B}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_JM9130013}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
Consensus	*****	*****	*****	*****	*****
	601				619
msa72034.2{173_090}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_18RS21}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_2603}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_A909}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_CJB110}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_COH1}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_M732}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_M781}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_1169NT}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_H36B}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_JM9130013}	KWMKSSVKNK	psvmay---			
Consensus	*****	-----			

Table 49: Comparative Sequences related to SAG1502

SEQ ID NO: 4901

STRAIN 2603

aaacatccgatacttaatgatcaaaaatccttagcaattgttgaacagat  
 agaatatgatttttgataaattcgataattcagaagcttctttttatgcaa  
 cattagctagawttcgcggttatggatagagaaatcaaaaatttattaga  
 gaaaatccaaatagtc aaatcctttcaattgggtgtggacttgatacaag  
 gtttgaaagagtcgataatggacaaattaggtggatataaccttgatttgc  
 cagaggttatggagataagaaaattatttttgaagagcatgaaagagtt  
 actaatatagcaaaaatcagccctagatgaaacttggacacgggaggtaaa  
 tccccaaaatgcccccttttctaactcgtgtcagaagggtgttttaattgtttc  
 taaaagaagatgacgtagagacttttcttcatatcctgacaaattcattt  
 agccaattttatggcacaatttgatttgggtcataaggaaatgatttaataa  
 aggaaagcaacatgatagcaagtaagtatatggatagacaatttcoagtttg  
 gtatcacagatgggtcatgagatttgggttagaccctaaattaaagcaa  
 ataatctgatttaactttacagatgagatgagcaaatgtgagttaggcac  
 acttcgctctttacttccaacaattcgtaaatataaattgttttaggtg  
 tgtacgaatataaagcatc

SEQ ID NO: 4902

STRAIN 090

TAATGATCAAAAATCCTTAGCAATTGTTGAACAGATAGAATATGATTTTG  
 ATAAATTGCGATAAATTGAGAAGCTTCTTTTATGCAACATTAGCTAGAATT  
 CGCGTTATGGATAGAGAAATCAAAAATTTATTAGAGAAAATCCAATAG  
 TCAAAATCCTTTCAATTGGTGTGGACTTGATACAAGGTTTGAAAGAGTCCG  
 ATAAATGGACAAAATTAGGTGGTATAACCTTGATTGGCAGAGGTTATGGAG  
 ATAGAAAATTTATTTTGAAGAGCATGAAGAGTTACTAATATAGCAAAA  
 ATCAGCCATAGATGAAACTTGGACACGGGAGGTAAATCCCCAAAATGCCC  
 CTMTTCTAATCGTGTGAGAAGGTGTTTAAATGTTTCTAAAAGAAGATGAC  
 GTAGAGACTTTTCTTCATATCTGACAAAATTCATTAGCCAATTTATGGC  
 ACAATTTGATTGTGTGATAAGGAAATGATTAAATAAGGAAAGCAACATG  
 ATACAGTAAAGTATATGGATACAGAATTTCAAGTTTGGTATCAGATGGT  
 CATGAGATTGTGGATTAGACCCCTAAATTAAGCAAAATAAATCTGATTAA  
 CTTCACAGATGAGATGAGCAAAATTTGAGTTAGGCACACTTCGCTCTTTAC  
 TTCCAACAATTCGTAATTTAATAATTGTTTAGGTGTGTACGAATATAAA  
 GCATC

SEQ ID NO: 4903

STRAIN A909

AAACATCCGATACTTAATGA

TCAAAAATCCTTAGCAATTGTTGAACAGATAGAATATGATTTTGATAAAAT  
 TCGATAAATTGAGAAGCTTCTTTTATGCAACATTAGCTAGAATTGCGGTT  
 ATGGATAGAGAAATCAAAAATTTATTAGAGAAAATCCAATAGTCAAAAT  
 CcTTTCaATTGGTGTGGACTTGATACAAGGTTTGAAAGAGTCGATAATG  
 GACAAATTAGGTGGTATAACCTTGATTGGCAGAGGTTATGGAGATAAGA  
 AAATTaTTTTTGAAGAGCATGAAAGAGTTACTAATATAGCAAAAATCAGC  
 CCTAGATGaAACTTGGACACGGGAGGTAAATCCCCAAAATGCCCCCTTTTC  
 TAATCGGTGTGAGAAGGTGTTTAAATGTTTCTAAAAGAAGATGACGTAGAG  
 ACTTTTCTTCATATCTGACAAAATTCATTAGCCAATTTATGGCACAATT  
 TGATTGTGTGATAAGGAAATGATTAAATAAGGAAAGCAACATGATACAG  
 TAAAGTATATGGATACAGAATTTCAAGTTTGGTATCAGATGGTCTAGAG  
 ATTTGTGATTAGACCCCTAAATTAAGCAAAATAAATCTGATTAACTTTAC  
 AGATGAGATGAGCAAAATTTGAGTTAGGCACACTTCGCTCTTTACTTCCAA  
 CAATTCGTAAATTTAATAATTGTTTAGGTGTGTACGAATATAAGCATC

SEQ ID NO: 4904

STRAIN H36B

AAACATCCGATACTTAATGATCAAAAATCCTTAGCA

ATTGTTGAACAGATAGAATATGATTTTGATAAAATTCGATAATTCAGAAGC  
 TTCTTTTATGCAaCATTAGCTAGAATTGCGGTTATGGATAGAGAAATCA  
 AAAAAATTATTAGAGAAAATCCAATAGTCATATCCTTTCAATTGGCTGT  
 GgACTTGATACAAGGTTTGAAAGAGTCGATAATGGACAAATTAGGTGGTA  
 TAACCTTGATTGGCAGAGGTTATGGAGATAAGAAAATTATTTTTGAAG  
 AGCATGAAAGAGTTACTAATATAGCAAAAATCAGCCcTAGATGAAACTTGG  
 ACACGGGAGGTAAATCCCCAAAATGCCCCCTTTCTAATCGTGTGAGAAG  
 TGTTTAAATGTTTCTAAAAGAAGATGACGTAGAGACTTTCTTCATATCC  
 TGACAAAATTCATTAGCCAATTTATGGCACAATTGATTGTGTGcAGAG  
 GAAATGATTAAATAAGGAAAGCAACATGATACAGTAAAGTATATGGATAC  
 AGAATTTCAAGTTGGGTATCAGATGGTCAAGAAATTGTGGATTTAGACC  
 CTAAATTAAGCAAAATAAATCTGATTAACTTTACAGATGAGATGAGCAAA  
 TTTGAGTTAGGCACACTTCGCTCTTTACTTCCAACAATTCGTAATTTAA  
 TAATTGTTTAGGTGTGTACGAATATAAGCATC

SEQ ID NO: 4905

STRAIN 18RS21

AACATCCGATACTTAATGATCAAAAATCCTTAGCAAT

TGTTGAACAGATAGAATATGATTTTGATAAAATTCGATAATTCAGAAGCTT  
 CTTTTATGCAACATTAGCTAGAATTGCGGTTATGGATAGAGAAAATCAAA  
 AAATTTATTAGAGAAAATCCAATAGTCaAATCCTTTCAATTGGTGTGG  
 ACTTGATACAAGGTTTGAAAGAGTCGATAATGGACAAATTAGGTGGTATA  
 ACCTTGATTGGCAGAGGTTATGGAGATAAGAAAATTATTTTTGAAGAG  
 CATGAAAGAGTTACTAATATAGCAAAAATCAGCCCTAGATGAAACTTGGAC  
 ACCGGAGGTAAATCCCCAAAATGCCCCCTTTCTAATCGTGTGcAGAGGTG  
 TTTTAAATGTTTCTAAAAGAAGATGACGTAGAGACTTTCTTCATATCCTG

Table 49: Comparative Sequences related to SAG1502

ACAAATTCATTTAGCCAAATTTATGGCACaATTTGATTGTGTGCATaAGGA  
AATGATTAAATAAGGAAAGCAACATGATACAGTAAAGTATATGGATACAG  
AATTTCAAGTTGGTATCACAGATGGTCATGAGATTGTGGATTAGACCCT  
AAATTAAGCAAATAAATCTGATTAACTTTACAGATGAGATGAGCAAAT  
TGAGTTAGGCACACTTCGCTCTTTACTTCCAACAATTCGTAATTTAATA  
ATTGTTTAGGTGTGTACGAATATAaAGCATC

SEQ ID NO: 4906

STRAIN M732

AAACATCCGATACCTTAATGATCAAAAATCCTTAGCAATTGTTGAACA  
GATAGAAATATGATTGGATAAATTCGATAATTCAGAAGCTTCTTTTATG  
CAACATTAGCTAGAATTCGCGTTATGGATAGAGAAATCAAAAATTTATT  
AGAGAAAATCCAAATAGTCAAAATCCTTTCAATTGGTTGTGGACTTGATC  
AAGGTTTGAAAGAGTCGATAATGGACAAATTAGGTGGTATAACCTTGATT  
TGCCAGAGGTTATGGAGATAAGAAAATTTATTTTGAAGAGCATGAAAGA  
GTTACTAATATAGCAAAATCAGCCCTAGATGAACTTGACACGGGAGGT  
AAATCCCCAAAATGCCCCCTTTCTAATCGTGTGAGAAGGTGTTTAAATGT  
TTCTAAAAGAAAGATGACGTAGAGACTTTCTTCATATCCTGACAAATTC  
TTTAGCCAAATTTATGGGCaCAATTTGATTTGTGTGCATAGGAAATGATTAA  
TAAAGGAAAGCAACATGATACAGTAAAGTATATGGATACAGAAATTTCAAT  
TTGGTATCACAGATGGTCATGAGATTGTGGATTAGACCCTAAATTAAG  
CAAATAAATCTGATTAACTTTACAGATGAGATGAGCAAATTTGAGTTAGG  
CACACTTCGCTCTTTACTTCCAACAATTCGTAATTTAATAATTTGTTAG  
GtGTGTACGAATATAAAGCATC

SEQ ID NO: 4907

STRAIN COH1

AAACATCCGATACCTTAATGATCAAAAATCCTTAGCAA  
TTGTTGAACAGATAGAATATGATTGGATAAATTCGATAATTCAGAAGCT  
TCITTTTATGCAACATTAGCTAGAATTCGCGTTATGGATAGAGAAATCAA  
AAAATTTATTAGAGAAAATCCAAATAGTCAAAATCCTTTCAATTGGTTGTG  
GACTTGATACAAGGTTTGAAAGAGTCGATAATGGACAAATTAGGTGGTAT  
AACCTTGATTGCGCAGAGGTTATGGAGATAAGAAAATTTATTTTGAAGA  
GCATGAAAGAGTTACTAATATAGCAAAATCAGCCCTAGATGAACTTGGA  
CACGGGAGGTAAATCCCCAAAATGCCCCCTTTCTAATCGTGTGAGAAGGT  
GTTTTAATGTTTCTAAAAGAAGATGACGTAGAGACTTTTCTTCATATCCT  
GACAAATTCATTTAGCCAAATTTATGGCACAATTTGATTGTGTGCATAAGG  
AAATGATTAAATAAGGAAAGCAACATGATACAGTAAAGTATATGGATACA  
GAATTTCAAGTTGGTATCACAGATGGTCATGAGATTGTGGATTAGACCC  
TAAATTAAGCAAATAAATCTGATTAACTTTACAGATGAGATGAGCAAAT  
TTGAGTTAGGCACACTTCGCTCTTTACTTCCAACAATTCGTAATTTAAT  
AATGTTTAGGTGTGTACGAATATAAAGCATC

SEQ ID NO: 4908

STRAIN M781

AAACATCCGATACCTTAATGATCA  
AAAATCCTTAGCAATTTGTAACAGATAGAATATGATTGGATAAATTCG  
ATAATTCAGAAGCTTCTTTTATGCAACATTAGCTAGAATTCGCGTTATG  
GATAGAGAAATCAAAAATTTATTAGAGAAAATCCAAATAGTCAAATCCT  
TTCAATTGGTTGTGGACTTGATACAAGGTTTGAAAGAGTCGATAATGGAC  
AAATTAGGTGGTATAACCTTGATTGCGCAGAGGTTATGGAGATAAGAAAA  
TTATTTTGAAGAGCATGAAAGAGTTACTAATATAGCAAAATCAGCCCT  
AGATGAAACTTGACACCGGAGGTAAATCCCCAAAATGCCCCCTTTTCTAA  
TCGTGTGAGAAGGTGTTTTAATGTTTCTAAAAGAAAGTACGTAGAGACT  
TTTCTTCATATCCTGACAAATTCATTAGCCAAATTTATGGCACAATTTGA  
TTGTGTGCATAAGGAAATGATTAAATAAGGAAAGCAACATGATACAGTAA  
AGTATATGGATACAGAAATTCAGTTGGTATCACAGATGGTCATGAGATT  
GTGGATTAGACCCCTAAATTAAGCAAATAAATCTGATTAACTTTACAGA  
TGAGATGAGCAAATTTGAGTTAGGCACACTTCGCTCTTTACTTCCAACAA  
TTCGTAATTTAATAATGTTTAGGTGTGTACGAATATAAAGCATC

SEQ ID NO: 4909

STRAIN CJB110

AAACATCCGATACCTTAATGATCAAAAATCCTTAGCAA  
TTGTTGAACAGATAGAATATGATTGGATAAATTCGATAATTCAGAAGCT  
TCITTTTATGCAACATTAGCTAGAATTCGCGTTATGGATAGAGAAATCAA  
AAAATTTATTAGAGAAAATCCAAATAGTCAAAATCCTTTCAATTGGTTGTG  
GACTTGATACAAGGTTTGAAAGAGTCGATAATGGACAAATTAGGTGGTAT  
AACCTTGATTGCGCAGAGGTTATGGAGATAAGAAAATTTATTTTGAAGA  
GCATGAAAGAGTTACTAATATAGCAAAATCAGCCCTAGATGAACTTGGA  
CACGGGAGGTAAATCCCCAAAATGCCCCCTTTCTAATCGTGTGAGAAGGT  
GTTTTAATGTTTCTAAAAGAAGATGACGTAGAGACTTTTCTTCATATCCT  
GACAAATTCATTTAGCCAAATTTATGGCACAATTTGATTGTGTGCATAAGG  
AAATGATTAAATAAGGAAAGCAACATGATACAGTAAAGTATATGGATACA  
GAATTTCAAGTTGGTATCACAGATGGTCATGAGATTGTGGATTAGACCC  
TAAATTAAGCAAATAAATCTGATTAACTTTACAGATGAGATGAGCAAAT  
TTGAGTTAGGCACACTTCGCTCTTTACTTCCAACAATTCGTAATTTAAT  
AATGTTTAGGTGTGTACGAATATAAAGCATC

SEQ ID NO: 4910

STRAIN 1169NT

AAACATCCGATACCTTAATGATCAAAAATCCTTAGCAAT  
TGTTGAACAGATAGAATATGATTGGATAAATTCGATAATTCAGAAGCTT

Table 49: Comparative Sequences related to SAG1502

CTTTTATGCAACATTAGCTAGAAATTCGCGTTATGGATAGAGAAATCAAA AAATTTATTAGAGAAAAATCCAAATAGTCATATCCTTTCTATTGGTTGTGG ACTTGATACAAGGTTTGAAAGAGTCGATAATGGACAAATAGGTGGTATA ACCTTGATTTGCCAGAGGTTATGGAGATAAGAAAATTATTTTGAAGAG CATGAAAGAGTTACTAATATAGCAAAATCAGCCCTAGATGAACTTGGAC ACAGGAGGTAATCCCCAAATGCCCTTTTCTGATCGTGTGAGAGGTG TTTAAATGTTTCTAAAGAGATGACGTAGAGACTTTTCTCATATCCTG ACAAATTCATTTAGCCAATTTATGGCACAATTTGATTGTGTGAGAAAGGA AATGATTAAAGGAAAGCAACATGATACAGTAAAGTATATGGATACAG AATTTAGTTTGGTATCACAGATGGTCATGAAATTTGGGATTAGACCCCT AAATTAAGCAAAATAATCTGATTAACTTTACAGATGAGATGAGCAAAAT TGAGTTAGGCACACTTCGCTCTTTACTTCCAACAATTCTGTAATTTAATA ATTGTTAGGTGTGTACGAATATAAAGCATC									
SEQ ID NO: 4911 STRAIN JM9130013 AGCAATGTGTGAACAGATAGAAATGATT TTGATAAATTCGATAATTCAGAAGCTTCTTTTATGCAACATTAGCTAG ATTTCGCGTTATGGATAGAGAAATCAAAAAATTTATTAGAGAAAAATCCAA TAGTCATATCCTTTCAATTTGGCTGTGGACTTGATACAAGGTTTGAAAGAG TCGATAATGGACAAATAGGTGGTATAACCTTGATTGCCAGAGGTTATG GAGATAAGAAAAATTATTTTGAAGAGCATGAAAGAGTTACTAATATAGC AAAATCAGCCCTAGATGAACTTGGACACGGGAGGTAAATCCCCAAATG CCCCCTTTCTAATCGTGTGAGAAGGTGTTTAAATGTTTCTAAAGAAAGAT GACGTAGAGACTTTTCTCATATCCTGACAAATTCATTAGCCAATTTAT GGCACAATTTGATTGTGTGAGAAGGAAATGATTAAATAAGGAAAGCAAC ATGATACAGTAAAGTATATGGATACAGAAATTTAGTTTGGTATCACAGAT GGTCATGAAATTTGGATTAGACCCCTAAATTAAGCAAAATAAATCTGAT TAACTTTACAGATGAGATGAGCAAAATTTAGTTAGGCACACTTCGCTCTT TACTTCCAACAATTCGTAAATTTAATAATTTGTTAGGTGTGTACGAATAT AAAGCATC									
PRETTY of: /biotmp/mta42193.2{*} January 21, 2003 05:04 ..									
msa42193.2{176_090}	1	-----	-----	taatga	tcaaaaatcc	ttAGCAATTG	TTGAACAGAT	50	
msa42193.2{176_CJB110}		AAACATCCGA	TACTtaatga	tcaaaaatcc	ttAGCAATTG	TTGAACAGAT			
msa42193.2{176_18RS21}		-AACATCCGA	TACTtaatga	tcaaaaatcc	ttAGCAATTG	TTGAACAGAT			
msa42193.2{176_2603}		AAACATCCGA	TACTtaatga	tcaaaaatcc	ttAGCAATTG	TTGAACAGAT			
msa42193.2{176_A909}		AAACATCCGA	TACTtaatga	tcaaaaatcc	ttAGCAATTG	TTGAACAGAT			
msa42193.2{176_COH1}		AAACATCCGA	TACTtaatga	tcaaaaatcc	ttAGCAATTG	TTGAACAGAT			
msa42193.2{176_M732}		AAACATCCGA	TACTtaatga	tcaaaaatcc	ttAGCAATTG	TTGAACAGAT			
msa42193.2{176_M781}		AAACATCCGA	TACTtaatga	tcaaaaatcc	ttAGCAATTG	TTGAACAGAT			
msa42193.2{176_H36B}		AAACATCCGA	TACTtaatga	tcaaaaatcc	ttAGCAATTG	TTGAACAGAT			
msa42193.2{176_JM9130013}		-----	-----	-----	-----	-----			
msa42193.2{176_1169NT}		AAACATCCGA	TACTtaatga	tcaaaaatcc	ttAGCAATTG	TTGAACAGAT			
Consensus		*****	*****	-----	-----	*****	*****		
msa42193.2{176_090}	51	AGAATATGAT	TTtGATAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA	100		
msa42193.2{176_CJB110}		AGAATATGAT	TTtGATAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA			
msa42193.2{176_18RS21}		AGAATATGAT	TTtGATAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA			
msa42193.2{176_2603}		AGAATATGAT	TTtGATAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA			
msa42193.2{176_A909}		AGAATATGAT	TTtGATAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA			
msa42193.2{176_COH1}		AGAATATGAT	TTtGATAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA			
msa42193.2{176_M732}		AGAATATGAT	TTtGATAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA			
msa42193.2{176_M781}		AGAATATGAT	TTtGATAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA			
msa42193.2{176_H36B}		AGAATATGAT	TTtGATAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA			
msa42193.2{176_JM9130013}		AGAATATGAT	TTtGATAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA			
msa42193.2{176_1169NT}		AGAATATGAT	TTtGATAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA			
Consensus		*****	***-*****	*****	*****	*****	*****		
msa42193.2{176_090}	101	CATTAGCTAG	AaTTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA	150		
msa42193.2{176_CJB110}		CATTAGCTAG	AaTTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA			
msa42193.2{176_18RS21}		CATTAGCTAG	AaTTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA			
msa42193.2{176_2603}		CATTAGCTAG	AaTTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA			
msa42193.2{176_A909}		CATTAGCTAG	AaTTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA			
msa42193.2{176_COH1}		CATTAGCTAG	AaTTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA			
msa42193.2{176_M732}		CATTAGCTAG	AaTTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA			
msa42193.2{176_M781}		CATTAGCTAG	AaTTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA			
msa42193.2{176_H36B}		CATTAGCTAG	AaTTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA			
msa42193.2{176_JM9130013}		CATTAGCTAG	AaTTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA			
msa42193.2{176_1169NT}		CATTAGCTAG	AaTTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA			
Consensus		*****	*-*****	*****	*****	*****	*****		
msa42193.2{176_090}	151	GAAAAATCCAA	ATAGTCaAaT	CCITTCaATT	GGtTGTGGAC	TTGATACAAG	200		
msa42193.2{176_CJB110}		GAAAAATCCAA	ATAGTCaAaT	CCITTCaATT	GGtTGTGGAC	TTGATACAAG			
msa42193.2{176_18RS21}		GAAAAATCCAA	ATAGTCaAaT	CCITTCaATT	GGtTGTGGAC	TTGATACAAG			
msa42193.2{176_2603}		GAAAAATCCAA	ATAGTCaAaT	CCITTCaATT	GGtTGTGGAC	TTGATACAAG			
msa42193.2{176_A909}		GAAAAATCCAA	ATAGTCaAaT	CCITTCaATT	GGtTGTGGAC	TTGATACAAG			
msa42193.2{176_COH1}		GAAAAATCCAA	ATAGTCaAaT	CCITTCaATT	GGtTGTGGAC	TTGATACAAG			

Table 49: Comparative Sequences related to SAG1502

msa42193.2{176_M732}	GAAATCCAA	ATAGTCAaAT	CCTTTCaATT	GGtTGTGGAC	TTGATACAAG
msa42193.2{176_M781}	GAAATCCAA	ATAGTCAaAT	CCTTTCaATT	GGtTGTGGAC	TTGATACAAG
msa42193.2{176_H36B}	GAAATCCAA	ATAGTCAaAT	CCTTTCaATT	GGtTGTGGAC	TTGATACAAG
msa42193.2{176_JM9130013}	GAAATCCAA	ATAGTCAaAT	CCTTTCaATT	GGtTGTGGAC	TTGATACAAG
msa42193.2{176_1169NT}	GAAATCCAA	ATAGTCAaAT	CCTTTCaATT	GGtTGTGGAC	TTGATACAAG
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	201	250			
msa42193.2{176_CJB110}	GTTTGAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTGTC
msa42193.2{176_18RS21}	GTTTGAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTGTC
msa42193.2{176_2603}	GTTTGAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTGTC
msa42193.2{176_A909}	GTTTGAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTGTC
msa42193.2{176_COH1}	GTTTGAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTGTC
msa42193.2{176_M732}	GTTTGAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTGTC
msa42193.2{176_M781}	GTTTGAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTGTC
msa42193.2{176_H36B}	GTTTGAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTGTC
msa42193.2{176_JM9130013}	GTTTGAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTGTC
msa42193.2{176_1169NT}	GTTTGAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTGTC
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	251	300			
msa42193.2{176_CJB110}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_18RS21}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_2603}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_A909}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_COH1}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_M732}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_M781}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_H36B}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_JM9130013}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_1169NT}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	301	350			
msa42193.2{176_CJB110}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_18RS21}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_2603}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_A909}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_COH1}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_M732}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_M781}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_H36B}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_JM9130013}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_1169NT}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	351	400			
msa42193.2{176_CJB110}	TCCCCAAAAT	GCCCCCTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_18RS21}	TCCCCAAAAT	GCCCCCTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_2603}	TCCCCAAAAT	GCCCCCTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_A909}	TCCCCAAAAT	GCCCCCTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_COH1}	TCCCCAAAAT	GCCCCCTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_M732}	TCCCCAAAAT	GCCCCCTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_M781}	TCCCCAAAAT	GCCCCCTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_H36B}	TCCCCAAAAT	GCCCCCTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_JM9130013}	TCCCCAAAAT	GCCCCCTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_1169NT}	TCCCCAAAAT	GCCCCCTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	401	450			
msa42193.2{176_CJB110}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_18RS21}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_2603}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_A909}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_COH1}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_M732}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_M781}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_H36B}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_JM9130013}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_1169NT}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	451	500			
msa42193.2{176_CJB110}	AGCCAATTTA	TGGCACAATT	TGATTGTGTG	CaTAAGGAAA	TGATTAATAA
msa42193.2{176_18RS21}	AGCCAATTTA	TGGCACAATT	TGATTGTGTG	CaTAAGGAAA	TGATTAATAA
msa42193.2{176_2603}	AGCCAATTTA	TGGCACAATT	TGATTGTGTG	CaTAAGGAAA	TGATTAATAA
msa42193.2{176_A909}	AGCCAATTTA	TGGCACAATT	TGATTGTGTG	CaTAAGGAAA	TGATTAATAA



Table 49: Comparative Sequences related to SAG1502

msa42193.2{176_COH1}	AGCCAATT	TGGCACA	TGATTTGT	CAT	AAGGAAA	TGATTAATAA
msa42193.2{176_M732}	AGCCAATT	TGGCACA	TGATTTGT	CAT	AAGGAAA	TGATTAATAA
msa42193.2{176_M781}	AGCCAATT	TGGCACA	TGATTTGT	CAT	AAGGAAA	TGATTAATAA
msa42193.2{176_H36B}	AGCCAATT	TGGCACA	TGATTTGT	CAG	AAGGAAA	TGATTAATAA
msa42193.2{176_JM9130013}	AGCCAATT	TGGCACA	TGATTTGT	CAG	AAGGAAA	TGATTAATAA
msa42193.2{176_1169NT}	AGCCAATT	TGGCACA	TGATTTGT	CAG	AAGGAAA	TGATTAATAA
Consensus	*****	*****	*****	***	*****	*****
msa42193.2{176_090}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG	
msa42193.2{176_CJB110}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG	
msa42193.2{176_18RS21}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG	
msa42193.2{176_2603}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG	
msa42193.2{176_A909}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG	
msa42193.2{176_COH1}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG	
msa42193.2{176_M732}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG	
msa42193.2{176_M781}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG	
msa42193.2{176_H36B}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG	
msa42193.2{176_JM9130013}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG	
msa42193.2{176_1169NT}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG	
Consensus	*****	*****	*****	*****	*****	*****
msa42193.2{176_090}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA	
msa42193.2{176_CJB110}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA	
msa42193.2{176_18RS21}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA	
msa42193.2{176_2603}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA	
msa42193.2{176_A909}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA	
msa42193.2{176_COH1}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA	
msa42193.2{176_M732}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA	
msa42193.2{176_M781}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA	
msa42193.2{176_H36B}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA	
msa42193.2{176_JM9130013}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA	
msa42193.2{176_1169NT}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA	
Consensus	*****	*****	*****	*****	*****	*****
msa42193.2{176_090}	ATAAATCTGA	TAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC	
msa42193.2{176_CJB110}	ATAAATCTGA	TAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC	
msa42193.2{176_18RS21}	ATAAATCTGA	TAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC	
msa42193.2{176_2603}	ATAAATCTGA	TAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC	
msa42193.2{176_A909}	ATAAATCTGA	TAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC	
msa42193.2{176_COH1}	ATAAATCTGA	TAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC	
msa42193.2{176_M732}	ATAAATCTGA	TAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC	
msa42193.2{176_M781}	ATAAATCTGA	TAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC	
msa42193.2{176_H36B}	ATAAATCTGA	TAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC	
msa42193.2{176_JM9130013}	ATAAATCTGA	TAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC	
msa42193.2{176_1169NT}	ATAAATCTGA	TAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC	
Consensus	*****	*****	*****	*****	*****	*****
msa42193.2{176_090}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG	
msa42193.2{176_CJB110}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG	
msa42193.2{176_18RS21}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG	
msa42193.2{176_2603}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG	
msa42193.2{176_A909}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG	
msa42193.2{176_COH1}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG	
msa42193.2{176_M732}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG	
msa42193.2{176_M781}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG	
msa42193.2{176_H36B}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG	
msa42193.2{176_JM9130013}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG	
msa42193.2{176_1169NT}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG	
Consensus	*****	*****	*****	*****	*****	*****
msa42193.2{176_090}	TGTACGAATA	TAAAGCATC				
msa42193.2{176_CJB110}	TGTACGAATA	TAAAGCATC				
msa42193.2{176_18RS21}	TGTACGAATA	TAAAGCATC				
msa42193.2{176_2603}	TGTACGAATA	TAAAGCATC				
msa42193.2{176_A909}	TGTACGAATA	TAAAGCATC				
msa42193.2{176_COH1}	TGTACGAATA	TAAAGCATC				
msa42193.2{176_M732}	TGTACGAATA	TAAAGCATC				
msa42193.2{176_M781}	TGTACGAATA	TAAAGCATC				
msa42193.2{176_H36B}	TGTACGAATA	TAAAGCATC				
msa42193.2{176_JM9130013}	TGTACGAATA	TAAAGCATC				
msa42193.2{176_1169NT}	TGTACGAATA	TAAAGCATC				
Consensus	*****	*****				

SEQ ID NO: 4912

STRAIN 2603 frame: 1

KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARKXRVMDREIKKFIRENPNSQILSI  
 CGGLDTRFRVNDGQIRWYNLDLFEVMEIRKLFFEEHERVTNIAKSALDETWTRVNPQN  
 APPLIVSEGVLMFLKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGKHQDITVKYMDTE

Table 49: Comparative Sequences related to SAG1502

FQFGITDGHEIVDLDPKQKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVYEYKA

**SEQ ID NO: 4913**

STRAIN 090 frame: 2

NDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSIGCGLD  
TRFERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSAIDETWTREVPQNAPFLI  
VSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGQHDVTKYMDTEFQFGI  
TDGHEIVDLDPKQKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVYEYKA

**SEQ ID NO: 4914**

STRAIN A909 frame: 1

KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSI  
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTREVPQN  
APFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGQHDVTKYMDTE  
FQFGITDGHEIVDLDPKQKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVYEYKA

**SEQ ID NO: 4915**

STRAIN H36B frame: 1

KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSHILSI  
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTREVPQN  
APFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGQHDVTKYMDTE  
FQFGITDGHEIVDLDPKQKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVYEYKA

**SEQ ID NO: 4916**

STRAIN 18RS21 frame: 3

HPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSIG  
CGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTREVPQNA  
PFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGQHDVTKYMDTEF  
QFGITDGHEIVDLDPKQKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVYEYKA

**SEQ ID NO: 4917**

STRAIN M732 frame: 1

KHPILNDQKSLAIVEQIEYDLDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSI  
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTREVPQN  
APFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGQHDVTKYMDTE  
FQFGITDGHEIVDLDPKQKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVYEYKA

**SEQ ID NO: 4918**

STRAIN COH1 frame: 1

KHPILNDQKSLAIVEQIEYDLDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSI  
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTREVPQN  
APFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGQHDVTKYMDTE  
FQFGITDGHEIVDLDPKQKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVYEYKA

**SEQ ID NO: 4919**

STRAIN M781 frame: 1

KHPILNDQKSLAIVEQIEYDLDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSI  
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTREVPQN  
APFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGQHDVTKYMDTE  
FQFGITDGHEIVDLDPKQKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVYEYKA

**SEQ ID NO: 4920**

STRAIN CJB110 frame: 1

KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSI  
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSAIDETWTREVPQN  
APFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGQHDVTKYMDTE  
FQFGITDGHEIVDLDPKQKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVYEYKA

**SEQ ID NO: 4921**

STRAIN 1169NT frame: 1

KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSHILSI  
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTQEVNPQN  
APFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGQHDVTKYMDTE  
FQFGITDGHEIVDLDPKQKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVYEYKA

**SEQ ID NO: 4922**

STRAIN JM9130013 frame: 2

AIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSHILSIGCGLDTRFERV  
DNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTREVPQNAPFLIVSEGVL  
MLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGQHDVTKYMDTEFQFGITDGHEI  
VDLDPKQKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVYEYKA

PRETTY of: /biotmp/msa42204.2{\*} January 21, 2003 05:05 ..

	1		50
msa42204.2{176_H36B}	khpilndqks	LAIVEQIEYD fDKFDNSEAS FYATLARiRV MDREIKKFIR	
msa42204.2{176_JM9130013}	-----	-AIVEQIEYD fDKFDNSEAS FYATLARiRV MDREIKKFIR	
msa42204.2{176_090}	-----ndqks	LAIVEQIEYD fDKFDNSEAS FYATLARiRV MDREIKKFIR	
msa42204.2{176_18RS21}	-hpiilndqks	LAIVEQIEYD fDKFDNSEAS FYATLARiRV MDREIKKFIR	
msa42204.2{176_2603}	khpilndqks	LAIVEQIEYD fDKFDNSEAS FYATLARxRV MDREIKKFIR	
msa42204.2{176_A909}	khpilndqks	LAIVEQIEYD fDKFDNSEAS FYATLARiRV MDREIKKFIR	
msa42204.2{176_CJB110}	khpilndqks	LAIVEQIEYD fDKFDNSEAS FYATLARiRV MDREIKKFIR	

Table 49: Comparative Sequences related to SAG1502

msa42204.2{176_COH1}	khpilndqks	laIVEQIEYD	ldKFDNSEAS	FYATLARiRV	MDREIKKFIR
msa42204.2{176_M732}	khpilndqks	laIVEQIEYD	ldKFDNSEAS	FYATLARiRV	MDREIKKFIR
msa42204.2{176_M781}	khpilndqks	laIVEQIEYD	ldKFDNSEAS	FYATLARiRV	MDREIKKFIR
msa42204.2{176_1169NT}	khpilndqks	laIVEQIEYD	fdKFDNSEAS	FYATLARiRV	MDREIKKFIR
Consensus	-----	*****	*****	*****	*****
51					
msa42204.2{176_H36B}	ENPNShILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_JM9130013}	ENPNShILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_090}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_18RS21}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_2603}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_A909}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_CJB110}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_COH1}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_M732}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_M781}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_1169NT}	ENPNShILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
Consensus	*****	*****	*****	*****	*****
101					
msa42204.2{176_H36B}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_JM9130013}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_090}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_18RS21}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_2603}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_A909}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_CJB110}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_COH1}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_M732}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_M781}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_1169NT}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
Consensus	*****	***	*****	*****	*****
151					
msa42204.2{176_H36B}	SQFMAQFDLC	qKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_JM9130013}	SQFMAQFDLC	qKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_090}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_18RS21}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_2603}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_A909}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_CJB110}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_COH1}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_M732}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_M781}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_1169NT}	SQFMAQFDLC	qKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
Consensus	*****	*****	*****	*****	*****
201					
msa42204.2{176_H36B}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_JM9130013}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_090}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_18RS21}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_2603}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_A909}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_CJB110}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_COH1}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_M732}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_M781}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_1169NT}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
Consensus	*****	*****	*****	*****	
239					

Table 50: Comparative Sequences relating to SAG 1024

## SEQ ID NO. 5001

## STRAIN 2603

ATGAAAAACAAAACTATTACTGCTTATTGGAGGCTTATTAATAATGATAATGATGACA  
 GCATGTAAGGATTCAAAAATCCAGAAAACCGCACAAAGGAAGAGTACCAAGCTGAACAA  
 AATTTTAAACCGTTTTTTGAGTTTGTAGCAGAAAAGATAAGATTGAGCAAAATACAA  
 AAATACTTACTATTAGTATCGGATTCAGGTGATGCATTAGATTAGAAATATTTCTATAGT  
 ATTCAAGATTTAAAAAAAATAAGGATTTAGGGAAGTTTGAACAAGAAAAGTCAAATA  
 GAAAAGCCGGTGGCTATAATGAGTTAGAAAATAAGAGGTCCCAITTTGAATATTTTAA  
 AATAATATAGTTTATCCAAAAGGAAAACCGAATATTACATTTGATGACTTTATTATCGGA  
 GCAATGGATACTAAAGAATTAAAGAATTAAAAAATTAAAAAGTAAAAAGTTATTATTA  
 AAACATCCGGAACCTGAGTTGAAGATATAACATATGAATTGCCGACACAGTCAAGCTT  
 ATTAATAAA

## SEQ ID NO. 5002

## STRAIN 090

TAAGGATTCAAAAATCCAGAAAACCGCACAAAG  
 GAAGAGTACCAAGCTGAACAAAATTTTAACTGTTTTTGGAGTTTTTGTAGC  
 ACAAATATATAAGATTGAAACAAAATACAAAATACCTACTATTAGTAT  
 CGGATTCAGGTGATGCATTAGATTAGAAATATTTCTATAGTATTCAGAT  
 TTAATAAAAAATAAGGATTTAGGGAAGTTTGAACAAGAAAAGTCAAAAT  
 AGAAAAGCCGGTGGCTATAATGAGTTAGAAAATAAGAGGTCCCATTTG  
 AATATTTTAAAAATAATATAGTTTATCCAAAAGGAAAACCGAATATTACA  
 TTTGATGACTTTATTATCGGAGCAATGGATATAAGAAATTAAAAAATT  
 AAAAGTAAAAAGTTATTTATTAACATCCGGAACCTGAGTTGAAAGATA  
 TAACATATGAATTGCCGACACAGTCAAGCTTATTAATAAA

## SEQ ID NO. 5003

## STRAIN 18RS21

TAAGGATTCAAAAATCCAGAAAACCGCACAAAGGAAG  
 AGTACCAAGCTGAACAAAATTTTAAACCGTTTTTGGAGTTTTTGTAGCAGAA  
 AAGATATAAGATTGAGCAAAATACAAAATACCTACTATTAGTATTCGGA  
 TTCAGGTGATGCATTAGATTAGAAATATTTCTATAGTATTCAGATTTAA  
 AAAAAATAAGGATTTAGGGAAGTTTGAACAAGAAAAGTCAAAATAGAA  
 AAGCCGGTGGCTATAATGAGTTAGAAAATAAGAGGTCCCATTTGAATA  
 TTTTAAAAATAATATAGTTTATCCAAAAGGAAAACCGAATATTACATTTG  
 ATGACTTTATTATCGGAGCAATGGATATAAGAAATTAAAGAATTAAAA  
 GAATTAATAAAATTAAAGTAAAAAGTTATTTATTAACATCCGGAAC  
 TGAGTTGAAAGATATAACATATGAATTGCCGACACAGTCAAGCTTATTA  
 AAAAA

PRETTY of: /biotmp/msa212269.2{\*} February 10, 2003 05:07 ..

msa212269.2{184_090}	1	50
msa212269.2{184_2603}	atgaaaaaac aaaaaactatt actgcttatt ggaggcttat taataatgat	
msa212269.2{184_18RS21}	*****	
Consensus	*****	
msa212269.2{184_090}	51	100
msa212269.2{184_2603}	-----TAAGG ATTCAAAAAT CCCAGAAAAC CGCACAAAGG	
msa212269.2{184_18RS21}	aatgatgaca gcatgTAAGG ATTCAAAAAT CCCAGAAAAC CGCACAAAGG	
Consensus	*****	
msa212269.2{184_090}	101	150
msa212269.2{184_2603}	AAGAGTACCA AGCTGAACAA AATTTTAAAC tGTTTTTTGA GTTTTTAGCA	
msa212269.2{184_18RS21}	AAGAGTACCA AGCTGAACAA AATTTTAAAC cGTTTTTTGA GTTTTTAGCA	
Consensus	*****	
msa212269.2{184_090}	151	200
msa212269.2{184_2603}	CAAAAAtATA AAGATTTGaa CAAAATACAA AAATACTTAC TATTAGTATC	
msa212269.2{184_18RS21}	CAAAAAGATA AAGATTTGag CAAAATACAA AAATACTTAC TATTAGTATC	
Consensus	*****	
msa212269.2{184_090}	201	250
msa212269.2{184_2603}	GGATTTCAGGT GATGCATTAG ATTAGAAATA TTTCTATAGT ATTCAAGATT	
msa212269.2{184_18RS21}	GGATTTCAGGT GATGCATTAG ATTAGAAATA TTTCTATAGT ATTCAAGATT	
Consensus	*****	
msa212269.2{184_090}	251	300
msa212269.2{184_2603}	TAAAAAATAA TAAGGATTTA GGAAGTTTG AAACAAGAAA AAGTCAAATA	
msa212269.2{184_18RS21}	TAAAAAATAA TAAGGATTTA GGAAGTTTG AAACAAGAAA AAGTCAAATA	
Consensus	*****	
msa212269.2{184_090}	301	350
msa212269.2{184_2603}	GAAAAGCCCG GTGGCTATAA TGAGTTAGAA AATAAAGAGG TCCCATTGTA	
msa212269.2{184_18RS21}	GAAAAGCCCG GTGGCTATAA TGAGTTAGAA AATAAAGAGG TCCCATTGTA	
Consensus	*****	

Table 50: Comparative Sequences relating to SAG 1024

msa212269.2{184_090}	351	400
msa212269.2{184_2603}	ATATTTTAAA AATAATATAG TTTATCCAAA AGGAAAACCG AATATTACAT	
msa212269.2{184_18RS21}	ATATTTTAAA AATAATATAG TTTATCCAAA AGGAAAACCG AATATTACAT	
Consensus	*****	*****
msa212269.2{184_090}	401	450
msa212269.2{184_2603}	TTGATGACTT TATTATCGGA GCAATGGATA CT.....	.....
msa212269.2{184_18RS21}	TTGATGACTT TATTATCGGA GCAATGGATA CT.....	..aaagaatta
Consensus	*****	-----
msa212269.2{184_090}	451	500
msa212269.2{184_2603}	AAAGAATTAA AAAAATTAAA AGTAAAAAGT TATTATTATA AACATCCGGA	
msa212269.2{184_18RS21}	AAAGAATTAA AAAAATTAAA AGTAAAAAGT TATTATTATA AACATCCGGA	
Consensus	*****	*****
msa212269.2{184_090}	501	550
msa212269.2{184_2603}	AACTGAGTTG AAAGATATAA CATATGAATT GCCGACACAG TCGAAGCTTA	
msa212269.2{184_18RS21}	AACTGAGTTG AAAGATATAA CATATGAATT GCCGACACAG TCGAAGCTTA	
Consensus	*****	*****
msa212269.2{184_090}	551	
msa212269.2{184_2603}	TTAAAAAA	
msa212269.2{184_18RS21}	TTAAAAAA	
Consensus	*****	
SEQ ID NO. 5004		
STRAIN 2603 frame: 1		
MKKQKLLLLIGLLIMIMMTACKDSKIPENRTKEEYQAEQNFKPFEEFLAQKDKDLSKIQ		
KYLIVSDSGDALDLEYFYISIQDLKKNKDLGKFETRKSQIEKPGGYNELENKEVPFEYFK		
NNIVYPKGKPNITFDDFIIGAMDTKELKELKLVKSYLLKHPETELKDITYELPTQSKL		
IKK		
SEQ ID NO. 5005		
STRAIN 090 frame: 2		
KDSKIPENRTKEEYQAEQNFKPFEEFLAQKYKDLNKIQKYLIVSDSGDALDLEYFYISIQ		
DLKKNKDLGKFETRKSQIEKPGGYNELENKEVPFEYFKNNIVYPKGKPNITFDDFIIGAM		
DTKELKELKLVKSYLLKHPETELKDITYELPTQSKLIKK		
SEQ ID NO. 5006		
STRAIN 18RS21 frame: 2		
KDSKIPENRTKEEYQAEQNFKPFEEFLAQKDKDLSKIQKYLIVSDSGDALDLEYFYISIQ		
DLKKNKDLGKFETRKSQIEKPGGYNELENKEVPFEYFKNNIVYPKGKPNITFDDFIIGAM		
DTKELKELKLVKSYLLKHPETELKDITYELPAQSKLIKK		
PRETTY of: /biotmp/msa212547.2{*} February 10, 2003 05:11 ..		
msa212547.2{184_18RS21}	1	50
msa212547.2{184_2603}	-----	-----
msa212547.2{184_090}	-----	-----
Consensus	*****	*****
msa212547.2{184_18RS21}	51	100
msa212547.2{184_2603}	QKdKDLsKIQ KYLLLVSDSG DALDLEYFYIS IQDLKKNKDL GKFETRKSQI	
msa212547.2{184_090}	QKdKDLsKIQ KYLLLVSDSG DALDLEYFYIS IQDLKKNKDL GKFETRKSQI	
Consensus	***-***	*****
msa212547.2{184_18RS21}	101	150
msa212547.2{184_2603}	EKPGGYNELE NKEVPFEYFK NNIVYPKGKP NITFDDFIIG AMDTkelkel	
msa212547.2{184_090}	EKPGGYNELE NKEVPFEYFK NNIVYPKGKP NITFDDFIIG AMDT.....	
Consensus	*****	*****
msa212547.2{184_18RS21}	151	186
msa212547.2{184_2603}	KELKLVKVS YLLKHPETEL KDITYELPaQ SKLIKK	
msa212547.2{184_090}	KELKLVKVS YLLKHPETEL KDITYELPtQ SKLIKK	
Consensus	*****	*****

Table 51: Comparative Sequences relating to SAG0677

SEQ ID NO. 5101

STRAIN 2603

ttgaataataaagggtgtcggtggcgatgggtgtccaaatattatcaatacta  
 tatcaaaatggacaacaataaaccttacttaagtcccaaagataagacta  
 ctgtagagaagttagaagatcgctggaaaaaatctcttcaaagttcag  
 gatactggcattgggtttgaaagacgtttatcttcaatctgttaagtattgt  
 tgggtgggtggcaataataatttagacctatcacacctccaggatttaaaa  
 aagaagataaaaaagttgaaaaaccaaatttagacctccaccaggaatt  
 gatttaccagcaccaacttcaatgagaagttttgattattcaacccacc  
 gggaactaagccaagcaaacccaaagatagtttatcaactcctccaggtt  
 tcccagatttaaacacgcccggatgaagcaccacaaaggtatgtaaaaa  
 gacgctattgaagataaatcaggagcaatataatagctaaagtctctca  
 acttagctttgtgatggccctatttttagctagcaaaagtaaatggcaaaa  
 tattacaagtogaatctgatggcaaattagtcatctctagaatgctttg  
 tcagctaataatcaatttgatgacactagtcttaaaatttatcgtaataata  
 tcgcaataaagaaattactatcacacagattatttgcagatacaaaat  
 atgtcaatatcacagcgggtgactatttgagcaataactacttttgagcaa  
 tttagctactgggtgaaacagtagattaccatgccattgtattttcaagct  
 tgctgctatttaagacaaggggtggaagatttatgttaacgataaattgc  
 aagaaactctcgtagcgcttaagataaatctgttaagattgggtatt  
 gaattaccaaattgatgtcagacatatgtatgtttatctgttctgtctt  
 gaatgaggttaaaactgttgataaatcttgaaaaatgatgaacaagaca  
 ttaactcagcaaaaacttaccatttaaaatacaacccgacaaatcgctgt  
 cttagagttactatataaacttaactcaagttcagaaatcatgaccac  
 ttccaagatggaaagatgccagaattgggtgaacaaaaagatgtttctt  
 tggatataaacgatattggacatgagtaagtttaaaactattcgacttgg  
 cgaagaggttctgaatttaaggggacaacttattgcaaaaactggaacagt  
 tgaattagatatgtttttcaacaatctcaagaccagcttcaattatta  
 aaaaaatataccttatccaaatgggtgttccaaatgaattgaaaaaatt  
 gactctgattttgggttaactgaaagttagatagatggatactatatata  
 taagatgcaattaaccttaatttaaatcaaccagtggtgcaagctctta  
 aagttgtttataaagggcaagaagatccatatagtcacagaagaagat  
 atgactaaaaaaggtgaacagctcagtcattcaactcaagccaatgaaaa  
 tacagcaaaagtaacctttgctaatatgactgggtcacattatagtaagg  
 ttactgtgaatggaaagaagttgttaaaaggtagtgagtacctttaact  
 aaaggatggacaacatttgtattacataaaacagaaaaattcatataatgt  
 taaaagtttgattatggagacgggttagtgtaagtaagaaagtcaacaac  
 ttcttttaagtcctagatttatctaaaaatagcatatgagggatatgcta  
 ctactatgcaaaaagattcagcgtatcacgaaacagtgacagctcagtc  
 ccttcgaattaatctcactgcagatactaaacttaattttaatgctgtta  
 aaggagcagtgctcttactgaaaatgatgatgagacagtttgagtt  
 gctggaccacaagatgatcctgttagtgaaacataaatacccatcagttat  
 tctcttaactcctgccttatggaaactgctagtgaggcaactcctaatg  
 gtaaggaatcacagcatctggtattatcggtcacatcaaggatgggtgat  
 aaaaacagcatgttgaagtcaaaatgggtgaatgaaaaatggagacatgct  
 aggaacccctgttatattcaaggttaagacttgactaatcgacacaaac  
 cattaatgagtggaagcgtagagtaactttatgcccgttaacaatatgagttc  
 cgggctaaattaccacttagtcgttttaacacttggattagggttgaagt  
 ggttaacagaagcaggagagaagcaagttatgttctgcgcagttctcttg  
 accaactcagttccagagcttaacacagcagtttgctaaacgtgatttgact  
 tctgatactgctcttatccacatcggtgccaagatgactctctaaact  
 aaaaattatatcaagatgattcattacttgaatctgttgataaaacccggtc  
 tttagtgttttagaaatgggttagaaatcactaaagatatgacagtacca  
 ctagaatttggagataatatatttaagttatctgctgttgacttatcaaa  
 ttatcgctgtaagtagagaccttatatatctatagaacccgttttgatgtta  
 aagcaagccaaatgacagctgacaaaggagctaaagttaactgtggatattg  
 ttgatgaagcacttagttgttccagaatggcaggagcttatacattaac  
 aatcgacgaagctccaaacacaaatgaatcaggaatgttaacaaacgcta  
 aagttatcgattcattatgtaaatgggtgttgataaagttgatgttccg  
 attaaagtagttgacttagaagctattcgtaagctgaagaagcagtaaa  
 agctgaagaagcagctaaagctgaagaagcagtaaaagctgaagaggac  
 ataaaacccaagaagcactatagttgaagaaggctacaaggttaataac  
 gttcatcaaaactgatactacagtttaagcgtctgatttaccaaagactaa  
 gacagtttccgagttcatatggctagaacagacaataaacagataaactt  
 cacatcagacacatgttgaaaaacaaataaaaatacattgccatccact  
 ggtgacagcaaacgtgggtatttatatcactggaaatggctatcggttatgct  
 gagtgattattttagtttagctaaaaagtttaaaagcaaatat

SEQ ID NO. 5102

STRAIN A909

TTGAATAATAAAGGTGTCGGTGGCGAT

GGTGTCCAAATTTATCAATACTATATCAAAATGGACAACAATAAACCTTA  
 CTTAAGTCCCAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGCTGGA  
 AAAAAATTACTTTCAAAGTTCAAGATATCGGCATTGGTTTGAAGACGTT  
 TATCTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACCT  
 TATCACACCTCCAGGATTTAAAAAAGAGATAAAAAAGTTGAAAAACCAA  
 AATTAGACCGTCCACCAGGAATTGATTACCAACCAACTTCAATGAGA  
 AGTTTGTATTATCAACCCACCGGGAAGTAAGCCAAGCAAAACCAAGA  
 TAGTTTATCAACTCTCCAGGTTTCCAGATTTAACACGCGCCGGATG  
 AAGCACTAAAGGATAGTAAAAAAGACGCTATTGAAGATAAATCAGGAGCA  
 ATTAATATGCTAAGTCTCTTCAACTTAGCTTTGTTGATGACCTATTTT  
 AGCTAGCAAAAGTAAATGGCAAAATATTACAAGTCGAATCTGATGGCAAT  
 TAGTCATTCCTAGAAATGCTTTGTGAGTAAATCAATTTGATGACACTAGT

Table 51: Comparative Sequences relating to SAG0677

CTTAAATTTTATCGTAATAATAATCGCAATAAGAAATTACTATCACAAC  
 AGATTATTTTGCAGATACAAAATATGTCAATATCACAGCGGTGACTATT  
 TGAGCAATACACTTTTGAGCAATTAGCTACTGGTGAAACAGTAGATTAC  
 CATGCCATTGTATTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGGTAA  
 GATTTATGTTAAACGATAAATTGCAAGAACTTCTCGTATAGCGCTTAAAG  
 ATAAATCTGTTAAGATTGGTATTGAATTACCAATGATGTGAGACATATT  
 GATAGTTTATCTGTTCTGTTGAATGAGGTTAAACTGTTGATAATAT  
 CTTGAAAAATGATGAACAAGACATTAACTCTCAGCAAACTTACCAATTAA  
 AATACAAACCCGACAAATCGTCTAGAGTTTACTATTAAATAACATTAAAC  
 TCAAGTTTCAGAAATCATGACCACTTCAAAGATGGAAAGATGCCAGAATT  
 GGTGTAaCAAAAAGATGTTCTTTGGATATAaCGATATGGACATGAGTA  
 AGTTTAAAACTATTGCACTTGGACGAAAGGATTCTGAATTTAAGGACAA  
 CTTATTGCAAAAACCTGGAACAGTTGAATTAGATATGTTTTCAAACAATC  
 TCAAGACCCAGCTTCAATTATTTAAAAAATATACCTTATCCAAAATGGTG  
 TTCCAAATGAATTGAAAAAATTGACTCTAGTTTGGTTTAACTGAAAGT  
 CAGATAGTGGATATATATTTATAAAGATGCAATTAACTTAAATTTAA  
 ATTAACAGTGGTGCAAGTCTTAAAGTTGTTTATAAAGGCAAGAAGATC  
 CATATAGTCATCAGAAAGAAGATATGACTAAAAAAGGTGAACAGCTCAGT  
 CATTTCACTCAAGCCAATGAAATACAGCAAAAGTAACTTTGCTAATAT  
 TGAATGCTGACATTATAGTAAGTTACTGTGAATGGAAAGAAGTTGGTA  
 AAGGTAGTGAGTTACTTTAACTAAAGGATGGACAACATTTGATTACAT  
 AAAAAAGAAATTTCAATTAATGTTTAAAGTTGATTATGGAGACGGTAG  
 TGTAAGTAAGAAAGTTCAACAACCTTCTTTAAGTCTAGATTATCTAAAA  
 ATAAAGCATATGAGGGATATGCTACTTACTATGCAAAAAGATTGAGGTAT  
 TACGAaaCAAGTGAAGTCTAGTCCCTCGAATTAACTCTCACTGCAGATC  
 TAACTTAAATTTAATGCTGTTAAAGGAGCGAGTCTCTTACTGAAAATA  
 TGATGATGAGACAGTTTGCAGTTGCTGGACCAAGATGATCCTGTTAGT  
 GAACATAAATACCCATCAGTATTTCTCTTAACTCCTGCTTATTGGAAAC  
 TGCTAGTGAGGCAACTCTaAATGGTAAGGAATCACAGCATCTGGTATTA  
 TCCGTACATCAAGGATGGTGATAAAAGCAAGCATGTTGAAGTCAAAATG  
 GTGAATGAAATGGAGACATGCTAGGAACCCCTGTTATTATTCAAGGTAA  
 AGACTTGACTAATCGAACAAAACCAATTAATGAGTGGACGTAGAGTACTTT  
 ATGCCGGTAAACAATATGAGTTCCGGGCTAAATTACCCTTAGTCTGTTTT  
 AACACTTGGATTAGGGTTGAAGTGGTAACAGAAGCAGGAGAGAAAGCAAG  
 TATTGTTGCTCGCATGTTCTTTGACCAATCAGTCCAGAGCTTAAACAG  
 CAGTTGCTAAACGATTTGACTTCTGATCTGCTCTTATCCACATCGTT  
 GCCAAGATGACTCTCTAAACTTAAATTATATCAAGATGATTCTTACT  
 TGAATCTGTTGATAAAACCGGTCTTTATAGTTTTAGAAATGGTGTAGAAA  
 TCACTAAAGATATGACAGTACCCTAGAAATTTGGAGATAATATTATTAAG  
 TTATCTGCTGTTGACTTATCAAAATATCGTCTGTAATGAGACCCCTTCATAT  
 CTATAGAAACCGTTTTGATGTTAAAGCAAGCCAATGACAGCTGACAAAG  
 GAGCTAAAGTAACTGTGGATATGTTGATGAAGCACTTAGTTGTTCCAGAA  
 ATGGCAGGAGCTTATACATTAACAATCGACGAAGATCCAACACAATGTA  
 ATCAGGAATGTTAAACAACGCTAAAGATCGATTCAATTATGTAATGGTG  
 GTGTTGATAAAGTTGATGTTCCGATTAAAGTGAAGTGAAGTGAAGGCTATT  
 CGTAAAGCTGAAGAAGCACATAAGCTGACGAAGCACGTAAAGCTGAAGA  
 AGCAGCTAAAGCTGAAGAAGCACGTAAAGCTGAAGAAGCACGTAAAGCTG  
 AAGAGGGACATaAAAACCAAGAACCTTATAGTTGAAGAAGGCTACAAG  
 GTTAATAACGTTTCATCAAACTGATCTACAGTTAAAGCGTCTGATTTACC  
 AAAGACTAAGACAGTTTCCGAGTTTCATATGGCTAGAACAGACAATAAAC  
 AGATAACTTCATCAGACATGTTGAAAAACAATTTAAAAATA

SEQ ID NO. 5103

STRAIN H3B

TGGTGTCCAAATTTATCAATACTATATCAAAATGGACAACAATAAACCTT  
 ACTTAAGTCCCAAGATAAGACTACTGTAGAGAAGTTAGaaGATCGCTGG  
 AAAAAAATTACTTTCAAAGTTCCAGGATACTGGCATTGGTTTGAAGACGT  
 TTATCTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACC  
 TTATCACACCTCCAGGATTAAAAAAGAAGATAAAAAAGTTGAAAAACCA  
 AAATTAGACCGTCCACCAGGAATTGATTTACCAGCACCAACTTCAATGAG  
 AAGTTTGTATTATCAACCCACCGGGAACCTAAGCCAAGCAAAACCAAG  
 ATAGTTTATCAACTCTCCAGGTTTCCAGATTTTAAACAGCCGCGCGGAT  
 GAAGCACTAAAGGATAGTAAAAAAGACGCTATTGAAGATAAATCAGGAGC  
 AATTAAATATGCTAAGTCTCTTCAACTAGCTTTGTTGATGACCCCTATTT  
 TAGCTAGCAAAAGTAAATGGCAAAATATTACAAGTCAATCTGATGGCAAA  
 TTAGTCATTCTTGAATGCTTTGTGAGCTAATCAATTTGATGACACTAG  
 TCTTAAATTTTATCGTAATAATAATCGCAATAAAGAAATTTacTATCACAA  
 CAGATTATTTTGCAGATACAAAATATGTCAATATCACAGCGGTGACTAT  
 TTGAGCAATACTACTTTTGAAGCAATTAGCTACTGGTGAAaCAGTAGATTA  
 CCATGCCATTGTaTCTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGGTA  
 AGATTTATGTCAACGATAAATTGCAAGAACTTCTCGTATAGCGCTTAAAG  
 GATAAATCTGTTAAGATTGGTATTGAATTACCAATGATGTGACAGATAT  
 TGATAGTTTATCTGTTCTGTTGAATGAGGTTAAACTGTTGATAATA  
 TCTTGAAAAATGATGAACAAGACATTAACTCTCAGCAAACTTACCAATTA  
 AAATACAACCCGACAAATCGTCTAGAGTTTACTATTAAATAACATTAA  
 CTAAGTTTCAGAAATCATGACCACTTCAAAGATGGAAAGATGCCGAAT  
 TGGTTGAACAAAAGATGTTCTTTGGATATAAACGATATGGACATGAGT  
 AAGTTTAAACTATTGCACTTGGACGAAAGGATTCTGAATTTAAGGGACA  
 ACTTATTGCAAAAACCTGGAACAGTTGAATTAGATATGTTTTCAAACAAT  
 CTCAAGACCCAGCTTCAATTATTTAAAAAATATACCTTATCCAAAATGGT  
 GTTCCAAATGAATTGAAAAAATTGACTCTAGTTTGGTTTAACTGAAAG  
 TCAGATAGATGGATCTATATTTATAAAGATGCAATTAACTTAAATTTA  
 AATTAACAGTGGTGCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGAT

Table 51: Comparative Sequences relating to SAG0677

CCATATAGTCATCAGAAAGAAGATATGACTAAAAAGGTGAACAGCTCAG  
 TCATTCAACTCAAGCCAATGAAATACAGCAAAAGTAACCTTTGCTAATA  
 TTGACTGGTCACATTATAGTAAGGTTACTGTGAATGGAAAAGAAGTTGGT  
 AAAGGTAGTGAGTTACCTTTAACTAAAGGATGGACAACATTTGTATTACA  
 TAAAACAGAAAAATTCATTAAATGTTAAAGTTTGATTATGGAGACGGGTA  
 GTGTAAGTAAGAAAGTTCAACAACCTCCCTTAAAGTCCTAGATTATCTAAA  
 AATAAGCATATGAGGGATATGCTACTTACTATGCAAAAAGATTGAGCGTA  
 TTACGAAACAAGTGACAGTCTAGTCTTCCGAATTAATCTCACTGCAGATA  
 CTAAACCTTAATTTTAATGCTGTTAAAGGAGCGAGTGTCTTACTGAAAAT  
 ATGATGATGAGACAGTTTGCAAGTTGCTGGACCACAAGATGATCCTGTTAG  
 TGAACATAAATACCCATCAGTATTTCTCTTAACCTCCTGCCTTATTGGAAA  
 CTGCTAGTGAGGCACTCTAAATGGTAAGGAAATCACAGCATCTGGTATT  
 ATCGGTCACATCAAGGATGGTGATAAAGCAAGCATGTTGAAGTCAAAAT  
 GGTGAATGAAAATGGAGACATGCTAGGAACCCCTGTTATTATCAAGGTA  
 AAGACTTGACTAATCGAACAAAACCATTAATGAGTGGACGTAGAGTACTT  
 TATGCCGGTAAACAATATGAGTTCGGGGCTAAATTACCACCTAGTCTGTTT  
 TAAcAaCTTGGATTAGGGTTGAAGTGGTAACAGAGCAGGAGAGAAAGCAA  
 GTATTGTTTCGTCGCGATGTTCTTTGACCAATCAGTTCAGAGCTTAACACA  
 GCAGTTGCTAAACGCTGATTGACTTCTGATAGTCTCTTATCCACATCGT  
 TGCCAAAGATGACTCTCTAAAACTAAAAATTATATCAAGATGATTCAATTAC  
 TTGAATCTGTGATAAAACCGGCTCTTATAGTTTGAAGATGGGTAGAA  
 ATCACTAAAGATATGACAGTACCCTAGAAATTTGGAGATAATATTACTAA  
 GTTATCTGCTGTTGACTTATCAAATTTATCGTCTGTAATGAGACCCCTTCATA  
 TCTATAGAAACCGTTTGTATGTTAAAGCAAGCCAAATGACAGCTGACAAA  
 GGAGCTAAAGTAAGTACTGTGGATATGTTGATGAAGCACTAGTGTTCAGA  
 AATGGCAGGAGCTTATACATTAACTCGACGAAGCTCCAAACACAAATG  
 AATCAGGAATGTTAACAACCGCTAAAGTATCGATTCAATTATGTAATGGT  
 GGTGTTGATAAAGTtGATGTTCCGATTAAAGTAGTTGACTTAGAAGCTAT  
 TCGTAAAGCTGAAGAAGCACATAAAGCTGACGAAGCAGTAAAGCTGAAG  
 AAGCAGTAAAGCTGACGAAGCACATAAAGCTGAAGAAGTACGTAAGCT  
 GAAGAAGCACATAAAGCTCGAAGAAGCAGTAAAGCTGAAGAGGGACATAA  
 AACCCAAGAAGCACCTATAGTTGAAGAAGGCTACAAGTTAATAACGTTT  
 ATCAAACTGATACTACAGTTAAAGCGTCTGATTACCAAGACTAAGACA  
 GTTTCGCAGTTTATATGGCTAGAACAGACAATAAACAGATAAATTCACA  
 TCAGACACATG

SEQ ID NO. 5104

STRAIN 18RS21

TTGAATAATAAGGTGTGCGTGGCGATGGTGTCCAA  
 ATTTATCAATACTATATCAAAATGGACAACAATAAACCTTACTTAAGTCC  
 CAAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGCTGGAAAAAATTA  
 CTTTCAAGTTTCAAGATACTGGCATTGGTTTGAAGACGTTTATCTTCAA  
 TCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACCTTATCACACC  
 TCCAGGATTTAAAAAAGAAGATAAAAAAGTTGAAAAACCAAATTAGACC  
 GTCCACCAGGAATTGATTACCAGCACCACTCAATGAGAAGTTTGTAT  
 TATTCACCCCAACCGGAACTAAGCCAGCAACCCAAAGATAGTTTATC  
 AACTCCTCCAGGTTTCCCAGATTAAACACGCCGCCGCGGATGAAGCACCAA  
 AGGATAGTAAAAAAGACGCTATTGAAGATAAATCAGGAGCAATTAATAT  
 GCTAAGTCTCTCAACTTAGCTTTGTTGATGACCCATTTTAGCTAGCAA  
 AGTAAATGGCAAAATATTACAAGTCGAATCTGATGGCAAAATTAGTCATTC  
 CTAGAAATGCTTTGTCAGCTAATCAATTTGATGACACTAGTCTTAAATTT  
 TATCGTAATAATAATCGCAATAAAGAAATTACTATCACACAGATTATTT  
 TGAGATACAAAATATGTCAATATCACAGCGTTGACTATTTGAGCAATA  
 CTACTTTTGAAGCAATTAGCTACTGGTGAACAGTAGATTACCATGCCATT  
 GTATTTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGGTAAGATTTATGT  
 TAACGATAAATTGCAAGAACTTCTCGTATAGCGCTTAAAGATAAATCTG  
 TTAAGATTGGTATTGAATTAACCAATGATGTCAGACATATTGATAGTTTA  
 TCTGTTCTGTCGTTTGAATGAGGTTAAACTGTGATAATATCTTGAAAAA  
 TGATGAACAAGCATTAAATCTCAGCAAaACTTACCAATTAATAACAAACC  
 CGACAATCGTCGTCTAGAGTTTACTATTAATAACATTAACTCAAGTTCA  
 GAAATCATGACCACTTTCAAAGATGGAAGATGCCAGAAATGGTTGAACA  
 AAAAGATGTTCTTTGGATATaAACGATATGGACATGAGTAAGTTTAAAA  
 CTATTCGACTTGACGAAAGGATTCTGAATTTAAGGGACAACCTTATTGCA  
 AAAACTGGAACAGTTGAATTAGATATGTTTTCAACAATCTCAAGACCC  
 AGCTTCAATTTATAAAAAAATATACCTTATCCAAATGGTGTTCCAAATG  
 AATTGAAAAAATTTGACTCTAGTTTGGTTTAACTGAAAGTCAGATAGAT  
 GGATACTATATTATAAAGATGCAATTAACCTTAATTTAAATTAACAGG  
 TGGTCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGATCCATATAGTC  
 ATCAGAAAGAAGATATGACTAAAAAAGGTGAACAGCTCAGTCATTCAACT  
 CAAGCCAATGAAATACAGCAAAAGTAACCTTTGCTAATATTGACTGGTC  
 ACATTATAGTAAGGTTACTGTGAATGGAAGAAGTTGTTAAAGGTAGTG  
 AGTTACCTTTAACTAAAGGATGGACAACATTTGTATTACATAAAACAGAA  
 AATTCAATTAATGTTAAAGTTTGTATTATGGAGACGGGTAGTGAAGTAA  
 GAAAGTTCAACAACCTCCTTTAAGTCTTAGATTATCTAAAAATTAAGCATA  
 TGAGGGATATGCTACTTACTATGCAAAAAGATTGAGCGTATTACGAAACA  
 AGTGACAGTCTAGTCTTTCGAATTAATCTCACTGCAGATACTAACTTAA  
 TTTTAAATGCTGTTAAAGGAGCGAGTGTCTTACTGAAAAATATGATGATGA  
 GACAGTTTGCAGTTGCTGGACCACAAGATGATCCTGTTAGTGAACATAAA  
 TACCCATCAGTATTTCTTAACTCCTGCCTTATTGGAACCTGCTAGTGA  
 GGCAACTCTAAATGGTAAGGAAATCACAGCATCTGGTATTATCGGTCA  
 TCAAGGATGGTGATAAAGCAAGCATGTTGAAGTCAAAATGGTGAATGAA  
 AATGGAGACATGCTAGGAACCCCTGTTATTATCAAGGTAAAGACTTGAC  
 TAATCGAACAAAACCATTAATGAGTGGACGTAGAGTACTTTATGCCGGTA



Table 51: Comparative Sequences relating to SAG0677

AACAATATGAGTTCCGGGCTAAATTACCACTTAGTCGTTTAACTTGG  
 ATTAGGGTTGAAGTGGTAACAGAAGCAGGAGAGAAAGCAAGTATTGTTCC  
 TCGCATGTTCTTTGACCAATCAGTTCCAGAGCTTAACACAGCAGTTGCTA  
 AACGTGATTTGACTTCIGATACTGCTCTTATCCACATCGTTGCCAAAGAT  
 GACTCTCTAAAACCTAAAATTATATCAAGATGATTCAATACCTGAATCTGT  
 TGATAAAACCGGTCCTTATAGTTTGAAGATGGTGTAGAAATCACTAAAG  
 ATATGACAGTACCCTAGAAATTGGAGATAATATATTAAGTTATCTGCT  
 GTTGACTTATCAAAATTATCGTCGTAATGAGACCCCTTCATATCTATAGAAA  
 CCGTTTGTATGTTAAAGCAAGCCAAATGACAGCTGACAAAGGAGCTAAAG  
 TAACTGTGGATATGTTGATGAAGCACTTAGTTGTTCCAGAAATGGCAGGA  
 GCTTATACATTAACAATCGACGAAGCTCCAAACACAAATGAATCAGGAAT  
 GTTAACAAACCGCTAAAGTATCGATTCAATTATGTAATGGTGGTGTGATA  
 AAGTTGATGTTCCGATTAAAGTAGTTGACTTAGAAGCTATTTCGTAAGCT  
 GAAGAAGCACGTAAGCTGAAGAAGCACGTAAGCTGAAGAGGGACATAA  
 AACCCAAAGACCTATAGTTGAAGAAGGCTACAAAGTTAATAACGTTTC  
 ATCAAACTGATACATACATTAAAGCGTCTGATTACCAAAAGCTAAGACA  
 GTTTCGCGAGTTTATATGGCTAGAACAGACAATAACAGATAACTTCACA  
 TCAGACACATGTTGAA

SEQ ID NO. 5105

STRAIN M732

TTGAATAATAAAGGTGTCGGTGGCGATGGTGTCC

AAATTTATCAATACTATATCAAAATGGACAACAATAAACCTTACTTAAGT  
 CCCAAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGCTGGAAAAAAT  
 TACCTTCAAAGTTCCAGGATACTGGCATTGGTTTGAAGACGTTTATCTTC  
 AATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACCTTATCACA  
 CCTCCAGGATTTAAAAAGAAAGATAAAAAAGTTGAAAAACCAAAATTAGA  
 CCGTCCACACAGGAATTGATTTACCAGCACCAACTCAATGAGAAGTTTGT  
 ATTATTCAACCCACCGGGAACCTAAGCCAAAGCAACCCAAAGATAGTTTA  
 TCAACTCTCCAGGTTTCCAGATTAAACACGCGCCGATGAAGCCAC  
 CAAAGGATAGTAAAAAGACGCTATTGAAGATAAATCAGGAGCAATTAAA  
 TATGCTAAGTCTCTCAACTTAGCTTTGTTGATGACCTATTTTAGCTAG  
 CAAAGTAAATGGCAAAATATTACAAGTCGAATCTGATGGCAAAATTAGTCA  
 TTCTTAGAAATGCTTTGTGAGCTAATCAATTTGATGACACTAGTCTTAAA  
 ATTTATCGTAATAATAATCGCAATAAAGAAATTACTATCACACAGATTA  
 TTTTGCAGATACAAAATATGTCAATATCACAGCGGTTGACTATTTGAGCA  
 ATACTACTTTTGGAGCAATAGCTACTGGTGAACAGTAGATTACCATGCC  
 ATTGTATTTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGGTAAGATTTA  
 TGTTAACGATAAAATGCAAGAACTTCTCGTATAGCGCTTAAAGATAAAT  
 CTGTTAAGATTGGTATTGAATTACCAATGATGTCAGACATATTGATAGT  
 TTATCTGTTCTCGTTTGAATGAGGTTAAACTGTTGATAATATCTTGAA  
 AAATGATGAACAAGACATTAATCTCAGCAAACTTACCAATTAATAATACA  
 ACCGACAAATCGTCTGCTAGAGTTTACTATTAATAACATTAACTCAAGT  
 TCAGAAATCATGACCACTTTCAAAGATGGAAGATGCCAGAAATGGTTGA  
 ACAAAAAGATGTTTCTTTGGATATAAACGATATGGACATGAGTAAGTTTA  
 AAACATTTTCGACTTGGACGAAAGGATTCTGAATTTAAGGACAACTTATT  
 GCAAAAACCTGGAAACAGTTGAATTAGATATGTTTTCAAACAATCTCAAGA  
 CCCAGCTTCAATTTAATAAAAAATATACCTTATCCAAATGGTGTTCCAA  
 ATGAATGAAAAAATTTGACTCTAGTTTGGTTTAACTGAAAGTCAGATA  
 GATGATACTATATTTATAAAGATGCAATTAACTTAAATTTAAATTAAC  
 CAGTGGTGCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGATCCATATA  
 GTCATCAGAAAGAAATATGACTAAAAAAGGTGAACAGCTCAGTCATTCA  
 ACTCAAGCCAATGAAAATACAGCAAAAGTAACCTTTGCTAATATTGACTG  
 GTCACATTATAGTAAGGTTACTGTGAATGGAAGAAAGTTGGTAAAGGTA  
 GTGAGTTACCTTTAACTAAGGATGGACAACTTTGTATTACATAAAACA  
 GAAAATTCAATTAATGTTAAAGTTTGAATTATGGAGACGGGTAGTGTAAAG  
 TAAGAAAGTTCAACAACTTCTTTAAGTCTTAGATTATCTAAAAATTAAGC  
 ATATGAGGGATATGCTACTTACTATGCAAAAAGATTGAGCGTATTACGAA  
 ACAAGTGACAGTCTAGTCTTCGAATTAATCTCACTGCAGATACTAACT  
 TAATTTAATGCTGTTAAAGGAGCGAGTCTCTTACTGAAAATATGATGA  
 TGAGACAGTTTGCAGTTGCTGGACCAAGATGATCCTGTTaGTGAACAT  
 AAATACCCATCAGTaTTCTCTTAACTCCTGCCCTATTGGAAaCTGCTAG  
 TGAGGCAACTCTAAATGGTAAGGAAATCACAGCATCTGGTATTATCGGTC  
 ACATCAAGGATGGTGATAAAGCAAGCATGTGAAGTCAAAATGGTGAAT  
 GAAATGGAGACATGCTAGAACCCCTGTTATTATTCAAGGTAAGACTT  
 GACTAATCGAACAAAACCTAATGAGTGGACGTAGAGTACTTTATGCCG  
 GTAAACAATATGAGTTCCGGGCTAAATTACCACCTAGTCTGTTTAACT  
 TGGATTAGGGTTGAAGTGGTAACAGAAGCAGGAGAGAAAGCAAGTATTGT  
 TCGTGCATGTTCTTTGACCAATCAGTCCAGAGCTTAACACAGCAGTTG  
 CTAAACGTGATTTGACTTCTGATACTGCTCTTATCCACATCGTTGCCAAA  
 GATGACTCTCTAAAACCTAAAATTATATCAAGATGATTCAATCTTGAATC  
 TGTGTATAAAACCGGTCCTTATAGTTTGAAGATGGTGTAGAAATCACTA  
 AAGATATGACAGTACCCTAGAAATTGGAGATAATATTTAAGTTATCT  
 GCTGTTGACTTATCAAAATTATCGTCGTAATGAGACCCCTTCATATCTATAG  
 AAACCGTTTGTATGTTAAAGCAAGCCAAATGACAGCTGACAAAGGAGCTA  
 AAGTAACTGTGGATATGTTGATGAAGCACTTAGTTGTTCCAGAAATGGCA  
 GGAGCTTATACATTAACAATCGACGAAGCTCCAAACACAAATGAATCAGG  
 AATGTTAACAAACGCTAAAGTATCGATTCAATTATGTAATGGTGGTGTG  
 ATAAAGTTGATGTTCCGATTAAAGTAGTTGACTTAGAAGCTATTTCGTAA  
 GCTGAAGAGACATAAAGCTGACGAAGCACGTAAGCTGAAGAAGCACG  
 TAAAGCTGAAGAAGCACATAAAGCTGAAGAAGTACGTAAGCTGAAGAAG  
 CACATAAAGTGAAGAAGCACGTAAGCTGAAGAAGGACATAAACCACAA  
 GAAGCACCTATAGTTGAAGAAGGCTACAAAGTTAATAACGTTTCATCAAC

Table 51: Comparative Sequences relating to SAG0677

TGATACTACAGTTAAAGCGTCTGATTACCAAAGACTAAGACAGTTTCCG  
CAGTTTCATATGGCTAGAACAGACAATAAACAGATAACTTCACATCAGACA  
CATGTTGAAAA

SEQ ID NO. 5106

STRAIN COH1

TTGAATAATAAAGGTGTCCGGTGGCGATGGT  
GTCCAAATTTATCAATACTATATCAAAATGGACAACAATAAACCTTACTT  
AAGTCCCAAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGCTGGAAAA  
AAATTACTTTCAAAGTTCAGGATACTGGCATTGGTTTGAAAGACGTTTAT  
CTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACCTTAT  
CACACCTCCAGGATTAAAAAAGAAGATAAAAAAGTTGAAAAACCAAAAT  
TAGACCGTCCACCAGGAATTGATTTACCAGCACCAACTTCAATGAGAAGT  
TTTGATTATTCAACCCACCGGGAAGTAAGCCAAGCAACCCAAAGATAG  
TTTATCAACTCCTCCAGGTTCCAGATTAAACACGCCGCCGGATGAAG  
CCaCCAAAGGATAGTAAAAAAGACGCTATTGAAGATAAATCAGGAGCAAT  
TAAATATGCTAAGTCTTCAACTTAGCTTGTGTGATGACCTATTATTAG  
CTAGCAAGATAAATGGCAAAATATTACAAGTCGAATCTGATGGCAAAATTA  
GTCAATCTAGAAATGCTTGTGAGCTAATCAATTTGATGACACTAGTCT  
TAAATTTATCGTAATAATAATCGCAATAAAGAAATTACTATCACAACAG  
ATTATTTTGCAGATACAAATATGTCATATCAGACGGTTGACTATTG  
AGCAATACTACTTTTGAGCAATTAGCTACTGGTGAAACAGTAGATTACCA  
TGCCATTGTATTTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGGTAAGA  
TTTATGTTAAGCATAAATGCAAGAACTTCTCGTATAGCGCTTAAAGAT  
AAATCTGTTAAGATTGCTATTGAATTACCAATGATGTCAGACATATTGA  
TAGTTTATCTGTTTCGTCGTTTGAATGAGGTTAAACTGTTGATAATATCT  
TGAAAAATGATGAACAAGACATTAACTCTAGCAAACTTACCAATTAAAA  
TACAACCCGACAAATCGTCTGCTAGAGTTTACTATTAATAACATTAACTC  
AAGTTTCAAGAAATCATGACCACTTTCAAAGATGGAAGATGCCAGAAATGG  
TTGAACAAAAAGATGTTCTTTGGATATAAACGATATGGACATGAGTAAG  
TTTAAACTATTTCGACTTGGACGAAAGGATTCTGAATTTAAGGGCAACT  
TATTTGCAAAACTGGAACAGTTGAATTAGATATGTTTTCAAACAACTCTC  
AAGACCCAGCTTCAATTATTAATAAATATACCTTATCCAAATGGTGT  
CCAAATGAATTGAAAAAATTTGACTCTAGTTTGGTTTAACTGAAAGTCA  
GATAGATGGATACTATATTATAAAGATGCAATTAACTTAAATTTAAAT  
TAACCAAGTGGTCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGATCCA  
TATAGTCATCAGAAAGAAGATATGACTAAAAAAGGTGAACAGCTCAGTCA  
TTCAACTCAAGCCAATGAAATACAGCAAAAGTAACCTTTGCTTAATATTG  
ACTGGTCACATTATAGTAAGGTTACTGTGAATGGAAGAAGTTGGTAAA  
GGTAGTGAGTTACCTTTAACTAAAGGATGGACAACATTTGTATTACATAA  
AACAGAAAAATTCATTAAATGTTAAAGTTTGATTATGGAGACGGGTAGTG  
TAAGTAAGAAAGTTCAACAACTTCTTTAAGTCTTAGATTATCTAAAAAT  
AAGCATATGAGGGATATGCTACTTACTATGCAAAAAGATTGAGCGTATTA  
CGAAACAAGTGACAGTCTAGTCTTCAATTAATCTCACTGCAGATACTA  
AACTTAATTTAATGCTGTTAAAGGAGCGAGTGTCTTACTGAAAAATATG  
ATGATGAGACAGTTTGCAGTTGCTGGACCACAAGATGATCCTGTTAGTGA  
ACATAAATACCCATCAGTATTTCTTAACTCTGCTTATTGGAAGTCT  
CTAGTGAGGCAACTCTAAATGGTAAGGAAATCACAGCATCTGGTATTATC  
GGTCACATCAAGGATGGTGATAAAGCAAGCATGTTGAAGTCAAAATGGT  
GAATGAAAAATGGAGACATGCTAGGAACCCCTGTTATTATTCAAGGTAAAG  
ACTTGACTAATCGAACAAAACCAATTAATGAGTGGACGTAGAGTACTTTAT  
GCCGGTAAACAAATATGAGTTCCGGGCTAAATTACCCTTAGTCTGTTTAA  
CACTTGGATTAGGGTTGAAGTGGTAACAGAAGCAGGAGAGAAAGCAAGTA  
TTGTTCTGTCGATGTTCTTTGACCAATCAGTTCCAGAGCTTAAACAGCA  
GTTGCTAAACGTGATTGACTTCTGATATGCTCTTATCCACATCGTTGTC  
CAAGATGACTCTCTAAACCTAAATTTATATCAAGATGATTCAATTACTTG  
AATCTGTTGATAAAACCGGCTCTTATAGTTTGAAGATGGTGTAGAAATC  
ACTAAAGATATGACAGTACCCTAGAAATTTGGAGATAATAATTATTAAAGTT  
ATCTGCTGTTGACTTATCAAATTATCGTCTGAATGAGACCTTCATATCT  
ATAGAAACCGTTTGTATGTTAAAGCAAGCCAAATGACAGCTGACAAAGGA  
GCTAAAGTAACGTGGATATGTTGATGAAGCACTAGTTGTTCCAGAAAT  
GGCAGGAGCTTATACATTAACTCGACGAAGCTCCAAACACAAATGAAT  
CAGGAATGTTAAACAAACGCTAAAGTATCGATTCTATTATGTAATGGTGGT  
GTTGATAAAGTTGATGTTCCGATTAAAGTAGTTGACTTAGAAGCTATTTCG  
TAAAGCTGAAGAAGCACATAAAGCTGACGAAGCAGTAAAGCTGAAGAAG  
CAGTAAAGCTGAAGAAGCACATAAAGCTGAAGAAGTACGTAAAGCTGAA  
GAAGCACATAAAGCTGAAGAAGCAGTAAAGCTGAAGAAGGACATAAAAC  
CCAAGAAGCACCTATAGTTGAAGAAGGCTACAAAGTTAATAAGGTTTATC  
AACTGATACTACAGTTTAAAGCGTCTGATTACCAAGACTAAGACAGTT  
TCCGCGATTCTATGCTAGAACAGACAATAAACAGATAACTTCACATCA  
GACACATGT

SEQ ID NO. 5107

STRAIN M781

TTGAATAATAAAGGTGTCCGGTGGCGATGGT  
GTCCAAATTTATCAATACTATATCAAAATGGACAACAATAAACCTTACTT  
AAGTCCCAAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGCTGGAAAA  
AAATTACTTTCAAAGTTCAGGATACTGGCATTGGTTTGAAAGACGTTTAT  
CTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACCTTAT  
CACACCTCCAGGATTAAAAAAGAAGATAAAAAAGTTGAAAAACCAAAAT  
TAGACCGTCCACCAGGAATTGATTTACCAGCACCAACTTCAATGAGAAGT  
TTTGATTATTCAACCCACCGGGAAGTAAGCCAAGCAACCCAAAGATAG  
TTTATCAACTCCTCCAGGTTTCCAGATTAAACACGCCGCCGGATGAAG

Table 51: Comparative Sequences relating to SAG0677

CCaCCAAAGGATAGTAAAAAGACGCTATTGAAGATAAATCAGGAGCAAT  
TAAATATGCTAAGTCTCTTCAACTAGCTTTGTTGATGACCCATATTTAG  
CTAGCAAAGTAAATGGCAAAATATTACAAGTCGAATCTGATGGCAAATTA  
GTCAATTCCTAGAAATGCTTTGTGACGTAATCAATTTGATGACACTAGTCT  
TAAaATTATCGTAATAATAATCGCAATAAGAAATTaCTATCACAACAG  
ATTATTTTGAGATACAAAATATGTCAATATCACAGCGGTTGACTATTTG  
AGCAATACTACTTTTGAGCAATTAGCTACTGGTGAAACAGTAGATTACCA  
TGCCATTTGATTTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGGTAAGA  
TTTATGTTAAGATAAATTCGAAGAACTTCTCGTATAGCGCTTAAAGAT  
AAATCTGTTAAGATTGGTATTGAATTACCAATGATGTCAGACATATTGA  
TAGTTTATCTGTTCTGTTGAAATGAGGTTAAACTGTTGATAATATCT  
TGAAAAATGATGAACAAGACATTAATCTCAGCAAACTTACCAATTAAAA  
TACAACCCGACAAATCGTCTGCTAGAGTTTACTATTAAATACATTAACTC  
AAGTTCGAAATCATGACCCTTTCAAAGATGGAAGATGCCAGAAATGG  
TTGAACAAAAAGATGTTTCTTTGGATATAACGATATGACATGAGTAAG  
TTTAAAACTATTGCACTTGGACGAAAGGATTCTGAATTAAGGGCAAACT  
TATTTGCAAAACTGGAACAGTTGAATTAGATATGTTTTCAAACCAATCTC  
AAGACCCAGCTTCAATTATTAAAAAATATACCTTATCCAAATGGTGT  
CCAAATGAATTAAGAAATTTGACTCTAGTTTGGTTTAACTGAAAGTCA  
GATAGATGGATACATATTTATAAAGATGCAATTAACCTTAAATTTAAAT  
TAACCAAGTGGTCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGATCCA  
TATAGTCATCAGAAAGAAGATATGACTAAAAAGGTGAACAGCTCAGTCA  
TTCAACTCAAGCCAAATGAAAATACAGCAAAAGTAACCTTTGCTAATATTG  
ACTGGTCACATTATAGTAAGGTTACTGTGAATGGAAGAAGTTGGTAAAG  
GGTAGTGAGTTACCTTTAACTAAAGGATGGACAACATTGTTATTACATAA  
AACAGAAATTCATTAAATGTTAAAGTTTGAATTATGAGAGCGGGTAGTG  
TAAGTAAGAAAGTTCAACCACTTCTTTAAGTCTTAGATTATCTAAAAAT  
AAGCATATGAGGGATATGCTACTTACTATGCAAAAAGATTGAGCGTATTA  
CGAAACAGTGACAGTCTAGTCTTGAATTAATCTCAGTCAGATACTA  
AACTTAATTTTAAATGCTGTTAAAGGAGCGAGTGCTTACTGAAAATATG  
ATGATGAGACAGTTGCAAGTCTGAGGACCAAGATGATCCTGTTAGTGA  
ACATAAATACCCATCAGTATTTCTTAACTCTGCTTATTGGAACCTG  
CTAGTGAGGCAACTCTAATGTTAAGGAAATCACAGCATCTGGTATTATC  
GGTCACATCAAGGATGGTGATAAAAGCAAGCATGTTGAAGTCAAAATGGT  
GAATGAAAATGGAGACATGCTAGGAACCCCTGTTATTATTCAAGGTAAAG  
ACTTGACTAATCGAACAAACCAATTAATGAGTGGACGTAGAGTACTTTAT  
GCCGGTAAACCAATATGAGTTCCGGGCTAAATTACCACTTAGTCGTTTAA  
CACTTGGATTAGGGTTGAAGTGGTAAACAGAGCAGGAGAGAAAGCAAGTA  
TTGTTCTGTCGATGTTCTTTGACCAATCAGTTCAGAGCTTAAACAGCA  
GTTGCTAAACGTTGATTGACTCTGATAGTCTTATCCACATCGTTGC  
CAAAGATGACTCTCTAAACTAAAATTTATATCAAGATGATTCACTACTTG  
AATCTGTTGATAAAACCGGTCTTTATAGTTTGAAGTGGTGTAGAAATC  
ACTAAAGATATGACAGTACCCTAGAAATTTGGAGATAATATTATTAGTT  
ATCTGCTGTTGACTTATCAAAATATCGTCTGAATGAGACCCCTCATATCT  
ATAGAAAACCGTTTGTATGTTAAAGCAAGCAAAATGACAGCTGACAAAGGA  
GCTTAAAGTAACTGTGGATATGTTGATGAAGCACTTAGTTGTTCCAGAAAT  
GGCAGGAGCTTATACATTAAACCAATCGACGAAGCTCCAAACCAAAATGAAT  
CAGGAATGTTTAAACAAAGCTAAGTATCGATTCAATTATGTAATGGTGGT  
TTTGATAAAGTTGATGTTCCGATTAAAGTAGTTGACTTAGAAGCTATTCG  
TAAAGCTGAAGAAGCACATAAAGCTGACGAAGCAGTAAAGCTGAAGAAG  
CACGTAAAGCTGAAGAAGCACATAAAGCTGAAGAAGTACGTAAAGCTGAA  
GAAGCACATAAAGCTGAAGAAGCACCGTAAAGCTGAAGAGGGACATAAAA  
CCCAAGAGCACCTATAGTTGAAGAAGGCTACAAAGTTAATAACGTTTAT  
CAAACTGATACATAGTTAAAGCGTCTGATTACCAAGACTAAGACAGT  
TTCCGCAAGTTATATGGCTAGAACAGACAATAAACAGATAAATTCATC  
AGACACATGTTG

SEQ ID NO. 5109

STRAIN JM9130013

TGGTGTCCAAATTTATCAATACTATATCAAAATGGACAACAATAAAC  
CTTACTTAAAGTCCAAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGC  
TGGAAAAAATTTACTTTCAAAGTTTCAAGATCTGGCATTGGTTTGAAGA  
CGTTTATCTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTAG  
ACCTTATCACACCTCCAGGATTTAAAAAAGAAGATAAAAAAGTTGAAAAA  
CCAAAAATTAGACCGTCCACCAGGAATTGATTACCAGCACCAACTTCAAT  
GAGAAGTTTGTATTATCAACCCACCGGGAATTAAGCCAAAGCAACCCA  
AAGTAGTTTATCAACTCTTCCAGGTTTCCAGATTAAACACGCGCGCG  
GATGAAGCACCAAGGATAGTAAAAAAGACGCTATTGAAGATAAATCAGG  
AGCAATTAATATGCTAAGTCTCTTCAACTAGCTTTGTTGATGACCCTA  
TTTTAGCTAGCAAGTAAATGGCAAAATATTACAAGTCGAATCTGATGGC  
AAATTAGTCATTCTAGAAATGCTTTGTGAGCTAATCAATTTGATGACAC  
TAGTCTTAAATTTATCGTAATAATAATCGCAATTAAGAAATTAATATCA  
CAACAGATTATTTGAGATACAAAATATGTCAATATCACAGCGGTTGAC  
TATTTGAGCAaTACTACTTTTGAAGCAATTAGCTACTGGTGAAACAGTAGA  
TTACCATGCCATTGTATTTCAAGCTTTGCTGCTATTAAAGACAAGGGTG  
GTAAGATTATGTTAAGGATAAATTGCAAGAACTTCTCGTATAGCGCTT  
AAAGATAAATCTGTTAAGATTGGTATTGAATTACCAATGATGTCAGACA  
TATTGATAGTTTATCTGTTCTGTTGAATGAGGTTAAACTGTTGATA  
ATATCTTGAATAATGATGAACAAGACATTAACTCAGCAAACTTACCA  
TTAAATACAAACCCGACAAATCGTCTGCTAGAGTTTACTATTAAATACAT  
TAATCTAAGTTTCAAGAAATCATGACCCTTCAAAGATGGAAGATGCCAG  
AATTGGTTGAACAAAAAGATGTTTCTTTGGATATAAACGATATGGACATG  
AGTAAGTTTAAACTATTGCACTTGGACGAAGGATTCTGAATTTAAGGG

Table 51: Comparative Sequences relating to SAG0677

ACAACCTTATTGCAAAACTGGAACAGTTGAATTAGATATGTTTTTCAAAC  
 AATCTCAAGACCCAGCTTCAATTATTAATAAATATACCTTATCCAAAT  
 GGTGTTCGAATGAATGAAAAAATTTGACTCTAGTTTGGTTTAACTGA  
 AAGTCAGATAGATGGATACATATTTATAAAGATGCAATTAACCTTAAAT  
 TTAAATTAAACAGTGGTGCAGTCTTAAAGTTGTTTATAAGGGCAAGAA  
 GATCCATATAGTCATCAGAAAGAGATATGACTAAAAAGGTGAACAGCT  
 CAGTCATTCAACTCAAGCCATGAAAAATACAGCAAAAGTAACCTTTGCTA  
 ATATTGACTGGTCACATTATAGTAAGGTTACTGTGAATGGAAAAGAGTT  
 GGTAAAGGTAGTGAGTTACCTTTAACTAAAGGATGGCAACATTGTATT  
 ACATAAAACAGAAAAATTCATTAAATGTTAAAGTTTGATTATGGAGACGG  
 GTAGTGAAGTAAGAAAGTTCAACAACTTCCCTTAAAGTCCAGATTATCT  
 AAAAAATAAGCATATGAGGGATATGCTACTTACTATGCAAAAAGATTGAG  
 GTATTACGAACAAGTGACAGTCTAGTCCTTCGAATTAACTCTACTGCAG  
 ATACTAAACTTAATTTTAAATGCTGTTAAAGGAGCGAGTCTCTTACTGAA  
 AATATGATGATGAGACAGTTTGCACTTGGTGGACCAAGATGATCCTGT  
 TAGTGAACATAAATACCCATCAGTATTTCTCTTAACTCCTGCCTTATTGG  
 AAACCTGCTAGTGAGGCAACTCTAAATGGTAAGGAAATCACAGCATCTGGT  
 ATTATCGGTACATCAAGGATGGTGATAAAAGCAAGCATGTTGAAGTCAA  
 AATGGTGAATGAAATGGAGACATGCTAGGAACCCCTGTTTATTATCAAG  
 GTAAGACTTGACTAATCGAACAACCAATTAATGAGTGGACGTAGAGTA  
 CTTTATGCCGGTAAACAATATGAGTTCCGGGCTAAATTAACCACTTAGTCG  
 TTTTAACTTTGATTAGGGTTGAAGTGGTAACAGAAGCAGGAGaGaaag  
 cAaGTATTGTTTCGTCGATGTTCTTTGACCAATCAGTTCAGAGCTTAAC  
 ACAGCAGTTGCTAAACGTGATTGACTTCTGATAGTCTCTTATCCACAT  
 CGTTGCCAAGATGACTCTCTAAACTAAAATTATATCAAGATGATTCTAT  
 TACTTGAATCTGTGATAAAACCGGCTTTTATAGTTTGAAGATGGTGA  
 GAAATCACTAAAGATATGACAGTACCACTAGAAATTTGGAGATAATATTAT  
 TAAGTTATCTGCTGTTGACTTATCAAATTTATCGTGAATGAGACCCCTC  
 ATATCTATAGAAACCGTTTGTATGTTAAAGCAAGCCAAATGACAGCTGAC  
 AAAGGAGCTAAAGTAACGTGTGATATGTTGATGAAGCACTTAGTTGTTCC  
 AGAAATGGCAGGAGCTTATACATTAAACAATCGACGAAGCTCCAAACACAA  
 ATGAATCAGGAATGTTAAACAACGCTAAAGTATCGATTCAATTATGTAAT  
 GGTGGTGTGATAAAGTTGATGTTCCGATTAAAGTAGTTGACTTAGAAGC  
 TATTTCGTAAAGCTGAAGAAGCACATAAAGCTGACGAAGCAGTAAAGCTG  
 AAGAAGCACGTAAAGCTGAAGAAGCACATAAAGCTGAAGAAGTACGTAA  
 GCTGAAGAAGCACATAAAGCTGAAGAAGCACCGTAAAGCTGAAGAGGGAC  
 ATAAAACCCGAAGCACCTATAGTTGAAGAAGCTACAAGTTAATAAC  
 GTTCATCAAACTGATACACTACAGTTAAAGCGTCTGATTACCAAAGACTAA  
 GACAGTTTCGCGAGTTCATATGGCTAGAACAGACAATAAACAGATAAAT  
 CATATCAGACACATGTTG

## MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa235280.2{\*} December 10, 2002 05:12 ..

	1		50
msa235280.2{195_COH1}	ttgaataata aaggtgtcgg tggcgaTGGT	GTCCAAATTT ATCAATACTA	
msa235280.2{195_M732}	ttgaataata aaggtgtcgg tggcgaTGGT	GTCCAAATTT ATCAATACTA	
msa235280.2{195_M781}	ttgaataata aaggtgtcgg tggcgaTGGT	GTCCAAATTT ATCAATACTA	
msa235280.2{195_H36B}	-----TGGT	GTCCAAATTT ATCAATACTA	
msa235280.2{195_JM9130013}	-----TGGT	GTCCAAATTT ATCAATACTA	
msa235280.2{195_18RS21}	ttgaataata aaggtgtcgg tggcgaTGGT	GTCCAAATTT ATCAATACTA	
msa235280.2{195_2603}	ttgaataata aaggtgtcgg tggcgaTGGT	GTCCAAATTT ATCAATACTA	
msa235280.2{195_A909}	ttgaataata aaggtgtcgg tggcgaTGGT	GTCCAAATTT ATCAATACTA	
Consensus	-----*****	*****	
	51		100
msa235280.2{195_COH1}	TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAA	GATAAGACTA	
msa235280.2{195_M732}	TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAA	GATAAGACTA	
msa235280.2{195_M781}	TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAA	GATAAGACTA	
msa235280.2{195_H36B}	TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAA	GATAAGACTA	
msa235280.2{195_JM9130013}	TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAA	GATAAGACTA	
msa235280.2{195_18RS21}	TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAA	GATAAGACTA	
msa235280.2{195_2603}	TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAA	GATAAGACTA	
msa235280.2{195_A909}	TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAA	GATAAGACTA	
Consensus	*****	*****	
	101		150
msa235280.2{195_COH1}	CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT	CAAAGTTCAG	
msa235280.2{195_M732}	CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT	CAAAGTTCAG	
msa235280.2{195_M781}	CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT	CAAAGTTCAG	
msa235280.2{195_H36B}	CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT	CAAAGTTCAG	
msa235280.2{195_JM9130013}	CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT	CAAAGTTCAG	
msa235280.2{195_18RS21}	CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT	CAAAGTTCAG	
msa235280.2{195_2603}	CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT	CAAAGTTCAG	
msa235280.2{195_A909}	CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT	CAAAGTTCAG	
Consensus	*****	*****	
	151		200
msa235280.2{195_COH1}	GATACTGGCA TTGGTTTGAA AGACGTTTAT CTTCAATCTG	TTAAGTATGT	
msa235280.2{195_M732}	GATACTGGCA TTGGTTTGAA AGACGTTTAT CTTCAATCTG	TTAAGTATGT	
msa235280.2{195_M781}	GATACTGGCA TTGGTTTGAA AGACGTTTAT CTTCAATCTG	TTAAGTATGT	
msa235280.2{195_H36B}	GATACTGGCA TTGGTTTGAA AGACGTTTAT CTTCAATCTG	TTAAGTATGT	

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_JM9130013}	GATACTGGCA	TTGGTTTGAA	AGACGTTTAT	CTTCAATCTG	TTAAGTATGT
msa235280.2{195_18RS21}	GATACTGGCA	TTGGTTTGAA	AGACGTTTAT	CTTCAATCTG	TTAAGTATGT
msa235280.2{195_2603}	GATACTGGCA	TTGGTTTGAA	AGACGTTTAT	CTTCAATCTG	TTAAGTATGT
msa235280.2{195_A909}	GATACTGGCA	TTGGTTTGAA	AGACGTTTAT	CTTCAATCTG	TTAAGTATGT
Consensus	*****	*****	*****	*****	*****
201					
msa235280.2{195_COH1}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_M732}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_M781}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_H36B}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_JM9130013}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_18RS21}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_2603}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_A909}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
Consensus	*****	*****	*****	*****	*****
250					
251					
msa235280.2{195_COH1}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_M732}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_M781}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_H36B}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_JM9130013}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_18RS21}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_2603}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_A909}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
Consensus	*****	*****	*****	*****	*****
300					
301					
msa235280.2{195_COH1}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCCAACC
msa235280.2{195_M732}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCCAACC
msa235280.2{195_M781}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCCAACC
msa235280.2{195_H36B}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCCAACC
msa235280.2{195_JM9130013}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCCAACC
msa235280.2{195_18RS21}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCCAACC
msa235280.2{195_2603}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCCAACC
msa235280.2{195_A909}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCCAACC
Consensus	*****	*****	*****	*****	*****
350					
351					
msa235280.2{195_COH1}	GGGAAGTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_M732}	GGGAAGTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_M781}	GGGAAGTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_H36B}	GGGAAGTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_JM9130013}	GGGAAGTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_18RS21}	GGGAAGTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_2603}	GGGAAGTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_A909}	GGGAAGTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
Consensus	*****	*****	*****	*****	*****
400					
401					
msa235280.2{195_COH1}	TCCCAGATT	AAACACGCCG	CCGGATGAAG	cCACcAAAGG	ATAGTAAAAA
msa235280.2{195_M732}	TCCCAGATT	AAACACGCCG	CCGGATGAAG	cCACcAAAGG	ATAGTAAAAA
msa235280.2{195_M781}	TCCCAGATT	AAACACGCCG	CCGGATGAAG	cCACcAAAGG	ATAGTAAAAA
msa235280.2{195_H36B}	TCCCAGATT	AAACACGCCG	CCGGATGAAG	.CACTAAAGG	ATAGTAAAAA
msa235280.2{195_JM9130013}	TCCCAGATT	AAACACGCCG	CCGGATGAAG	.CACcAAAGG	ATAGTAAAAA
msa235280.2{195_18RS21}	TCCCAGATT	AAACACGCCG	CCGGATGAAG	.CACcAAAGG	ATAGTAAAAA
msa235280.2{195_2603}	TCCCAGATT	AAACACGCCG	CCGGATGAAG	.CACcAAAGG	ATAGTAAAAA
msa235280.2{195_A909}	TCCCAGATT	AAACACGCCG	CCGGATGAAG	.CACTAAAGG	ATAGTAAAAA
Consensus	*****	*****	*****	*****	*****
450					
451					
msa235280.2{195_COH1}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_M732}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_M781}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_H36B}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_JM9130013}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_18RS21}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_2603}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_A909}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
Consensus	*****	*****	*****	*****	*****
500					
501					
msa235280.2{195_COH1}	AACCTAGCCT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_M732}	AACCTAGCCT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_M781}	AACCTAGCCT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_H36B}	AACCTAGCCT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_JM9130013}	AACCTAGCCT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_18RS21}	AACCTAGCCT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_2603}	AACCTAGCCT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_A909}	AACCTAGCCT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
Consensus	*****	*****	*****	*****	*****
550					

Table 51: Comparative Sequences relating to SAG0677

		551			600
msa235280.2{195_COH1}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAAATGCTTT
msa235280.2{195_M732}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAAATGCTTT
msa235280.2{195_M781}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAAATGCTTT
msa235280.2{195_H36B}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAAATGCTTT
msa235280.2{195_JM9130013}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAAATGCTTT
msa235280.2{195_18RS21}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAAATGCTTT
msa235280.2{195_2603}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAAATGCTTT
msa235280.2{195_A909}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAAATGCTTT
Consensus	*****	*****	*****	*****	*****
		601			650
msa235280.2{195_COH1}	GTCAGCTAAT	CAATTGTATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
msa235280.2{195_M732}	GTCAGCTAAT	CAATTGTATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
msa235280.2{195_M781}	GTCAGCTAAT	CAATTGTATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
msa235280.2{195_H36B}	GTCAGCTAAT	CAATTGTATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
msa235280.2{195_JM9130013}	GTCAGCTAAT	CAATTGTATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
msa235280.2{195_18RS21}	GTCAGCTAAT	CAATTGTATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
msa235280.2{195_2603}	GTCAGCTAAT	CAATTGTATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
msa235280.2{195_A909}	GTCAGCTAAT	CAATTGTATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
Consensus	*****	*****	*****	*****	*****
		651			700
msa235280.2{195_COH1}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
msa235280.2{195_M732}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
msa235280.2{195_M781}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
msa235280.2{195_H36B}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
msa235280.2{195_JM9130013}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
msa235280.2{195_18RS21}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
msa235280.2{195_2603}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
msa235280.2{195_A909}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
Consensus	*****	*****	*****	*****	*****
		701			750
msa235280.2{195_COH1}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
msa235280.2{195_M732}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
msa235280.2{195_M781}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
msa235280.2{195_H36B}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
msa235280.2{195_JM9130013}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
msa235280.2{195_18RS21}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
msa235280.2{195_2603}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
msa235280.2{195_A909}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
Consensus	*****	*****	*****	*****	*****
		751			800
msa235280.2{195_COH1}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAGGCT
msa235280.2{195_M732}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAGGCT
msa235280.2{195_M781}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAGGCT
msa235280.2{195_H36B}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAGGCT
msa235280.2{195_JM9130013}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAGGCT
msa235280.2{195_18RS21}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAGGCT
msa235280.2{195_2603}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAGGCT
msa235280.2{195_A909}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAGGCT
Consensus	*****	*****	*****	*****	*****
		801			850
msa235280.2{195_COH1}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
msa235280.2{195_M732}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
msa235280.2{195_M781}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
msa235280.2{195_H36B}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
msa235280.2{195_JM9130013}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
msa235280.2{195_18RS21}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
msa235280.2{195_2603}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
msa235280.2{195_A909}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
Consensus	*****	*****	*****	*****	*****
		851			900
msa235280.2{195_COH1}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
msa235280.2{195_M732}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
msa235280.2{195_M781}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
msa235280.2{195_H36B}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
msa235280.2{195_JM9130013}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
msa235280.2{195_18RS21}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
msa235280.2{195_2603}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
msa235280.2{195_A909}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
Consensus	*****	*****	*****	*****	*****
		901			950
msa235280.2{195_COH1}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT
msa235280.2{195_M732}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT
msa235280.2{195_M781}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT
msa235280.2{195_H36B}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT
msa235280.2{195_JM9130013}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_18RS21}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTCGTCGTT
msa235280.2{195_2603}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTCGTCGTT
msa235280.2{195_A909}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTCGTCGTT
Consensus	*****	*****	*****	*****	*****
951					1000
msa235280.2{195_COH1}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_M732}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_M781}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_H36B}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_JM9130013}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_18RS21}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_2603}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_A909}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
Consensus	*****	*****	*****	*****	*****
1001					1050
msa235280.2{195_COH1}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_M732}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_M781}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_H36B}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_JM9130013}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_18RS21}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_2603}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_A909}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
Consensus	*****	*****	*****	*****	*****
1051					1100
msa235280.2{195_COH1}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_M732}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_M781}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_H36B}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_JM9130013}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_18RS21}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_2603}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_A909}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
Consensus	*****	*****	*****	*****	*****
1101					1150
msa235280.2{195_COH1}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_M732}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_M781}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_H36B}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_JM9130013}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_18RS21}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_2603}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_A909}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
Consensus	*****	*****	*****	*****	*****
1151					1200
msa235280.2{195_COH1}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAACTA	TTCGACTTGG
msa235280.2{195_M732}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAACTA	TTCGACTTGG
msa235280.2{195_M781}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAACTA	TTCGACTTGG
msa235280.2{195_H36B}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAACTA	TTCGACTTGG
msa235280.2{195_JM9130013}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAACTA	TTCGACTTGG
msa235280.2{195_18RS21}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAACTA	TTCGACTTGG
msa235280.2{195_2603}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAACTA	TTCGACTTGG
msa235280.2{195_A909}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAACTA	TTCGACTTGG
Consensus	*****	*****	*****	*****	*****
1201					1250
msa235280.2{195_COH1}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
msa235280.2{195_M732}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
msa235280.2{195_M781}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
msa235280.2{195_H36B}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
msa235280.2{195_JM9130013}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
msa235280.2{195_18RS21}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
msa235280.2{195_2603}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
msa235280.2{195_A909}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
Consensus	*****	*****	*****	*****	*****
1251					1300
msa235280.2{195_COH1}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_M732}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_M781}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_H36B}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_JM9130013}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_18RS21}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_2603}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_A909}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
Consensus	*****	*****	*****	*****	*****
1301					1350

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_COH1}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT	
msa235280.2{195_M732}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT	
msa235280.2{195_M781}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT	
msa235280.2{195_H36B}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT	
msa235280.2{195_JM9130013}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT	
msa235280.2{195_18RS21}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT	
msa235280.2{195_2603}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT	
msa235280.2{195_A909}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT	
Consensus	*****	*****	*****	*****	*****	
1351						1400
msa235280.2{195_COH1}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT	
msa235280.2{195_M732}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT	
msa235280.2{195_M781}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT	
msa235280.2{195_H36B}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT	
msa235280.2{195_JM9130013}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT	
msa235280.2{195_18RS21}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT	
msa235280.2{195_2603}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT	
msa235280.2{195_A909}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT	
Consensus	*****	*****	*****	*****	*****	
1401						1450
msa235280.2{195_COH1}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT	
msa235280.2{195_M732}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT	
msa235280.2{195_M781}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT	
msa235280.2{195_H36B}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT	
msa235280.2{195_JM9130013}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT	
msa235280.2{195_18RS21}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT	
msa235280.2{195_2603}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT	
msa235280.2{195_A909}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT	
Consensus	*****	*****	*****	*****	*****	
1451						1500
msa235280.2{195_COH1}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA	
msa235280.2{195_M732}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA	
msa235280.2{195_M781}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA	
msa235280.2{195_H36B}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA	
msa235280.2{195_JM9130013}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA	
msa235280.2{195_18RS21}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA	
msa235280.2{195_2603}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA	
msa235280.2{195_A909}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA	
Consensus	*****	*****	*****	*****	*****	
1501						1550
msa235280.2{195_COH1}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA	
msa235280.2{195_M732}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA	
msa235280.2{195_M781}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA	
msa235280.2{195_H36B}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA	
msa235280.2{195_JM9130013}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA	
msa235280.2{195_18RS21}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA	
msa235280.2{195_2603}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA	
msa235280.2{195_A909}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA	
Consensus	*****	*-*****	*****	*****	*****	
1551						1600
msa235280.2{195_COH1}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG	
msa235280.2{195_M732}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG	
msa235280.2{195_M781}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG	
msa235280.2{195_H36B}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG	
msa235280.2{195_JM9130013}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG	
msa235280.2{195_18RS21}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG	
msa235280.2{195_2603}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG	
msa235280.2{195_A909}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG	
Consensus	*****	*****	*****	*****	*****	
1601						1650
msa235280.2{195_COH1}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC	
msa235280.2{195_M732}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC	
msa235280.2{195_M781}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC	
msa235280.2{195_H36B}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC	
msa235280.2{195_JM9130013}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC	
msa235280.2{195_18RS21}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC	
msa235280.2{195_2603}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC	
msa235280.2{195_A909}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC	
Consensus	*****	*****	*****-****	*****	*****	
1651						1700
msa235280.2{195_COH1}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG	
msa235280.2{195_M732}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG	
msa235280.2{195_M781}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG	
msa235280.2{195_H36B}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG	
msa235280.2{195_JM9130013}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG	
msa235280.2{195_18RS21}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG	



Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_2603}	TAAAGGATGG	ACAACATTGG	TATTACATAA	AACAGAAAAT	TCATTAAATG
msa235280.2{195_A909}	TAAAGGATGG	ACAACATTGG	TATTACATAA	AACAGAAAAT	TCATTAAATG
Consensus	*****	*****	*****	*****	*****
1701					
msa235280.2{195_COH1}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCACAA
msa235280.2{195_M732}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCACAA
msa235280.2{195_M781}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCACAA
msa235280.2{195_H36B}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCACAA
msa235280.2{195_JM9130013}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCACAA
msa235280.2{195_18RS21}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCACAA
msa235280.2{195_2603}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCACAA
msa235280.2{195_A909}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCACAA
Consensus	*****	*****	*****	*****	*****
1750					
1751					
msa235280.2{195_COH1}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_M732}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_M781}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_H36B}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_JM9130013}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_18RS21}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_2603}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_A909}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
Consensus	*****	*****	*****	*****	*****
1800					
1801					
msa235280.2{195_COH1}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_M732}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_M781}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_H36B}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_JM9130013}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_18RS21}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_2603}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_A909}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
Consensus	*****	*****	*****	*****	*****
1850					
1851					
msa235280.2{195_COH1}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_M732}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_M781}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_H36B}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_JM9130013}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_18RS21}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_2603}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_A909}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
Consensus	*****	*****	*****	*****	*****
1900					
1901					
msa235280.2{195_COH1}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
msa235280.2{195_M732}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
msa235280.2{195_M781}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
msa235280.2{195_H36B}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
msa235280.2{195_JM9130013}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
msa235280.2{195_18RS21}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
msa235280.2{195_2603}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
msa235280.2{195_A909}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
Consensus	*****	*****	*****	*****	*****
1950					
1951					
msa235280.2{195_COH1}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_M732}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_M781}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_H36B}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_JM9130013}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_18RS21}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_2603}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_A909}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
Consensus	*****	*****	*****	*****	*****
2000					
2001					
msa235280.2{195_COH1}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_M732}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_M781}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_H36B}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_JM9130013}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_18RS21}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_2603}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_A909}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
Consensus	*****	*****	*****	*****	*****
2050					
2051					
msa235280.2{195_COH1}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
2100					

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_M732}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_M781}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_H36B}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_JM9130013}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_18RS21}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_2603}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_A909}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_M732}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_M781}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_H36B}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_JM9130013}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_18RS21}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_2603}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_A909}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TGGAACAAAA
msa235280.2{195_M732}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TGGAACAAAA
msa235280.2{195_M781}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TGGAACAAAA
msa235280.2{195_H36B}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TGGAACAAAA
msa235280.2{195_JM9130013}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TGGAACAAAA
msa235280.2{195_18RS21}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TGGAACAAAA
msa235280.2{195_2603}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TGGAACAAAA
msa235280.2{195_A909}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TGGAACAAAA
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	CCATTAAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_M732}	CCATTAAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_M781}	CCATTAAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_H36B}	CCATTAAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_JM9130013}	CCATTAAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_18RS21}	CCATTAAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_2603}	CCATTAAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_A909}	CCATTAAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACCTGGATT	AGGGTTGAAG
msa235280.2{195_M732}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACCTGGATT	AGGGTTGAAG
msa235280.2{195_M781}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACCTGGATT	AGGGTTGAAG
msa235280.2{195_H36B}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACCTGGATT	AGGGTTGAAG
msa235280.2{195_JM9130013}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACCTGGATT	AGGGTTGAAG
msa235280.2{195_18RS21}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACCTGGATT	AGGGTTGAAG
msa235280.2{195_2603}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACCTGGATT	AGGGTTGAAG
msa235280.2{195_A909}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACCTGGATT	AGGGTTGAAG
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
msa235280.2{195_M732}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
msa235280.2{195_M781}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
msa235280.2{195_H36B}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
msa235280.2{195_JM9130013}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
msa235280.2{195_18RS21}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
msa235280.2{195_2603}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
msa235280.2{195_A909}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_M732}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_M781}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_H36B}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_JM9130013}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_18RS21}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_2603}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_A909}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_M732}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_M781}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_H36B}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_JM9130013}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_18RS21}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_2603}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_A909}	TTCTGTACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAAC		
Consensus	*****	*****	*****	*****	*****		
msa235280.2{195_COH1}	2451	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT	2500
msa235280.2{195_M732}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT	TAAAACCGGT	
msa235280.2{195_M781}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT	TAAAACCGGT	
msa235280.2{195_H36B}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT	TAAAACCGGT	
msa235280.2{195_JM9130013}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT	TAAAACCGGT	
msa235280.2{195_18RS21}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT	TAAAACCGGT	
msa235280.2{195_2603}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT	TAAAACCGGT	
msa235280.2{195_A909}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT	TAAAACCGGT	
Consensus	*****	*****	*****	*****	*****	*****	
msa235280.2{195_COH1}	2501	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC	2550
msa235280.2{195_M732}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC	TGACAGTACC	
msa235280.2{195_M781}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC	TGACAGTACC	
msa235280.2{195_H36B}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC	TGACAGTACC	
msa235280.2{195_JM9130013}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC	TGACAGTACC	
msa235280.2{195_18RS21}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC	TGACAGTACC	
msa235280.2{195_2603}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC	TGACAGTACC	
msa235280.2{195_A909}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC	TGACAGTACC	
Consensus	*****	*****	*****	*****	*****	*****	
msa235280.2{195_COH1}	2551	ACTAGAATTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA	2600
msa235280.2{195_M732}	ACTAGAATTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA	GACTTATCAA	
msa235280.2{195_M781}	ACTAGAATTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA	GACTTATCAA	
msa235280.2{195_H36B}	ACTAGAATTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA	GACTTATCAA	
msa235280.2{195_JM9130013}	ACTAGAATTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA	GACTTATCAA	
msa235280.2{195_18RS21}	ACTAGAATTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA	GACTTATCAA	
msa235280.2{195_2603}	ACTAGAATTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA	GACTTATCAA	
msa235280.2{195_A909}	ACTAGAATTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA	GACTTATCAA	
Consensus	*****	*****	***-*****	*****	*****	*****	
msa235280.2{195_COH1}	2601	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT	2650
msa235280.2{195_M732}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT	TTTTGATGTT	
msa235280.2{195_M781}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT	TTTTGATGTT	
msa235280.2{195_H36B}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT	TTTTGATGTT	
msa235280.2{195_JM9130013}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT	TTTTGATGTT	
msa235280.2{195_18RS21}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT	TTTTGATGTT	
msa235280.2{195_2603}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT	TTTTGATGTT	
msa235280.2{195_A909}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT	TTTTGATGTT	
Consensus	*****	*****	*****	*****	*****	*****	
msa235280.2{195_COH1}	2651	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT	2700
msa235280.2{195_M732}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT	CTGTGGATAT	
msa235280.2{195_M781}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT	CTGTGGATAT	
msa235280.2{195_H36B}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT	CTGTGGATAT	
msa235280.2{195_JM9130013}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT	CTGTGGATAT	
msa235280.2{195_18RS21}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT	CTGTGGATAT	
msa235280.2{195_2603}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT	CTGTGGATAT	
msa235280.2{195_A909}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT	CTGTGGATAT	
Consensus	*****	*****	*****	*****	*****	*****	
msa235280.2{195_COH1}	2701	GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA	2750
msa235280.2{195_M732}	GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA	TATACATTAA	
msa235280.2{195_M781}	GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA	TATACATTAA	
msa235280.2{195_H36B}	GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA	TATACATTAA	
msa235280.2{195_JM9130013}	GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA	TATACATTAA	
msa235280.2{195_18RS21}	GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA	TATACATTAA	
msa235280.2{195_2603}	GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA	TATACATTAA	
msa235280.2{195_A909}	GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA	TATACATTAA	
Consensus	*****	*****	*****	*****	*****	*****	
msa235280.2{195_COH1}	2751	CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT	2800
msa235280.2{195_M732}	CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT	AACAAACGCT	
msa235280.2{195_M781}	CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT	AACAAACGCT	
msa235280.2{195_H36B}	CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT	AACAAACGCT	
msa235280.2{195_JM9130013}	CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT	AACAAACGCT	
msa235280.2{195_18RS21}	CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT	AACAAACGCT	
msa235280.2{195_2603}	CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT	AACAAACGCT	
msa235280.2{195_A909}	CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT	AACAAACGCT	
Consensus	*****	***-*****	*****	*****	*****	*****	
msa235280.2{195_COH1}	2801	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC	2850
msa235280.2{195_M732}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC	TTGATGTTCC	

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_M781}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
msa235280.2{195_H36B}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
msa235280.2{195_JM9130013}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
msa235280.2{195_18RS21}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
msa235280.2{195_2603}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
msa235280.2{195_A909}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
msa235280.2{195_M732}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
msa235280.2{195_M781}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
msa235280.2{195_H36B}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
msa235280.2{195_JM9130013}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
msa235280.2{195_18RS21}	GATTAAAGTA	GTTGACTTAG	AAGCTATT..	.....	.....
msa235280.2{195_2603}	GATTAAAGTA	GTTGACTTAG	AAGCTATT..	.....	.....
msa235280.2{195_A909}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_M732}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_M781}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_H36B}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_JM9130013}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_18RS21}	.....	.....	.....	..CGTAAAGC	TGAaGAAGCA
msa235280.2{195_2603}	.....	....cgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_A909}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
Consensus	-----	-----	-----	-----	-----
msa235280.2{195_COH1}	CaTAAAGCTG	AAGAAGtAcg	taaagctgaa	gaagcacata	aagtcgaaga
msa235280.2{195_M732}	CaTAAAGCTG	AAGAAGtAcg	taaagctgaa	gaagcacata	aagtcgaaga
msa235280.2{195_M781}	CaTAAAGCTG	AAGAAGtAcg	taaagctgaa	gaagcacata	aagtcgaaga
msa235280.2{195_H36B}	CaTAAAGCTG	AAGAAGtAcg	taaagctgaa	gaagcacata	aagtcgaaga
msa235280.2{195_JM9130013}	CaTAAAGCTG	AAGAAGtAcg	taaagctgaa	gaagcacata	aagtcgaaga
msa235280.2{195_18RS21}	CgTAAAGCTG	AAGAAGcA..	.....	.....	.....
msa235280.2{195_2603}	CgTAAAGCTG	AAGAAGcA..	.....	.....	.....
msa235280.2{195_A909}	CgTAAAGCTG	AAGAAGcA..	.....	.....	.....
Consensus	*-*****	*****-*	-----	-----	-----
msa235280.2{195_COH1}	agca.CGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_M732}	agca.CGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_M781}	agcacCGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_H36B}	agca.CGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_JM9130013}	agcacCGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_18RS21}	....CGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_2603}	....CGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_A909}	....CGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
Consensus	-----	*****	*****	*****	*****
msa235280.2{195_COH1}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
msa235280.2{195_M732}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
msa235280.2{195_M781}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
msa235280.2{195_H36B}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
msa235280.2{195_JM9130013}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
msa235280.2{195_18RS21}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
msa235280.2{195_2603}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
msa235280.2{195_A909}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_M732}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_M781}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_H36B}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_JM9130013}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_18RS21}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_2603}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_A909}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGt	-----
msa235280.2{195_M732}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGt	TGAAAA----
msa235280.2{195_M781}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGt	TG-----
msa235280.2{195_H36B}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATG~	-----
msa235280.2{195_JM9130013}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGt	TG-----
msa235280.2{195_18RS21}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGt	TGAA-----
msa235280.2{195_2603}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGt	TGAAAAACAA
msa235280.2{195_A909}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGt	TGAAAAACAA

Table 51: Comparative Sequences relating to SAG0677

Consensus	*****	*****	*****	*****	*****
	3201				3250
msa235280.2{195_COH1}	-----	-----	-----	-----	-----
msa235280.2{195_M732}	-----	-----	-----	-----	-----
msa235280.2{195_M781}	-----	-----	-----	-----	-----
msa235280.2{195_H36B}	-----	-----	-----	-----	-----
msa235280.2{195_JM9130013}	-----	-----	-----	-----	-----
msa235280.2{195_18RS21}	-----	-----	-----	-----	-----
msa235280.2{195_2603}	ATTAAAAATA	cattgccatc	cactgggtgac	agcaaacgtg	gttattatat
msa235280.2{195_A909}	ATTAAAAATA	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	3251				3300
msa235280.2{195_COH1}	-----	-----	-----	-----	-----
msa235280.2{195_M732}	-----	-----	-----	-----	-----
msa235280.2{195_M781}	-----	-----	-----	-----	-----
msa235280.2{195_H36B}	-----	-----	-----	-----	-----
msa235280.2{195_JM9130013}	-----	-----	-----	-----	-----
msa235280.2{195_18RS21}	-----	-----	-----	-----	-----
msa235280.2{195_2603}	cactggaatg	gctatcgta	tgctgagtg	attatttagt	ttagctaaaa
msa235280.2{195_A909}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	3301	3317			
msa235280.2{195_COH1}	-----	-----			
msa235280.2{195_M732}	-----	-----			
msa235280.2{195_M781}	-----	-----			
msa235280.2{195_H36B}	-----	-----			
msa235280.2{195_JM9130013}	-----	-----			
msa235280.2{195_18RS21}	-----	-----			
msa235280.2{195_2603}	agtttaaaag	caaatat			
msa235280.2{195_A909}	-----	-----			
Consensus	*****	*****			

## SEQ ID NO. 5110

STRAIN 2603 frame: 1

LNKGVGGDGVQIYQYYIKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKD VY  
 LQSVKYVGGGNNNLDLITPPGFKKEDKKVEKPKLDRPPGIDLPAPTSMRSFDYSTPPG TK  
 PSKPKDLSLTPPGFPDLNTPPDEALDKSKDAIEDKSGAIKYAKSLQLSFVDDPILASKV  
 NGKILQVESDGLVI PRNALSANQFDDTSLKIYRNNRNKEITITTDYFADTKYVNITAV  
 DYLNTTTFEQLATGETVDYHAI VFSSFAAIKDKGGKIYVNDKLQETSRIALKDKSVKIGI  
 ELPNDVRHIDLSVRLNEVKTVDNILKNDQDINLSKTYQLKYNPTNRRLEFTINNINS  
 SSEIMTTFKDGKMPPELVEQKDVSLDINDMMSKFKTIRLGRKDSEFKGQLIAKTGTVELD  
 MFFKQSQDPASI IKKIYLIQNGVPNELKKFDSSFGLTESQIDGYIYKDAINLKFKLTS G  
 ASLKVYVYKGQEDPYSHQKEDMTKKGEQLSHSTQANENTAKVTFANIDWSHYSKVTVNGKE  
 VVGKSELPLTKGWTTFVLHKTENSLNVKSLIMETGSVSKKVQQLPLSPRLSKNKHMRDML  
 LTMQKDSAYYETSDSLVLRINLTADTKLNFNAVGASALTENMMMRQFAVAGPQDDPVSE  
 HKYPSVFLLTTPALLETASEATLNGKEITASGIIGHIKDGDKSKHVEVKMVNENGDM LGTP  
 VI IQGKDLTNRTPKPLMSGRRVL YAGKQYEFRAKLPLSRFNTWIRVEVVTEAGEKASIVRR  
 MFFDQSVPELNTAVAKRDLTSDTALIHIVAKDDSLKLKLYQDDSLLESVDKTGLYSFRNG  
 VEITKDMTVPLEFGDNI IKLSAVDLSNYRRNETLHIYRNRFDVKASQMTADKGAKVTVD M  
 LMKHLVVP EMAGAYTLTIDEAPNTNESGMLTNAKVSIIHYVNGGVDKVDVPIKVVDLEAIR  
 KAEEARKAEAEARKAEAEARKAEAEAGHKTQEAPIVEEGYKVN NVHQDTTIVKASDLPKTKTVS  
 AVHMARTDNKQITSHQTHVEKQIKNTLPSTGDSKRGYITGMAIVMLSVLFLSLAKKFKSK  
 Y

## SEQ ID NO. 5111

STRAIN A909 frame: 1

LNKGVGGDGVQIYQYYIKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKD VY  
 LQSVKYVGGGNNNLDLITPPGFKKEDKKVEKPKLDRPPGIDLPAPTSMRSFDYSTPPG TK  
 PSKPKDLSLTPPGFPDLNTPPDEALDKSKDAIEDKSGAIKYAKSLQLSFVDDPILASKV  
 NGKILQVESDGLVI PRNALSANQFDDTSLKIYRNNRNKEITITTDYFADTKYVNITAV  
 DYLNTTTFEQLATGETVDYHAI VFSSFAAIKDKGGKIYVNDKLQETSRIALKDKSVKIGI  
 ELPNDVRHIDLSVRLNEVKTVDNILKNDQDINLSKTYQLKYNPTNRRLEFTINNINS  
 SSEIMTTFKDGKMPPELVEQKDVSLDINDMMSKFKTIRLGRKDSEFKGQLIAKTGTVELD  
 MFFKQSQDPASI IKKIYLIQNGVPNELKKFDSSFGLTESQIDGYIYKDAINLKFKLTS G  
 ASLKVYVYKGQEDPYSHQKEDMTKKGEQLSHSTQANENTAKVTFANIDWSHYSKVTVNGKE  
 VVGKSELPLTKGWTTFVLHKTENSLNVKSLIMETGSVSKKVQQLPLSPRLSKNKHMRDML  
 LTMQKDSAYYETSDSLVLRINLTADTKLNFNAVGASALTENMMMRQFAVAGPQDDPVSE  
 HKYPSVFLLTTPALLETASEATLNGKEITASGIIGHIKDGDKSKHVEVKMVNENGDM LGTP  
 VI IQGKDLTNRTPKPLMSGRRVL YAGKQYEFRAKLPLSRFNTWIRVEVVTEAGEKASIVRR  
 MFFDQSVPELNTAVAKRDLTSDTALIHIVAKDDSLKLKLYQDDSLLESVDKTGLYSFRNG  
 VEITKDMTVPLEFGDNI IKLSAVDLSNYRRNETLHIYRNRFDVKASQMTADKGAKVTVD M  
 LMKHLVVP EMAGAYTLTIDEAPNTNESGMLTNAKVSIIHYVNGGVDKVDVPIKVVDLEAIR  
 KAEEAHKAEAEARKAEAEARKAEAEARKAEAEAGHKTQEAPIVEEGYKVN NVHQDTTIVKASDLPKTKTVS  
 AVHMARTDNKQITSHQTHVEKQIKNTLPSTGDSKRGYITGMAIVMLSVLFLSLAKKFKSK  
 Y

## SEQ ID NO. 5112

STRAIN H36B frame: 2

GVQIYQYYIKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKD VY LQSVKYVGG  
 GNNNLDLITPPGFKKEDKKVEKPKLDRPPGIDLPAPTSMRSFDYSTPPGTFPSKPKDLS  
 TTPGFPDLNTPPDEALDKSKDAIEDKSGAIKYAKSLQLSFVDDPILASKVNGKILQVES

**Table 51: Comparative Sequences relating to SAG0677**

DGKLVP1PRNALSANQFDDTSLK1YRNNNRNKE1T1ITDDYFADTKYVN1TAVDYLNSNTFFE  
QLATQETVDYSHA1VFSSFAA1KDKGGK1YVNDKLQETSRIALKDSVK1G1ELPNVDVRH1  
DLSVRR1LNEVKTVD1LNLKNDQD1NLSKTYQLKYNTNRLEFT1NNINSSE1MTTFY  
DGMPKPELVBQKVSLD1NDMDMSKFKT1RLRKQDSEFGKL1AKTQETVELDMDFPKQSQDP1  
AS1IKKI1YL1QNGVPELNBKFPDSSFLGTESDIGDY1YKDANLKFPLTSGASLQVNVYVK  
QEDPVSHQKEDMTKKGEQLSHSTQANENTAKVTANIDWSHYSKTVNGKVBGKGSELP1  
TKGWTT1FVHLKTENSLNVKSLM1QNETQSVSKVQQLPLSP1SRKKNHMRDMLTMQKDSAY  
YETSDSLVR1NLITAD1KLFNAVNGASAL1NNMMMRQFAVAGPQDDPVSEHKYPSVFLL  
TPALTEASEATENGKE1TAGS1IGH1KDGDGSKHVEYKVMNNGMDLGTVP1I1QCKDLT  
NRTKPLMSGRRLVYAGKQYEFRAKPLSRFNTW1RVEVUTEAGEAKS1VRMFPDQSVPE  
LNTAVAKRDLTSDPAL1IH1VAKDDSLKLQLYQDSSLSDVTK1GYSFRNGVET1KMTV  
PLEFGDN1TKLSAVDLSNRYRRNETL1H1YRNRFDVKASQMTADGKAKTV1DMLMKHLVUPE  
MAGAYTLT1DEAPNTNESGMLTNAKVS1IHYVNGGVDKVDVPI1KVVDLEAIRKAEAAHKAD  
EARKAEARKADAEAKAEVRKAEAAHKVEEARKAEABGHKTQEP1VEEGYKVNNVHQT  
TVKASDLPKTKTKSVAHMARTDNQK1TSHQTH

SEQ ID NO. 5113

STRAIN 18RS21 frame: 1

LNKKGVGGDGVQIYQYYIMKDNKNPKYLPSPDKTITVEKLEDRWKKITFKVQSDTQIGLKDQV  
LQSQVYVGGGNLNDLITPFGKEDKKVEKPLDRPPGIDLPTMSRFSFYTSPPGTK  
SPKPKDLSLTSPGFPDLNTPPDEAPKDSKKDAIEDKSGAIKYAKSLQLSFVDDPILASKY  
NGKTLQVBSDGKLVIERNALSANQFDDTSLKITRNNNNKAIITITDYFADTKYVNI  
DYLNTPEQLATGETVDYHAI VSSFAAI KDKGGKI YVNDKLBQTSRIALDKDSVKIGI  
ELPNDRVRIH DLSVLRLNEVQKTVDNILKNDEQDINLSKTYQLKYNPTRNRLEPTINN  
SEEMITTFDKGKQVNVKTQDVSLDINDMDSKFKTIRLGRKDSBFKGQLIAGTGTVELD  
MFFKQSQDPASIIKKIYILQNGVNELKFKDSFSGLTESQIDGYYIYKDAINLKFKLTSG  
ASLKVVYQGDSPDISHQKEDMTKKEGLSHSTQANENTAKTVYKDAINDWSHYSKTVNGKE  
VVGKSELPLTKGWTTFVLHKTENSNVKSILMETGVSXKVKVQDLPLSRLSKNHMRDML  
LTKQKDSAYETSDSLVRLNLTADTKLFNFVAKGASALTENMMRQFVAVAGDOPVSE  
HKYPSVFLTLPALLETASEATLNGKEITASGIIGHIGDKDQSKHVEVKVMNENGLMGT  
PVIQCKDLTNRTKPLMSGRRVLVYAGKQVEFRAKLPLSRFNTYIRVEVVTENGEBKASIVR  
MFFQDSVPELNTAVAKRDLSDTALIHIVAKDDSLKLKLYQDSSLSESSQMTADKGVSRNG  
VEITKDMTVPLEGPDNIILKSAVDLNSYRNRETLHIYRNRFDVKASQMTADKGAQVTDV  
LMKHLVPEMAGAYTLTILKSAVDLNTESGMLTNAKVISIYRNVGQVDKVDVPIKVVDLEAIR  
KAEARKAEAEARKAEEGHKTKQEAPIVEEGYKVNNVHQITDTTVKASDLPKTKTVAHVHAR  
TNDQKITSHQTHVE

SEQ ID NO. 5114

STRAIN M732 frame: 1

LNNGKVGGGDGVQIQYIQQYIKKNNKKPYLSPDKTKTVEKLEDRWKTKTFKVQDZTIGLKDQVY  
LQSVKQYVGGGNNLNDLITPPGFKKDDKVEKPKLDRPGDILEDAPTSMSFSDYSTPGTK  
SPKPKDYLSDGFGFPDLNTPDEATKG. .KRRY. R. IRSN. IC. VSTL. LC. .PYFS. QS  
KQWQNTSRI. WQISHS. KCFVS. SI. .H. S. NLS. .SC. RNYHYNRLPFCRYKICQYHS  
.LFEQYQYF. AISYW. NSRLPCHCIPFGLCCY. RGOW. DLR. R. IARNFSYSR. R. IC. DWY  
.ITK. CQTY. .FICSSPE. G. NC. .YLEK. .TRH. SQONLPKIQDPKSSRVY. .H. L  
KFRNHDFHQRWDKARDIG. TKRCFFGYKRYGHE. V. NYSTWTKGF. I. GTTYCKWNNS. IR  
VYFQTSIRPSFNY. KNIPYKPKWSCJ. IEKI. L. L. FWFN. KSDRWILYL. RCN. P. I. INQW  
KCS. SCL. RARRSI. SGERRYD. KR. TAQSFNSQ. KYSKNCL. Y. LVTL. .GYCEWKR  
SW. R. .VTFN. RMDNICIT. NRKFKIC. KFDYDGC. CK. ESSTSFKS. II. K. AYEGBYA  
TYYAKRFSVLNRK. QSPFSN. SHCRY. T. P. C. C. RSECYG. KYDDTBSCWITR. SC. .  
T. IPISISILNSCLIGNC. .GNSKW. GNHYSWYYRSHQGW. .KOAC. SONGE. KWRHARNP  
CYYSR. RLD. SNTKINETW. STLCTR. ITL. VPG. ITT. SF. HLD. G. SGNRSRRESKYCSS  
HVL. PISSRA. HSSC. T. DDF. YCYSPIRCQR. LSKTKIISR. FIT. IC. .NRSL. F. KW  
CRNH. RYDSTNRSLRY. YV. VTIC. LKILKS. .DPSYL. KPF. C. SKPNDS. QRS. SNGCY  
VDEALCSNRNGRIYLNRRSSKIK. IRNVNKR. SIDSLCKWVC. .S. CSD. SS. LRSYS  
.S. RST. S. RST. S. RST. S. RST. S. RST. S. RST. SRST. S. RGT. NPRSTYS. RRL  
QS. .RSSN. YYS. SV. FTKD. DFSRSSYG. NRQ. TDNFTSDTC. K

SEQ ID NO. 5115

STRAIN COH1 frame: 1

[illegible]

SEQ ID NO. 5116

STRAIN M781 frame: 1

STRAIN M/81 Iframe: 1  
LNNKVGVGSDGVQIYQYYIKMDNNKPYLSPDKTTVEKLEDRWKKITFKVQDTGIGLKDVY  
LQSVKYVGGGNNNLLDITPPGFKKEDKKVEKPKLDRPPGIDLPAPTSMRSFDYSTPPGK

Table 51: Comparative Sequences relating to SAG0677

PSKPKDSLSTPPGFPDLNTPPDEATKG..KRRY.R.IRSN.IC.VSST.LC..PYFS.QS  
 KWQNTSRI.WQISHS.KCFVS.SI..H.S.NLS...SQ.RNYHNLFCRYKICQYHSG  
 .LFEQYF.AISYW.NSRLPCHCIFLCCY.RQGW.DLC.R.IARNFSYSA.R.IC.DWY  
 .ITK.CQTY..FICSSFE.G.NC..YLEK..TRH.SQONLPKIQPDKSSSRVY..H.L  
 KFRNHDHFQRWKDARIG.TKRCFFGYKRYGHE.V.NYSTWTKGF.I.GITYCKNWS.IR  
 YVQTISRPSFNY.KNIPYKPKCSK.IEKI.L.FWFN.KSDRWILYL.RCN.P.I.INQW  
 CKS.SCL.RARRSI.SSERRYD.KR.TAQSFNSQ.KYSKSNLC.Y.LVTL..GYCEWKR  
 SW.R..VTFN.RMDNICIT.NRKFIKC.KFDYGDG.CK.ESSTTSFKS.II.K.AYEGYA  
 TTYAKRFSVLNKN.QSSPSN.SHCYR.T.F.CC.RSECSY.KYDDETVCSWTTT.RC..  
 T.IPISISLNSCLIGNC..GNSKW.GNHSIWYRSHQGW..KQAC.SQNGE.KWRHARNP  
 CYYSR.RLD.SNKTINWT.STLCR.TI.VPG.ITT.SF.HLD.G.SGNRSRRESKYCSS  
 HVL.PISSRA.HSSC.T.PDF.YCSYFHRQOR.LSKTKIISR.FIT.IC..NRSL.F.KW  
 CRNH.RYDSTTRIWR.YY.VICC.LIKLSS..DPSYL.KPF.C.SKPND.S.QRS.SNCGY  
 VDEALSCSRNGRSLYNNRRSSKHK.IRNVNKR.SIDSLCKWWC..S.CSD.SS.LRSYS  
 .S.RST.S.RST.S.RST.S.RST.S.RST.S.RST.SRRSTVKLRDIPKPKHL.LKKA  
 TKLITFIKLILQLKRLIYQRLRQFPQFIWLEQTINR.LHIRHML

## SEQ ID NO. 5117

STRAIN JM9130013 frame: 2

GVQIYQYIYIKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKDVYLQSVKYVGG  
 GNNLIDLITPPGFKKEDKKVEKPKLDRPPGIDLPAPTSMRSFDYSTPPGTPSKPKDSL  
 TTPGFPDLNTPPDEAPKDKSKDAIEDKSGAIKYAKSLQLSFVDDPILASKVNGKILQVES  
 DGKLVIPRNALSANQFDDTSLKIYRNNNRNKEITITTDYFADTKYVNITAVDYLNTTTFE  
 QLATGETVDYHAIVFSSFAAIKDKGKIYVNDKLQETSRIALDKDSVKIGIELPNDVRHI  
 DSLSVRLNEVKTVDNLIKNDQDINLSKTYQLKYNPTNRRLEFTINNINSSEIMTTFK  
 DGKMPLEVEQKDVSLDINMDMSKFKTIRLGRKDESEFGQLIAKTGTVELDMPFFKQSQDP  
 ASIKKIYLIQNGVPELKKFDSSFGLTESQIDGYIYKDAINLKFKLTSGASLKVYVYG  
 QEDPYSHQKEDMTKKGEQLSHSTQANENTAKVTTFANIDWSHYSKVTVNGKEVGKSGSELPL  
 TKGWTTFLVHTKENSINVKSLIMETGSGSVKVKQQLPLSPRLSKNKHMRDMLLTQKDSAY  
 YETSDSLVLRINLTADTKLNFNAVKGASALTENMMMRQFAVAGQDDPFVSEHKYPSVFL  
 TPALLEATSEATLNGKEITASGIIIGHIKDGGKSHVEVKMVNENGDMLGTPVILQKDLT  
 NRTKPLMSGRVLYACKQYEFRAKLPLSRFNTWIRVEVVTGEAKSIVRRMFDQSVPE  
 LNTAVAKRDLTSDTALIHIVAKDDSLKLKLYQDDSLLESVDKTLGYSFRNGVEITKDMTV  
 PLEFGDNI IKLSAVDLSNYYRNNETLHIYRNRFVVKASQMTADKGAKTVDMLMKHLVPE  
 MAGAYTLTIDEAPNTNESGMLTNAKVSIIHYVNGGVKDVDPVPIKVVLEAIRKAEAAHKA  
 EARKAEAEARKAEAAHKAEEVRKAEAAHKAEEAP.S.RGT.NPRSTYS.RRLQG..RSSN.  
 YYS.SV.FTKD.DSFRSSYG.NRQ.TDNFTSDTC

PRETTY of: /biotmp/msa235427.2{\*} December 10, 2002 05:18 ..

msa235427.2{195_H36B}	1	50
msa235427.2{195_JM9130013}	-----G	VQIYQYIYIKM DNNKPYLSPK DKTTVEKLED RWKKITFKVQ
msa235427.2{195_18RS21}	-----G	VQIYQYIYIKM DNNKPYLSPK DKTTVEKLED RWKKITFKVQ
msa235427.2{195_2603}	LNNKGVGGDG	VQIYQYIYIKM DNNKPYLSPK DKTTVEKLED RWKKITFKVQ
msa235427.2{195_A909}	LNNKGVGGDG	VQIYQYIYIKM DNNKPYLSPK DKTTVEKLED RWKKITFKVQ
msa235427.2{195_COH1}	LNNKGVGGDG	VQIYQYIYIKM DNNKPYLSPK DKTTVEKLED RWKKITFKVQ
msa235427.2{195_M732}	LNNKGVGGDG	VQIYQYIYIKM DNNKPYLSPK DKTTVEKLED RWKKITFKVQ
msa235427.2{195_M781}	LNNKGVGGDG	VQIYQYIYIKM DNNKPYLSPK DKTTVEKLED RWKKITFKVQ
Consensus	*****	*****
msa235427.2{195_H36B}	51	100
msa235427.2{195_JM9130013}	DTGIGLKDVY	LQSVKYVGGG NNNLIDLITPP GFKKEDKKVE KPCLDRPPGI
msa235427.2{195_18RS21}	DTGIGLKDVY	LQSVKYVGGG NNNLIDLITPP GFKKEDKKVE KPCLDRPPGI
msa235427.2{195_2603}	DTGIGLKDVY	LQSVKYVGGG NNNLIDLITPP GFKKEDKKVE KPCLDRPPGI
msa235427.2{195_A909}	DTGIGLKDVY	LQSVKYVGGG NNNLIDLITPP GFKKEDKKVE KPCLDRPPGI
msa235427.2{195_COH1}	DTGIGLKDVY	LQSVKYVGGG NNNLIDLITPP GFKKEDKKVE KPCLDRPPGI
msa235427.2{195_M732}	DTGIGLKDVY	LQSVKYVGGG NNNLIDLITPP GFKKEDKKVE KPCLDRPPGI
msa235427.2{195_M781}	DTGIGLKDVY	LQSVKYVGGG NNNLIDLITPP GFKKEDKKVE KPCLDRPPGI
Consensus	*****	*****
msa235427.2{195_H36B}	101	150
msa235427.2{195_JM9130013}	DLPaPTSMRS	FDYSTPPGK PSKPKDSLST PPGFPDLNTP PDEAlKdskK
msa235427.2{195_18RS21}	DLPaPTSMRS	FDYSTPPGK PSKPKDSLST PPGFPDLNTP PDEApKdskK
msa235427.2{195_2603}	DLPaPTSMRS	FDYSTPPGK PSKPKDSLST PPGFPDLNTP PDEApKdskK
msa235427.2{195_A909}	DLPaPTSMRS	FDYSTPPGK PSKPKDSLST PPGFPDLNTP PDEAlKdskK
msa235427.2{195_COH1}	DLPaPTSMRS	FDYSTPPGK PSKPKDSLST PPGFPDLNTP PDEAtKg..K
msa235427.2{195_M732}	DLPaPTSMRS	FDYSTPPGK PSKPKDSLST PPGFPDLNTP PDEAtKg..K
msa235427.2{195_M781}	DLPaPTSMRS	FDYSTPPGK PSKPKDSLST PPGFPDLNTP PDEAtKg..K
Consensus	***-*****	*****
msa235427.2{195_H36B}	151	200
msa235427.2{195_JM9130013}	daiedksgai	kyakslqlsf vddPilaskv ngkilqvess gklviprnl
msa235427.2{195_18RS21}	daiedksgai	kyakslqlsf vddPilaskv ngkilqvess gklviprnl
msa235427.2{195_2603}	daiedksgai	kyakslqlsf vdgPilaskv ngkilqvess gklviprnl
msa235427.2{195_A909}	daiedksgai	kyakslqlsf vddPilaskv ngkilqvess gklviprnl
msa235427.2{195_COH1}	rry.r.irs	ic.vsst.l c..Pyfs.qs kwqnitisri. wqishs.kcf
msa235427.2{195_M732}	rry.r.irs	ic.vsst.l c..Pyfs.qs kwqnitisri. wqishs.kcf
msa235427.2{195_M781}	rry.r.irs	ic.vsst.l c..Pyfs.qs kwqnitisri. wqishs.kcf
Consensus	-----	-----

Table 51: Comparative Sequences relating to SAG0677

		201			250
msa235427.2{195_H36B}	sanqfddtsl	kiyrnnnrnk	eitittddyFa	dtKyvntav	dylsnttFeq
msa235427.2{195_JM9130013}	sanqfddtsl	kiyrnnnrnk	eitittddyFa	dtKyvntav	dylsnttFeq
msa235427.2{195_18RS21}	sanqfddtsl	kiyrnnnrnk	eitittddyFa	dtKyvntav	dylsnttFeq
msa235427.2{195_2603}	sanqfddtsl	kiyrnnnrnk	eitittddyFa	dtKyvntav	dylsnttFeq
msa235427.2{195_A909}	sanqfddtsl	kiyrnnnrnk	eitittddyFa	dtKyvntav	dylsnttFeq
msa235427.2{195_COH1}	vs.si..h.s	.nls...sq.	rnyyhnrlFc	ryKicqyhsq	.lfeqyyF.a
msa235427.2{195_M732}	vs.si..h.s	.nls...sq.	rnyyhnrlFc	ryKicqyhsq	.lfeqyyF.a
msa235427.2{195_M781}	vs.si..h.s	.nls...sq.	rnyyhnrlFc	ryKicqyhsq	.lfeqyyF.a
Consensus		-----	-----*	-----*	-----*
		251			300
msa235427.2{195_H36B}	latgetvdyh	aivfssfaai	kdkGgkiyvn	dklqetsria	lkdksvkigi
msa235427.2{195_JM9130013}	latgetvdyh	aivfssfaai	kdkGgkiyvn	dklqetsria	lkdksvkigi
msa235427.2{195_18RS21}	latgetvdyh	aivfssfaai	kdkGgkiyvn	dklqetsria	lkdksvkigi
msa235427.2{195_2603}	latgetvdyh	aivfssfaai	kdkGgkiyvn	dklqetsria	lkdksvkigi
msa235427.2{195_A909}	latgetvdyh	aivfssfaai	kdkGgkiyvn	dklqetsria	lkdksvkigi
msa235427.2{195_COH1}	isyw.nsr1p	chcifklccy	.rqGw.dlc.	r.iarnfsys	a.r.ic.dwy
msa235427.2{195_M732}	isyw.nsr1p	chcifklccy	.rqGw.dlc.	r.iarnfsys	a.r.ic.dwy
msa235427.2{195_M781}	isyw.nsr1p	chcifklccy	.rqGw.dlc.	r.iarnfsys	a.r.ic.dwy
Consensus		-----	-----*	-----*	-----*
		301			350
msa235427.2{195_H36B}	elpndvrhid	slsvrrlnev	ktvndiLknd	eqdinlskty	qlKynPtnrr
msa235427.2{195_JM9130013}	elpndvrhid	slsvrrlnev	ktvndiLknd	eqdinlskty	qlKynPtnrr
msa235427.2{195_18RS21}	elpndvrhid	slsvrrlnev	ktvndiLknd	eqdinlskty	qlKynPtnrr
msa235427.2{195_2603}	elpndvrhid	slsvrrlnev	ktvndiLknd	eqdinlskty	qlKynPtnrr
msa235427.2{195_A909}	elpndvrhid	slsvrrlnev	ktvndiLknd	eqdinlskty	qlKynPtnrr
msa235427.2{195_COH1}	.itk.cqty.	.ficssfe.g	.nc..yLek.	.trh.sqgnl	piKiqPdkas
msa235427.2{195_M732}	.itk.cqty.	.ficssfe.g	.nc..yLek.	.trh.sqgnl	piKiqPdkas
msa235427.2{195_M781}	.itk.cqty.	.ficssfe.g	.nc..yLek.	.trh.sqgnl	piKiqPdkas
Consensus		-----	-----*	-----*	-----*
		351			400
msa235427.2{195_H36B}	leftinnins	sseimttFkd	gKmpelveqK	dvldindmd	mskfktirlg
msa235427.2{195_JM9130013}	leftinnins	sseimttFkd	gKmpelveqK	dvldindmd	mskfktirlg
msa235427.2{195_18RS21}	leftinnins	sseimttFkd	gKmpelveqK	dvldindmd	mskfktirlg
msa235427.2{195_2603}	leftinnins	sseimttFkd	gKmpelveqK	dvldindmd	mskfktirlg
msa235427.2{195_A909}	leftinnins	sseimttFkd	gKmpelveqK	dvldindmd	mskfktirlg
msa235427.2{195_COH1}	srvyv..h.l	kfrnhdhFqr	wKdarig.tK	rcffgykryg	he.v.nystw
msa235427.2{195_M732}	srvyv..h.l	kfrnhdhFqr	wKdarig.tK	rcffgykryg	he.v.nystw
msa235427.2{195_M781}	srvyv..h.l	kfrnhdhFqr	wKdarig.tK	rcffgykryg	he.v.nystw
Consensus		-----	-----*	-----*	-----*
		401			450
msa235427.2{195_H36B}	rKdsefkGql	iaKtgtveld	mfFkqsqdpA	siikKiyliq	ngvpnelkKf
msa235427.2{195_JM9130013}	rKdsefkGql	iaKtgtveld	mfFkqsqdpA	siikKiyliq	ngvpnelkKf
msa235427.2{195_18RS21}	rKdsefkGql	iaKtgtveld	mfFkqsqdpA	siikKiyliq	ngvpnelkKf
msa235427.2{195_2603}	rKdsefkGql	iaKtgtveld	mfFkqsqdpA	siikKiyliq	ngvpnelkKf
msa235427.2{195_A909}	rKdsefkGql	iaKtgtveld	mfFkqsqdpA	siikKiyliq	ngvpnelkKf
msa235427.2{195_COH1}	tKgf.i.Gtt	ycKnwns.ir	yvFqtisrPs	fny.Knipyp	kwcsk.ieKi
msa235427.2{195_M732}	tKgf.i.Gtt	ycKnwns.ir	yvFqtisrPs	fny.Knipyp	kwcsk.ieKi
msa235427.2{195_M781}	tKgf.i.Gtt	ycKnwns.ir	yvFqtisrPs	fny.Knipyp	kwcsk.ieKi
Consensus		-----	-----*	-----*	-----*
		451			500
msa235427.2{195_H36B}	dssFgltesq	idgyyiykda	inlkfkltsg	aslkvvykgq	edpyshqked
msa235427.2{195_JM9130013}	dssFgltesq	idgyyiykda	inlkfkltsg	aslkvvykgq	edpyshqked
msa235427.2{195_18RS21}	dssFgltesq	idgyyiykda	inlkfkltsg	aslkvvykgq	edpyshqked
msa235427.2{195_2603}	dssFgltesq	idgyyiykda	inlkfkltsg	aslkvvykgq	edpyshqked
msa235427.2{195_A909}	dssFgltesq	idgyyiykda	inlkfkltsg	aslkvvykgq	edpyshqked
msa235427.2{195_COH1}	.l.Fwfn.ks	drwilyl.rc	n.p.i.inqw	cks.scl.ra	rrsi.sserr
msa235427.2{195_M732}	.l.Fwfn.ks	drwilyl.rc	n.p.i.inqw	cks.scl.ra	rrsi.sserr
msa235427.2{195_M781}	.l.Fwfn.ks	drwilyl.rc	n.p.i.inqw	cks.scl.ra	rrsi.sserr
Consensus		-----	-----*	-----*	-----*
		501			550
msa235427.2{195_H36B}	mtkkgeqlsh	stqanentaK	vtfanidwsh	yskvtvngKe	vgkgselplt
msa235427.2{195_JM9130013}	mtkkgeqlsh	stqanentaK	vtfanidwsh	yskvtvngKe	vgkgselplt
msa235427.2{195_18RS21}	mtkkgeqlsh	stqanentaK	vtfanidwsh	yskvtvngKe	vgkgselplt
msa235427.2{195_2603}	mtkkgeqlsh	stqanentaK	vtfanidwsh	yskvtvngKe	vgkgselplt
msa235427.2{195_A909}	mtkkgeqlsh	stqanentaK	vtfanidwsh	yskvtvngKe	vgkgselplt
msa235427.2{195_COH1}	yd.kr.taqs	fnssq.kysK	snlc.y.lvt	l..gycewKr	sw.r..vtfn
msa235427.2{195_M732}	yd.kr.taqs	fnssq.kysK	snlc.y.lvt	l..gycewKr	sw.r..vtfn
msa235427.2{195_M781}	yd.kr.taqs	fnssq.kysK	snlc.y.lvt	l..gycewKr	sw.r..vtfn
Consensus		-----	-----*	-----*	-----*
		551			600
msa235427.2{195_H36B}	kgwttfvlhk	tenslnvksl	imetGsvskk	vqqlplsprl	sknkhmrdbl
msa235427.2{195_JM9130013}	kgwttfvlhk	tenslnvksl	imetGsvskk	vqqlplsprl	sknkhmrdbl
msa235427.2{195_18RS21}	kgwttfvlhk	tenslnvksl	imetGsvskk	vqqlplsprl	sknkhmrdbl
msa235427.2{195_2603}	kgwttfvlhk	tenslnvksl	imetGsvskk	vqqlplsprl	sknkhmrdbl



Table 51: Comparative Sequences relating to SAG0677

msa235427.2{195_A909}	kgwtffvlhk	tenslnvksl	imetGavskk	vqqlplsprl	sknkhmrndl
msa235427.2{195_COH1}	.rmdnicit.	nrkfiko.kf	dygdG.ck.e	ssttsfks.i	i.k.ayegy.
msa235427.2{195_M732}	.rmdnicit.	nrkfiko.kf	dygdG.ck.e	ssttsfks.i	i.k.ayegy.
msa235427.2{195_M781}	.rmdnicit.	nrkfiko.kf	dygdG.ck.e	ssttsfks.i	i.k.ayegy.
Consensus	-----	-----	-----*	-----	-----
msa235427.2{195_H36B}	601				650
msa235427.2{195_JM9130013}	lTmqkdsayy	etsdsivlri	Nltadtklmf	navkgaSalt	enmmmrqfav
msa235427.2{195_18RS21}	lTmqkdsayy	etsdsivlri	Nltadtklmf	navkgaSalt	enmmmrqfav
msa235427.2{195_2603}	lTmqkdsayy	etsdsivlri	Nltadtklmf	navkgaSalt	enmmmrqfav
msa235427.2{195_A909}	lTmqkdsayy	etsdsivlri	Nltadtklmf	navkgaSalt	enmmmrqfav
msa235427.2{195_COH1}	aTyyakrfsv	lrnk.qsps	N.shcry.t.	f.cc.rSecs	y.kyddetvc
msa235427.2{195_M732}	aTyyakrfsv	lrnk.qsps	N.shcry.t.	f.cc.rSecs	y.kyddetvc
msa235427.2{195_M781}	aTyyakrfsv	lrnk.qsps	N.shcry.t.	f.cc.rSecs	y.kyddetvc
Consensus	-----	-----	-----*	-----*	-----
msa235427.2{195_H36B}	651				700
msa235427.2{195_JM9130013}	agpqddpvse	hkypsvflit	palLetasea	tlngkeitaS	giighikdGd
msa235427.2{195_18RS21}	agpqddpvse	hkypsvflit	palLetasea	tlngkeitaS	giighikdGd
msa235427.2{195_2603}	agpqddpvse	hkypsvflit	palLetasea	tlngkeitaS	giighikdGd
msa235427.2{195_A909}	agpqddpvse	hkypsvflit	palLetasea	tlngkeitaS	giighikdGd
msa235427.2{195_COH1}	scwttr.sc.	.t.ipisisl	nscLignc..	gnskw.gnhS	iwyrrshqGw
msa235427.2{195_M732}	scwttr.sc.	.t.ipisisl	nscLignc..	gnskw.gnhS	iwyrrshqGw
msa235427.2{195_M781}	scwttr.sc.	.t.ipisisl	nscLignc..	gnskw.gnhS	iwyrrshqGw
Consensus	-----	-----	-----*	-----*	-----*
msa235427.2{195_H36B}	701				750
msa235427.2{195_JM9130013}	ksKhvevkmv	nEngdmlgtp	viiggkdltN	rtkplmsgr	vlyagkqyef
msa235427.2{195_18RS21}	ksKhvevkmv	nEngdmlgtp	viiggkdltN	rtkplmsgr	vlyagkqyef
msa235427.2{195_2603}	ksKhvevkmv	nEngdmlgtp	viiggkdltN	rtkplmsgr	vlyagkqyef
msa235427.2{195_A909}	ksKhvevkmv	nEngdmlgtp	viiggkdltN	rtkplmsgr	vlyagkqyef
msa235427.2{195_COH1}	.Kqac.sqn	gE.kwrharn	pcyyr.rld	.snktinewt	.stlcr.ti.
msa235427.2{195_M732}	.Kqac.sqn	gE.kwrharn	pcyyr.rld	.snktinewt	.stlcr.ti.
msa235427.2{195_M781}	.Kqac.sqn	gE.kwrharn	pcyyr.rld	.snktinewt	.stlcr.ti.
Consensus	-----	-----*	-----	-----	-----
msa235427.2{195_H36B}	751				800
msa235427.2{195_JM9130013}	raklplsrfrn	twirvevte	agekaSivrr	mffdqsvpel	ntavakrdlt
msa235427.2{195_18RS21}	raklplsrfrn	twirvevte	agekaSivrr	mffdqsvpel	ntavakrdlt
msa235427.2{195_2603}	raklplsrfrn	twirvevte	agekaSivrr	mffdqsvpel	ntavakrdlt
msa235427.2{195_A909}	raklplsrfrn	twirvevte	agekaSivrr	mffdqsvpel	ntavakrdlt
msa235427.2{195_COH1}	vpg.itt.sf	.hld.g.sgn	rsrreSkycs	shvl.pissr	a.hssc.t.f
msa235427.2{195_M732}	vpg.itt.sf	.hld.g.sgn	rsrreSkycs	shvl.pissr	a.hssc.t.f
msa235427.2{195_M781}	vpg.itt.sf	.hld.g.sgn	rsrreSkycs	shvl.pissr	a.hssc.t.f
Consensus	-----	-----	-----*	-----	-----
msa235427.2{195_H36B}	801				850
msa235427.2{195_JM9130013}	sdtalihiva	kddsLklkly	qddsllesvd	ktglysfng	veitkdmtp
msa235427.2{195_18RS21}	sdtalihiva	kddsLklkly	qddsllesvd	ktglysfng	veitkdmtp
msa235427.2{195_2603}	sdtalihiva	kddsLklkly	qddsllesvd	ktglysfng	veitkdmtp
msa235427.2{195_A909}	sdtalihiva	kddsLklkly	qddsllesvd	ktglysfng	veitkdmtp
msa235427.2{195_COH1}	df.ycsyphr	cqr.Lsktki	isr.fit.ic	.nrsl.f.k	wcrnh.ryds
msa235427.2{195_M732}	df.ycsyphr	cqr.Lsktki	isr.fit.ic	.nrsl.f.k	wcrnh.ryds
msa235427.2{195_M781}	df.ycsyphr	cqr.Lsktki	isr.fit.ic	.nrsl.f.k	wcrnh.ryds
Consensus	-----	-----*	-----	-----	-----
msa235427.2{195_H36B}	851				900
msa235427.2{195_JM9130013}	lefgdnitkl	savdlsnyrr	netlhiYrnr	fdvkaSqmta	dkgakvtvdm
msa235427.2{195_18RS21}	lefgdnitkl	savdlsnyrr	netlhiYrnr	fdvkaSqmta	dkgakvtvdm
msa235427.2{195_2603}	lefgdnitkl	savdlsnyrr	netlhiYrnr	fdvkaSqmta	dkgakvtvdm
msa235427.2{195_A909}	lefgdnitkl	savdlsnyrr	netlhiYrnr	fdvkaSqmta	dkgakvtvdm
msa235427.2{195_COH1}	tttriwr.yy	vicc.likls	s..dpsYl.k	pf.c.Skpnd	s.qrs.sncg
msa235427.2{195_M732}	tttriwr.yy	vicc.likls	s..dpsYl.k	pf.c.Skpnd	s.qrs.sncg
msa235427.2{195_M781}	tttriwr.yy	vicc.likls	s..dpsYl.k	pf.c.Skpnd	s.qrs.sncg
Consensus	-----	-----	-----*	-----*	-----
msa235427.2{195_H36B}	901				950
msa235427.2{195_JM9130013}	lmkhlvpem	aGaytltide	apntnesgml	tNakvSIhyv	nggvdkvdvp
msa235427.2{195_18RS21}	lmkhlvpem	aGaytltide	apntnesgml	tNakvSIhyv	nggvdkvdvp
msa235427.2{195_2603}	lmkhlvpem	aGaytltide	apntnesgml	tNakvSIhyv	nggvdkvdvp
msa235427.2{195_A909}	lmkhlvpem	aGaytltide	apntnesgml	tNakvSIhyv	nggvdkvdvp
msa235427.2{195_COH1}	yvdealcsr	nGrsllyinnr	rsakhhk.irn	vNkr.SIdsl	ckwwc..s.c
msa235427.2{195_M732}	yvdealcsr	nGrsllyinnr	rsakhhk.irn	vNkr.SIdsl	ckwwc..s.c
msa235427.2{195_M781}	yvdealcsr	nGrsllyinnr	rsakhhk.irn	vNkr.SIdsl	ckwwc..s.c
Consensus	-----	-----*	-----*	-----*	-----

Table 51: Comparative Sequences relating to SAG0677

		951			1000
msa235427.2{195_H36B}	ikvvdleair	kaeeahkade	arkaeeearka	deahkaeevr	kaeeahkvee
msa235427.2{195_JM9130013}	ikvvdleair	kaeeahkade	arkaeeearka	eeahkaeevr	kaeeahkvee
msa235427.2{195_18RS21}	ikvvdlea..	...irkaee	arkaeeearka	eeghktqeap	iveegykvnn
msa235427.2{195_2603}	ikvvdleair	kaeearkaee	arkaeeearka	eeghktqeap	iveegykvnn
msa235427.2{195_A909}	ikvvdleair	kaeeahkade	arkaeeearka	eearkaeeear	kaeehktqe
msa235427.2{195_COH1}	sd.ss.lrsy	s.s.rst.s.	rst.s.rst.	s.rst.s.rs	t.s.rst.sr
msa235427.2{195_M732}	sd.ss.lrsy	s.s.rst.s.	rst.s.rst.	s.rst.s.rs	t.s.rst.sr
msa235427.2{195_M781}	sd.ss.lrsy	s.s.rst.s.	rst.s.rst.	s.rst.s.rs	t.s.rst.sr
	Consensus	-----	-----	-----	-----
		1001			1050
msa235427.2{195_H36B}	arkaeeghkt	geapiveegy	kvnnvhqtdt	tvkasdlpkt	ktvsavhmar
msa235427.2{195_JM9130013}	ap.s.rgt.n	prstys.rri	gg..rssn.y	ys.sv.ftkd	.dsfrssyg.
msa235427.2{195_18RS21}	vhqtdttvka	sdipktktvs	avhmardnk	qitshqthve	-----
msa235427.2{195_2603}	vhqtdttvka	sdipktktvs	avhmardnk	qitshqthve	kqikntlpst
msa235427.2{195_A909}	apiveegykv	nnvhqtdttv	kasdlpktkt	vsavhmardt	nkqitshqth
msa235427.2{195_COH1}	rst.s.rgt.	nprstys.rr	lqs..rssn.	yps.sv.ftk	d.dsfrssyg
msa235427.2{195_M732}	rst.s.rgt.	nprstys.rr	lqs..rssn.	yps.sv.ftk	d.dsfrssyg
msa235427.2{195_M781}	rstvklrddi	kpkkh1.lkk	atklitfikl	ilqlkrliyy	rlrqfpqfiw
	Consensus	-----	-----	-----	-----
		1051		1081	
msa235427.2{195_H36B}	tdnkqitshq	th-----	-----	-----	~
msa235427.2{195_JM9130013}	nrq.tdnfts	dte-----	-----	-----	~
msa235427.2{195_18RS21}	-----	-----	-----	-----	~
msa235427.2{195_2603}	gdskrgyyit	gmaivmlsvl	fslakkfksk	y	
msa235427.2{195_A909}	vekqikn---	-----	-----	-----	~
msa235427.2{195_COH1}	.nrq.tdnft	sdTC-----	-----	-----	~
msa235427.2{195_M732}	.nrq.tdnft	sdTC.k----	-----	-----	~
msa235427.2{195_M781}	leqtinr.lh	irhml-----	-----	-----	~
	Consensus	-----	*****	*****	*

Table 52: Comparative Sequences relating to SAG 1823

## SEQ ID NO. 5201

## STRAIN 090

AGCGATACCTTTAATTTTGATATTGACCAAATTGCAGA  
 CAATGCTATCACTAAACAGATAAAACAACAGAAATTATTTCCAACCAGA  
 CAACAAGCCAAACTGGGCAAATTGCTTTTGTGAAAACTAACACCAGCA  
 CAAAAGTCTGCTATCTCTGAAAAAACACCAGCTTTGGTAGATACTTTTGT  
 CGGCGATCAAAATGCGCTCCTTGATTTTGGACAATCCGAGTAGAAGGCG  
 TTAATACCACTGTAAATCATATCTTGTCTGAGCAGAAAAAATTCAAATT  
 CCTCAAGTTGATGATTTACTAAAAAATGCTAATCGCGAACTAAATGGATT  
 TATTGCCAAATATAAGATGCTACTCCGGCAGAATTAGAGAAAAACCAA  
 ACTTGATTCAAAAATTATTCAAACAAAGCAAGACCTCGCTACAGGAATTT  
 TATTTTGACTCACAACATCGAGCAAAAAATGGATATGATGGCAGCGAA  
 TGTGTCAACAAGAGATACCTTTGGCAAGAAATATCGTCTCTGCTGAAA  
 TGCTCATTGAAGATAACTAAATCTATTGAAAAATTGGTTGGAGTTATT  
 GCTTCTATTGAATCGAGTCAAGCCGAGGCTGCTAATCGTGCAAGCCACTT  
 ACAACAAGAAATCTAGCATTAGATAGCCAAACGTCCGAGTATCAAAATTA  
 AAGTAAACCAATTAGCTCGAATGACTGAAGTTATCAATACCTCGAACAG  
 CAACATACTGAATATGTCAGCCGTCTCTACGTTGCATGGGCAACAACACC  
 ACAGATGCGAAACTTGGTCAAAGTATCGTCAGATATGCGTCAGAACTTG  
 GCATGTTACGTCGAAATACCATTTCCAACAATGAACTCTCAATCGCTCAG  
 TTAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTAT  
 TGTCAACGCTAATAATGACGATTTGCAGATGCTGGCTGAACTAGTAAAG  
 AAGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCACTGTTTCTATT  
 AAATCTGTCACTGCATTAGCTGAAAGCTTAGTGGCTCAAAATAATGGTAT  
 TATCGCTGCCATAGACAAAGGACGTAAGGAACGTGCCCAATTGGAATCTG  
 CTGTTATTAAATCGGCTGAAACAATCAATGATTCTGTCAAATTCGTGAT  
 AAAAAATAGTTGAAGCCTTACTCAACGAAGGTAAATCTACCCAAGAAAA  
 AGTTGATGAGTCT

## SEQ ID NO. 5202

## STRAIN A909

AGCGATACCTTTAATTTTGATATTGACCAAATTGCAGA  
 CAATGCTATCACTAAACAGATAAAACAACAGAAATTATTTCCAACCAGA  
 CAACAAGCCAAACTGGGCAAATTGCTTTTGTGAAAACTAACACCAGCA  
 CAAAAGTCTGCTATCTCTGAAAAAACACCAGCTTTGGTAGATACTTTTGT  
 CGGTGACCAAAATGCGCTCCTTGATTTTGGACAATCCGAGTAGAAGGCG  
 TTAATACCACTGTAAATCATATCTTGTCTGAGCAGAAAAAATTCAAATT  
 CCTCAAGTTGATGATTTACTAAAAAATGCTAATCGCGAACTAAATGGATT  
 TATTGCCAAATATAAGATGCTACTCCGGCAGAATTAGAGAAAAACCAA  
 ACTTGATTCAAAAATTATTCAAACAAAGCAAGACCTCGCTACAGGAATTT  
 TATTTTGACTCACAACATCGAGCAAAAAATGGATATGATGGCAGCGAA  
 TGTGTCAACAAGAGATACCTTTGGCAAGAAATATCGTCTCTGCTGAAA  
 TGCTCATTGAAGATAACTAAATCTATTGAAAAATTGGTTGGAGTTAWT  
 GCTTTTATTGAATCGAGTCAAGCCGAGGCTGCCAATCGTGCAAGCCACTT  
 ACAACAAGAAATCTAGCATTAGATAGCCAAACGTCCGAGTATCAAAATTA  
 AAGTAAACCAATTAGCTCGAATGACTGAAGTTATCAATACCTCGAACAG  
 CAACATACTGAATATGTCAGCCGTCTCTACGTTGCATGGGCAACAACACC  
 ACAGATGCGAAACTTGGTCAAAGTATCGTCAGATATGCGTCAGAACTTG  
 GCATGTTACGTCGAAATACCATTTCCAACAATGAACTCTCAATCGCTCAG  
 TTAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTAT  
 TGTCAACGCTAATAATGACGATTTGCAGATGCTGGCTGAACTAGTAAAG  
 AAGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCACTGTTTCTATT  
 AAATCTGTCACTGCATTAGCTGAAAGCTTAGTGGCTCAAAATAATGGTAT  
 TATCGCTGCCATAGACAAAGGACGTAAGGAACGTGCCCAATTAGAAATCTG  
 CTGTTATTAAATCGGCTGAAACAATCAATGATTCTGTCAAATTCGTGAT  
 AAAAAATAGTTGAAGCCTTACTCAACGAAGGTAAATCTACCCAAGAAAA  
 AGTGTGATGAGTCT

## SEQ ID NO. 5203

## STRAIN H36B

AGCGATACCTTTAATTTTGATATTGACCAAATTGCAGAC  
 AATGCTATCACTAAACAGATAAAACAACAGAAATTATTTCCAACCAGAC  
 AACAGCCAAACTGGGCAAATTGCTTTTGTGAAAACTAACACCAGCAC  
 AAAAGTCTGCTATCTCTGAAAAAACACCAGCTTTGGTAGATACTTTTGT  
 GTGACCAAAATGCGCTCCTTGATTTTGGACAATCCGAGTAGAAGGCGT  
 TAATACCACTGTAAATCATATCTTGTCTGAGCAGAAAAAATTCAAATTC  
 CTCAGTTGATGATTTACTAAAAAATGCTAATCGCGAACTAAATGGATT  
 ATTGCCAAATATAAGATGCTACTCCGGCAGAATTAGAGAAAAACCAA  
 CTTGATTCAAAAATTATTCAAACAAAGCAAGACCTCGCTACAGGAATTTT  
 ATTTTGACTCACAACATCGAGCAAAAAATGGATATGATGGCAGCGAAT  
 GTTGTCAACAAGAGATACCTTTGGCAAGAAATATCGTCTCTGCTGAAAT  
 GCTCATTGAAGATAACTAAATCTATTGAAAAATTGGTTGGAGTTATTG  
 CTCTATTGAATCGAGTCAAGCCGAGGCTGCCAATCGTGCAAGCCACTTA  
 CAACAAGAAATCTAGCATTAGATAGCCAAACGTCCGAGTATCAAAATTA  
 AAGTAAACCAATTAGCTCGAATGACTGAAGTTATCAATACCTCGAACAGC  
 AACATACTGAATATGTCAGCCGTCTCTACGTTGCATGGGCAACAACACCA  
 CAGATGCGAAACTTGGTCAAAGTATCGTCAGATATGCGTCAGAACTTG  
 CATGTTACGTCGAAATACCATTTCCAACAATGAACTCTCAATCGCTCAGT  
 TAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTATT  
 GTCAACGCTAATAATGACGATTTGCAGATGCTGGCTGAACTAGTAAAGA  
 AGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCACTGTTTCTATT  
 AATCTGTCACTGCATTATCTGAAAGCTTAGTGGCTCAAAATAATGGTATT  
 ATCGCTGCCATAGACAAAGGACGTAAGGAACGTGCCCAATTAGAAATCTGC

Table 52: Comparative Sequences relating to SAG 1823

TGTTATTAAATCGGCTGAAACAATCAATGATTCTGTCAAAATTCGTGATa  
 AAAAAATAGTTGAAGCCTTACTCAaCGAAGGTaAATCTACCCAAGAAAAA  
 GTTGATGAGTCT

SEQ ID NO. 5204

STRAIN 18RS21

TTTTGATATTGACCAAATTCAGACAATGCTATCACTAAAAACAGATAAAA  
 CAACAGAAATTATTTCCAACCAGACAACAAGCCAAACTGGGCAAAATGGCC  
 TTTTTTGAAAAAATAACACCAGCACAAAAGTCTGCTATCTCTGAAAAAAC  
 ACCAGCTTTGGTAGATACTTTTGTGGCGATCAAAATGCGCTCCTTGATT  
 TTGGACAATCCGCGTAGAAGGCGTTAATACCAGTGTAAATCATATCTTG  
 TCTGAGCAGAAAAAATTCAAATTCCTCAAGTTGATGATTTTACTAAAAAA  
 TGCTAATCGCGAACTAAATGGATTTATTGCCAAATATAAAGATGCTACTC  
 CGGCAGAAATTAGAGAAAAACCAAACTTGATTCAAAAATTATTCAAACAA  
 AGCAAGACCTCGCTACAGGAATTTTATTTTGACTCACAAAACATCGAGCA  
 AAAAATGGATATGATGGCAGCGAATGTTGTCAAACAAGAGATACCTTGG  
 CAAGAAATATCGTCTCTGCTGAAATGCTCATGAAGATAATCTAAATCT  
 ATTGAAAATTGGTTGGAGTTATTGCTTTTATTGAATCGAGTCAAGCCGA  
 GGTGCTTAATCGTGCAAGCCACTTACAACAGAAATTCTAGCATTAGATA  
 GCCAAACGCTCCGAGTATCAAATTAAGAATAACCAATTAGCTCGAATGACT  
 GAAGTTATCAATACCCTCGAACAGCAACATCCTGAATATGTCAGCCGTCT  
 CTACGTTGCATGGGCAACAACCAACAGATGCGAAACTTGGTCAAGTAT  
 CGTCAGATATGCGTCAGAACTTGGCATGTTACGTCGAAATACCAATCCCA  
 ACAATGAACTCTCAATCGCTCAGTTAGGCATGATGCAACAATCTGTCAA  
 ATCCGGTGTCACTGCTGATGCTATTGTCAACGCTAATAATGCAGCATTGC  
 AGATGCTGGCTGAACTAGTAAAGAAGCGATCCGATGTTAGAGAAGACC  
 GCACAAGCCCACTGTTTCTATTAAATCTGTCACTGCATTAGCTGAAAG  
 CTTAGTGGCTCAAAATAATGGTATTATCGCTGCCATAGACAAGGACGTA  
 AGGAACGTGCCCaATTGGAATCTGCTGTTATTAATCGGCTGAAACAATC  
 AATGATTCTGTCAAAATTCGTGATAAAAAAATAGTTGAAGCCTTACTCAA  
 CGAAGGTaAATCTACCCAAGAAAAGTTGATGAGTCT

SEQ ID NO. 5205

STRAIN M732

AGCGATACCTTTAAATTTTGATATTGACCAAATTCAGAC  
 AATGCTATCACTAAAACAGATAAAAACAAGAAATTTATTTCCAACCAGAC  
 AACAGGCCAACTGGGCAAAATGCGCTTTTGTGAAAACTAACACCAGCAC  
 AAAAGTCTGCTATCTCTGAAAAAACACAGCTTTGGTAGATACTTTTGTCT  
 GGTGACCAAAATGCGCTCCTTGATTTTGGACAATCCGCGTAGAAGGCGT  
 TAATACTACTGTTAATCATATCTTGTCTGAGCAGAAAAAATTCAAATTC  
 CTCAGTTGATGATTTACTAAAAAATGCTAATCGCGAACTAAATGGATT  
 ATTGCCAAATATAAAGATGCTACTCCGGCAGAAATTAGAGAAAAAACCAAA  
 CTTGATTCAAAAAATTATTCAAAACAAGCAAGACCTCGCTACAGGAATTTT  
 ATTTTGACTCACAAAACATCGAGCAAAAAATGGATATGATGGCAGCAAAAT  
 GTTGTCAAACAAGAAGATACTTTGGCAAGAATATCGTCTCTGCTGAAAT  
 GCTCATTGAAGATAATACTAAATCTATTGAAAATTTGGTTGGAGTTATTG  
 CTTTATTGAATCGAGTCAAGCCGAGGCTGCCAATCGTGCAAGCCACTTA  
 CAACAAGAAATTTCTAGCATTAGATAGCCAAACGTCGGAATATCAAATTAA  
 AGTAACCAATTAGCCCGAATGACTGAAGTTATCAATACCCTCGAACAGC  
 AACATACGGAATATGTCAGCCGTCTCTACGTTGCATGGGCAACAACCCA  
 CAGATGCGAACTTGGTCAAAGTATCGTCAGATATGCGTCAGAACTTGG  
 TAGTGTACGTCGAAATACCAATCCAACAATGAACTCTCAATCGCTCAGT  
 TAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTATT  
 GTCACCGCTAATAATGCAGCATTGCAAAATGCTGGCTGAAACTAGTAAAGA  
 AGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCACTGTTTCTATTA  
 AATCTGTCACTGCATTAGCTGAAAGCTTAGTGGCTCAAAATAATGGTATT  
 ATCGCTGCCATAGACAAGGACGTAAGGAACGTCGCCAATTAGAATCTGC  
 TGTATTAAATCGGCTGAAACAATCAATGATTCTGTCAAAATTCGTGATA  
 AAAAAATAGTTGAAGCCTTACTCAACGAAGGTAAATCTACCCAAGAAAAA  
 G

SEQ ID NO. 5206

STRAIN COH1

CTAAAAACAGATAAAAACAAGAAATTTTCCAACCAGACAACAAGCCAA  
 ACTGGGCAAAATGCGCTTTTGTGAAAACTAACACCAGCACAAAAGTCTGC  
 TWTCTCTGAAAAAACACAGCTTTGGTAGATACTTTGTGCGTGACCAAA  
 ATGCGCTCCTTGATTTTGGACAATCCGCGTAGAAGGCGTTAATACTACT  
 GTTAAATCATATCTTGTCTGAGCAGAAAAAATTCAAATTCCTCAAGTTGA  
 TGATTTACTAAAAAATGCTAATCGCGAACTAAATGGATTATTGCCAAAT  
 ATAAAGATGCTACTCCGGCAGAAATTAGAGAAAAAACCAAACTTGATTCAA  
 AATATTCTCAAAACAAGCAAGACCTCGCTACAGGAATTTTATTTTGACTC  
 ACAAAACATCGAGCAAAAAATGGATATGATGGCAGCAAAATGTTGTCAAAC  
 AAGAAGTACTTTTGGCAAGAAATATCGTCTCTGCTGAAATGCTCATTGAA  
 GATAATACTAAATCTATTGAAAATTTGGTTGGAGTTATTGCTTTTATTGA  
 ATCGAGTCAAGCCGAGGCTGCCAATCGTGCAAGCCACTTACAACAAGAAA  
 TTCTAGCaATTAGATAGCCAAACGTCGGAATATCAAATTAAGAATAACCAA  
 TTAGCCCGAATGACTGAaGTTATCAaTaCCCTCGAACAGCAACATACGGA  
 aTATGTCAGCCGTCTCTACGTTGCATGGGCAACAACACACAGATGCGAA  
 ACTTGGTCAAAGTATCGTCAGATATGCGTCAGAACTTGGTATGTTACGT  
 CGAAATACCAATCCAACAATGAACTCTCAATCGCTCAGTTAGGCATGAT  
 GCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTATTGTCAACGCTA  
 ATAATGCAGCATTGCAAATGCTGGCTGAACTAGTAAAGAAGCGATTCCG  
 ATGTTAGAGAAGACCGCACAAAGCCCACTGTTTCTATTAAATCTGTCAC

Table 52: Comparative Sequences relating to SAG 1823

TGCATTAGCTGAAAGCTTAGTGGCTCAAATAATGGTATTATCGCTGCCA  
TAGACAAAGGACGTAAGGAACGTGCCCAATTAGAATCTGCTGTTATTAA  
TCGGCTGAAACAATCAATGATTCTGTCAAATTCGTGATAAAAAAATAGT  
TGAAGCCCTACTCAaCGAAGGTAAATCTACCCAAGAAAAAGTTGATGAGT  
CT

SEQ ID NO. 5207

STRAIN M781

TTTTGATATTGACCAAATTCAGACAATGCTATCACTAAAAACAGATAAAA  
CAACAGAAATTAATTCCAACCAGACAACAAGCCAACTGGGCAAAATGGCC  
TTTTTTGAAAACTAACACCAGCACAAAAGTCTGCTATCTCTGAAAAAAC  
ACCAGCTTTGGTAGATACTTTTGTGGTGACCAAAATGCGCTCCTTGATT  
TTGGACAATCCGCGAGTAGAAGGCGTTAATACTACTGTAAATCATATCTTG  
TCTGAGCAGAAAAAATTCAAATTCCTCAAGTTGATGATTTACTAAAAAA  
TGCTAATCGCGAACTAAATGGATTATTGGCCAAATATAAGATGCTACTC  
CGGCAGAATTAGAGAAAAAACCAACTTGATTCAAAAATTATTCAAAACAA  
AGCAAGACCTCGCTACAGGAATTTTATTTTGACTCACAAAACATCGAGCA  
AAAAATGGATATGATGGCAGCAAAATGTTGTCAAACAAGAAGATACTTTGG  
CAAGAAATATCGTCTCTGCTGAAATGCTCATGAAGATAAATACTAAATCT  
ATTGAAAAATTGGTTGGAGTTATTGCTTTTATTGAATCGAGTCAAGCCGA  
GGCTGCCAATCGTGCAAGCCACTTACAACAAGAAATCTAGCATTAGATA  
GCCAAACGTCGGAATATCAAATTAAGTAACCAATTAGCCCGAATGACT  
GAAGTTATCAATACCCCTCGAACAGCAACATACGGAATATGTCAGCCGCTCT  
CTACGTTGATGGGCAACAACACCACAGATGCGAAACTTGGTCAAAGTAT  
CGTCAGATATGCGTCAGAAACTTGGTATGTTACGTCGAAATACCATTCOA  
ACAATGAAACTCTCAATCGCTCAGTTAGGCATGATGCAACAATCTGTCAA  
ATCCGGTGTCACTGCTGATGCTATTGTCAACGCTAATAATGCAGCATTGC  
AAATGCTGGCTGAAACTAGTAAAGAAGCGATTCCGATGTTAGAGAAGACC  
GCACAAAGCCCCACTGTTTCTATTAATCTGTCACTGCATTAGCTGAAAG  
CTTAGTGGCTCAAATAATGGTATTATCGCTGCCATAGACAAAGGACGTA  
AGGAACGTGCCCAATTAGAATCTGCTGTTTAAATCGGCTGAAACAATC  
AATGATTCTGTCAAATTCGTGATAAAAAAATAGTTGAAGCCTTACTCAA  
CGAAGGTAAATCTACCCAAGAAAAAGTTGATGAGTCT

SEQ ID NO. 5208

STRAIN CJB110

TTTTGATATTGACCAAATTCAGACAATGCTATCACTAAAAACAGATAAAA  
CAACAGAAATTAATTCCAACCAGACAACAAGCCAACTGGGCAAAATGGCC  
TTTTTTGAAAACTAACACCAGCACAAAAGTCTGCTATCTCTGAAAAAAC  
ACCAGCTTTGGTAGATACTTTTGTGGCGATCAAATGCGCTCCTTGATT  
TTGGACAATCCGCGAGTAGAAGGCGTTAATACTACTGTAAATCATATCTTG  
TCTGAGCAGAAAAAATTCAAATTCCTCAAGTTGATGATTTACTAAAAAA  
TGCTAATCGCGAACTAAATGGATTATTGGCCAAATATAAGATGCTACTC  
CGGCAGAATTAGAGAAAAAACCAACTTGATTCAAAAATTATTCAAAACAA  
AGCAAGACCTCGCTACAGGAATTTTATTTTGACTCACAAAACATCGAGCA  
AAAAATGGATATGATGGCAGCAAAATGTTGTCAAACAAGAAGATACTTTGG  
CAAGAAATATCGTCTCTGCTGAAATGCTCATGAAGATAAATACTAAATCT  
ATTGAAAAATTGGTTGGAGTTATTGCTTTTATTGAATCGAGTCAAGCCGA  
GGCTGCTAATCGTGCAAGCCACTTACAACAAGAAATCTAGCATTAGATA  
GCCAAACGTCGAGTATCAAATTAAGTAACCAATTAGCTCGAATGACT  
GAAGTTATCAATACCCCTCGAACAGCAaCATACTGAATATGTCAGCCGCTCT  
CTACGTTGATGGGCaCaACACCACAGATGCGAAACTTGGTCAAAGTAT  
CGTCAGATATGCGTCAGAAACTTGGCATGTTACGTCGAAATACCATTCOA  
ACAATGAAACTCTCAATCGCTCAGTTAGGCATGATGCAACAATCTGTCAA  
ATCCGGTGTCACTGCTGATGCTATTGTCAACGCTAATAATGCAGCATTGC  
AGATGCTGGCTGAAACTAGTAAAGAAGCGATTCCGATGTTAGAGAAGACC  
GCACAAAGCCCCACTGTTTCTATTAATCTGTCACTGCATTAGCTGAAAG  
CTTAGTGGCTCAAATAATGGTATTATCGCTGCCATAGACAAAGGACGTA  
AGGAACGTGCCCAATTGGAATCTGCTGTTTAAATCGGCTGAAACAATC  
AATGATTCTGTCAAATTCGTGATAAAAAAATAGTTGAAGCCTTACTCAA  
CGAAGGTAAATCTACCCAAGAAAAAGTTGATGAGTCT

SEQ ID NO. 5209

STRAIN 1169NT

GCAGACAATGCTATCACTAAAAACAGATAAAACAACAGAAATTAATTCCAA  
CCAGACAACAAGCCAACTGGGCAAAATGCTTTTGTGAAAACTAACAC  
CAGCACAAAAGTCTGCTATCTCTGAAAAAACACCAGCTTTGGTAGATACT  
TTTGTGGTGACCAAAATGCGCTCCTTGATTTTGGACAATCCGAGTAGA  
AGGCGTTAATACCACTGTTAATCATATCTTGTCTGAGCAGAAAAAATTC  
AAATTCCTCAAGTTGATGATTTACTAAAAAATGCTAATCGCGAACTAAAT  
GGATTATTGGCCAAATATAAGATGCTACTCCGGCAGAATTAGAGAAAAA  
ACCAAACTTGATCCAAAAATTATTCAAAACAAGCAAGACCTCACTACAGG  
AATTTTATTTTGACTCACAAAACATCGAGCAAAAATGGATATGATGGCA  
GCAAAATGTTGTCAAACAAGAAGATACTTTGGCAAGAAATATCGTCTCTGC  
TGAATGCTCATGAAGATAATACTAAATCTATTGAAATTTGGTTGGAG  
TTATTGCTTTTATTGAATCGAGTCAAGCCGAGGCTGCCAATCGTGCAAGC  
CACTTACAACAAGAAATTTAGCATTAGATAGCCAAACGTCGGAGTATCA  
AATTAAGTAACCAATTAGCTCGAATGACTGAAGTTATCAATACCTCTCG  
AaCAGCAACATACTGAATATGTCAGCCGCTCTCTACGTTGCATGGGCAACA  
aCACCACAGATGCGAACTTGGTCAAAGTATCGTCAGATATGCGTCAAAA  
ACTTGGCATGTTACGTCGAAATACCAATTCCAACAATGAAACTCTCAATCG  
CTCAGTTAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGAT  
GCTATTGTCAACGCTAATAATGCAGCATTGCAGATGCTGGCTGAAACTAG

Table 52: Comparative Sequences relating to SAG 1823

TAAAGAAGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCACTGTTT  
CTATTAAATCTGTCACTGCAATTAGCTGAAAGCTTAGTGCGCTCAAATAAT  
GGTATTATCGCTGCCATAGACAAAGGACGTAAGGAACGTGCCCAATTAGA  
ATCTGCTGTTATTAAATCGGCTGAAACAATCAATGATTCTGTCAAATTC  
GTGATAAAAAAATAGTTGAAGCCTTACTCAACGAAGGTAAATCTACCCAA  
GAAAAAGTTGATGAGTCT

SEQ ID NO. 5210

STRAIN JM9130013

AGCGATACCTTTAATTTTGATATTGACCAAATTGCAGAC  
AATGCTATCACTAAACAGATAAAACACAGAAATTATTTCCAACCAGAC  
AACAAGCCAAACTGGGCAAAATTGCCTTTTTTGA AAAA ACTAACACCAGCAC  
AAAAGTCTGCTATCTCTGAAAAAACACCAAGCTTTGGTAGATACCTTTGTC  
GGTGACCAAAATCGCTCCTTGATTTTGGACAATCCGAGTAGAAGGCGT  
TAATACCACTGTTAATCATATCTTGTCTGAGCAGAAAAAATCAAATTC  
CTCAAGTTGATGATTACTAAAAATGCTAATCGCGAACTAAATGGATT  
ATTGCCAAATATAAAGATGCTACTCCGGCAGAAATTAGAGAAAAAACCAA  
CTTGATTCAAAAAATTATCAAACAAAGCAGACCTCGCTACAGGAATTTT  
ATTTTGA CTACAAACATCGAGCAAAAAATGGATATGATGGCAGCGAAT  
GTTGTCAAACAAGAGATACCTTGGCAAGAAATATCGTCTCTGCTGAAAT  
GCTCAITGAAGATAATACTAAATCTATTGAAAAATTGGTTGGAGTTATTG  
CTTTTATGAATcGAGTCAAGCCGAGGCTGCCAATCGTGCAAGCCACTTA  
CAACAAGAAATTCTAGCATTAGATAGCCAAACGTCGAGTATCAAATtAA  
AAGTaACCAATTAGCTCGAATGACTGAAGTTATCAATACCCCTCGAACAGC  
AACATACCTGAATATGTGAGCGCTCTACGTTGCATGGGCAACAACCCA  
CAGATGCGAAACTTTGGTCAAAGTATCGTCAGATATGCGTCAAAAACTTGG  
CATGTTACGTCGAATACCAATCCAACATGAACTCTCAATCGCTCAGT  
TAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTATT  
GTCAACGCTAATAATGACGATGTCAGATGCTGGCTGAAACTAGTAAAGA  
AGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCACTGTTTCTATTA  
AATCTGTCACTGATTAGCTGAAAGCTTAGTGGCTCAAAATAATGTTATT  
ATCGCTGCCATAGACAAAGGACGTAAGGAACGTCGCCAATTAGAACTCTGC  
TGTATTAAATCCGCTGAAACAATCAATGATTCTGTCAAATTCGTGATA  
AAAAAATAGTTGAAGCCTTACTCAACGAAGGTAAATCTACCCAAGAAAAA  
GTTGATGAGTCT

SEQ ID NO. 5211

STRAIN 2603

agcgatacctttaattttgatattgaccaaattgcagacaatgctatcac  
taaaacagataaaaaacacagaaattttccaaccagacaacaagccaaa  
ctgggcaaatgtcctttttgaaaaactaacaccagcacaaaagtctgct  
atctctgaaaaaacaccagcttttggtagatacttttgcggcgatcaaaa  
tgcgctccttgatttttgacaatccgcagtagaaggcggttaataccactg  
ttaatcatatcttgtctgagcagaaaaaaattcaaattcctcaagttgat  
gatttactaaaaaatgctaatcgcgaaactaaattggatttattgccaata  
taaaagtgctactccggcagaatttagagaaaaaaccaacttgattcaaa  
aatttattcaaacaaagcaagacctcgctacaggaattttattttgactca  
caaacatcgagcaaaaaatggatgatggcagcgaatggtgtcaaca  
agaagatactttggcaagaaatcgtctctgctgaaatgctcattgaag  
ataatactaaatctattgaaaatttggttgaggatttattgctttattgaa  
tcgagtcgaagccgaggtgctaatcgtgcaagccacttacaacaagaaat  
tctagcattagatagccaaacgtccgagatcaaataaaagtaaccaat  
tagctcgaatgactgaagttatcaataccctcgaacagcaacatcctgaa  
tatgtcagcgtctctacgttgcatgggcaacaacaccacagatgcgaaa  
cttggtcaaaagtatcgtcagatagcgtcagaaaacttggtgctgtacgtc  
gaaataccattccaacaatgaaactctcaatcgtcagttaggcatgatg  
caacaatctgtcaaatccggtgtcactgctgattgtcaacgctaa  
taatgcagcatttgagatgctggtgaaactagtaagaagcgaattccga  
tgtagagaagaccgcacaaagccccactgtttctattaaatctgtcact  
gcattagctgaaagcttagtggtcaaaaataatggattatcgctgccat  
agacaaaggacgtaagggaacgtgcccattggaatctgctgttattaaat  
cggctgaaacaatcaatgattctgtcaaaattcgtgataaaaaaatagtt  
gaagccttactcaacgaaggttaattcaccgaagaaaagttgatgagtc  
t

PRETTY of: /biotmp/msa13607.2{\*} April 22, 2002 03:55 ..

	1				50
msa13607.2{201_COH1}	-----	-----	-----	-----	-----C
msa13607.2{201_M781}	-----	TTTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_090}	AGCGATACCT	TTAATTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_CJB110}	-----	TTTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_18RS21}	-----	TTTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_2603}	AGCGATACCT	TTAATTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_A909}	AGCGATACCT	TTAATTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_H36B}	AGCGATACCT	TTAATTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_JM9130013}	AGCGATACCT	TTAATTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_1169NT}	-----	-----	-----	GCAGACA	ATGCTATCAC
msa13607.2{201_M732}	AGCGATACCT	TTAATTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
Consensus	*****	*****	*****	*****	*****

Table 52: Comparative Sequences relating to SAG 1823

	51				100
msa13607.2{201_COH1}	TAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_M781}	TAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_090}	TAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_CJB110}	TAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_18RS21}	TAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_2603}	TAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_A909}	TAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_H36B}	TAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_JM9130013}	TAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_1169NT}	TAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_M732}	TAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
Consensus	*****	*****	*****	*****	*****
	101				150
msa13607.2{201_COH1}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_M781}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_090}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_CJB110}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_18RS21}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_2603}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_A909}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_H36B}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_JM9130013}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_1169NT}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_M732}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
Consensus	*****	*****	*****	*****	*****
	151				200
msa13607.2{201_COH1}	wTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCTG	GtGAcCAAAA
msa13607.2{201_M781}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCTG	GtGAcCAAAA
msa13607.2{201_090}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCTG	GcGatCAAAA
msa13607.2{201_CJB110}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCTG	GcGatCAAAA
msa13607.2{201_18RS21}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCTG	GcGatCAAAA
msa13607.2{201_2603}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCTG	GcGatCAAAA
msa13607.2{201_A909}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCTG	GtGAcCAAAA
msa13607.2{201_H36B}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCTG	GtGAcCAAAA
msa13607.2{201_JM9130013}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCTG	GtGAcCAAAA
msa13607.2{201_1169NT}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCTG	GtGAcCAAAA
msa13607.2{201_M732}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCTG	GtGAcCAAAA
Consensus	-*****	*****	*****	*****	*-***-*****
	201				250
msa13607.2{201_COH1}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATActACTG
msa13607.2{201_M781}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATActACTG
msa13607.2{201_090}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATAcCACTG
msa13607.2{201_CJB110}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATAcCACTG
msa13607.2{201_18RS21}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATAcCACTG
msa13607.2{201_2603}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATAcCACTG
msa13607.2{201_A909}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATAcCACTG
msa13607.2{201_H36B}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATAcCACTG
msa13607.2{201_JM9130013}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATAcCACTG
msa13607.2{201_1169NT}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATAcCACTG
msa13607.2{201_M732}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATActACTG
Consensus	*****	*****	*****	*****	*****-*****
	251				300
msa13607.2{201_COH1}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA	TTCAAATTCC	TCAAGTTGAT
msa13607.2{201_M781}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA	TTCAAATTCC	TCAAGTTGAT
msa13607.2{201_090}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA	TTCAAATTCC	TCAAGTTGAT
msa13607.2{201_CJB110}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA	TTCAAATTCC	TCAAGTTGAT
msa13607.2{201_18RS21}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA	TTCAAATTCC	TCAAGTTGAT
msa13607.2{201_2603}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA	TTCAAATTCC	TCAAGTTGAT
msa13607.2{201_A909}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA	TTCAAATTCC	TCAAGTTGAT
msa13607.2{201_H36B}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA	TTCAAATTCC	TCAAGTTGAT
msa13607.2{201_JM9130013}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA	TTCAAATTCC	TCAAGTTGAT
msa13607.2{201_1169NT}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA	TTCAAATTCC	TCAAGTTGAT
msa13607.2{201_M732}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA	TTCAAATTCC	TCAAGTTGAT
Consensus	*****	*****	*****	*****	*****
	301				350
msa13607.2{201_COH1}	GATTTACTAA	AAAATGCTAA	TCGCGAATA	AATGGATTAA	TTGCCAAATA

Table 52: Comparative Sequences relating to SAG 1823

msa13607.2{201_M781}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_090}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_CJB110}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_18RS21}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_2603}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_A909}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_H36B}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_JM9130013}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_1169NT}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_M732}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
Consensus	*****	*****	*****	*****	*****
	351				400
msa13607.2{201_COH1}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_M781}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_090}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_CJB110}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_18RS21}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_2603}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_A909}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_H36B}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_JM9130013}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_1169NT}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_M732}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
Consensus	*****	*****	*****	*****	*****
	401				450
msa13607.2{201_COH1}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_M781}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_090}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_CJB110}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_18RS21}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_2603}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_A909}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_H36B}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_JM9130013}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_1169NT}	AATTATTCAA	ACAAAGCAAG	ACCTCaCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_M732}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
Consensus	*****	*****	*****	*****	*****
	451				500
msa13607.2{201_COH1}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_M781}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_090}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_CJB110}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_18RS21}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_2603}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_A909}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_H36B}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_JM9130013}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_1169NT}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_M732}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
Consensus	*****	*****	*****	*****	*****
	501				550
msa13607.2{201_COH1}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_M781}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_090}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_CJB110}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_18RS21}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_2603}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_A909}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_H36B}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_JM9130013}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_1169NT}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_M732}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
Consensus	*****	*****	*****	*****	*****
	551				600
msa13607.2{201_COH1}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_M781}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_090}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_CJB110}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_18RS21}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA



Table 52: Comparative Sequences relating to SAG 1823

msa13607.2{201_2603}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_A909}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAwTGC	TTTTATTGAA
msa13607.2{201_H36B}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_JM9130013}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_1169NT}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_M732}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
Consensus	*****	*****	*****	*****-***	*****
601					
msa13607.2{201_COH1}	TCGAGTCAAG	CCGAGGCTGC	caATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_M781}	TCGAGTCAAG	CCGAGGCTGC	caATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_090}	TCGAGTCAAG	CCGAGGCTGC	taATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_CJB110}	TCGAGTCAAG	CCGAGGCTGC	taATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_18RS21}	TCGAGTCAAG	CCGAGGCTGC	taATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_2603}	TCGAGTCAAG	CCGAGGCTGC	taATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_A909}	TCGAGTCAAG	CCGAGGCTGC	caATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_H36B}	TCGAGTCAAG	CCGAGGCTGC	caATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_JM9130013}	TCGAGTCAAG	CCGAGGCTGC	caATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_1169NT}	TCGAGTCAAG	CCGAGGCTGC	caATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_M732}	TCGAGTCAAG	CCGAGGCTGC	caATCGTGCA	AGCCACTTAC	AACAAGAAAT
Consensus	*****	*****	-*****	*****	*****
651					
msa13607.2{201_COH1}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_M781}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_090}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_CJB110}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_18RS21}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_2603}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_A909}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_H36B}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_JM9130013}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_1169NT}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_M732}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAAA	AGTAACCAAT
Consensus	*****	*****	*****-**	*****	*****
701					
msa13607.2{201_COH1}	TAGCcCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCgGAA
msa13607.2{201_M781}	TAGCcCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCgGAA
msa13607.2{201_090}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_CJB110}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_18RS21}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATcCtGAA
msa13607.2{201_2603}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATcCtGAA
msa13607.2{201_A909}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_H36B}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_JM9130013}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_1169NT}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_M732}	TAGCcCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCgGAA
Consensus	****-*****	*****	*****	*****	****-***
751					
msa13607.2{201_COH1}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_M781}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_090}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_CJB110}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_18RS21}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_2603}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_A909}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_H36B}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_JM9130013}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_1169NT}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_M732}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
Consensus	*****	*****	*****	*****	*****
801					
msa13607.2{201_COH1}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGt	ATGTTACGTC
msa13607.2{201_M781}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGt	ATGTTACGTC
msa13607.2{201_090}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGc	ATGTTACGTC
msa13607.2{201_CJB110}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGc	ATGTTACGTC
msa13607.2{201_18RS21}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGc	ATGTTACGTC
msa13607.2{201_2603}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGc	ATGTTACGTC
msa13607.2{201_A909}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGc	ATGTTACGTC

Table 52: Comparative Sequences relating to SAG 1823

msa13607.2{201_H36B}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	aaAACTTGGc	ATGTTACGTC
msa13607.2{201_JM9130013}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	aaAACTTGGc	ATGTTACGTC
msa13607.2{201_1169NT}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	aaAACTTGGc	ATGTTACGTC
msa13607.2{201_M732}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGt	ATGTTACGTC
Consensus	*****	*****	*****	-*****-	*****
	851				900
msa13607.2{201_COH1}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_M781}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_090}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_CJB110}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_18RS21}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_2603}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_A909}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_H36B}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_JM9130013}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_1169NT}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_M732}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
Consensus	*****	*****	*****	*****	*****
	901				950
msa13607.2{201_COH1}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_M781}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_090}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_CJB110}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_18RS21}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_2603}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_A909}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_H36B}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_JM9130013}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_1169NT}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_M732}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
Consensus	*****	*****	*****	*****	*****
	951				1000
msa13607.2{201_COH1}	TAATGCAGCA	TTGCAaATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_M781}	TAATGCAGCA	TTGCAaATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_090}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_CJB110}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_18RS21}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_2603}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_A909}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_H36B}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_JM9130013}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_1169NT}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_M732}	TAATGCAGCA	TTGCAaATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
Consensus	*****	*****-*****	*****	*****	*****
	1001				1050
msa13607.2{201_COH1}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_M781}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_090}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_CJB110}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_18RS21}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_2603}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_A909}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_H36B}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_JM9130013}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_1169NT}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_M732}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
Consensus	*****	*****	*****	*****	*****
	1051				1100
msa13607.2{201_COH1}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_M781}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_090}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_CJB110}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_18RS21}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_2603}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_A909}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_H36B}	GCATTAtCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_JM9130013}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_1169NT}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT

Table 52: Comparative Sequences relating to SAG 1823

msa13607.2{201_M732}	GCATTAGCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
Consensus	*****-***	*****	*****	*****	*****
	1101				1150
msa13607.2{201_COH1}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_M781}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_090}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	gGAATCTGCT	GTTATTAAAT
msa13607.2{201_CJB110}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	gGAATCTGCT	GTTATTAAAT
msa13607.2{201_18RS21}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	gGAATCTGCT	GTTATTAAAT
msa13607.2{201_2603}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	gGAATCTGCT	GTTATTAAAT
msa13607.2{201_A909}	AGACAAAGGA	CGTAAaGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_H36B}	AGACAAAGGA	CGTAAaGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_JM9130013}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_1169NT}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_M732}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
Consensus	*****	*****-****	*****	*****	*****
	1151				1200
msa13607.2{201_COH1}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_M781}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_090}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_CJB110}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_18RS21}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_2603}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_A909}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_H36B}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_JM9130013}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_1169NT}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_M732}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
Consensus	*****	*****	*****	*****	*****
	1201				1250
msa13607.2{201_COH1}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_M781}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_090}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_CJB110}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_18RS21}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_2603}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_A909}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_H36B}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_JM9130013}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_1169NT}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_M732}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
Consensus	*****	*****	*****	*****	-----
	1251				
msa13607.2{201_COH1}	t				
msa13607.2{201_M781}	t				
msa13607.2{201_090}	t				
msa13607.2{201_CJB110}	t				
msa13607.2{201_18RS21}	t				
msa13607.2{201_2603}	t				
msa13607.2{201_A909}	t				
msa13607.2{201_H36B}	t				
msa13607.2{201_JM9130013}	t				
msa13607.2{201_1169NT}	t				
msa13607.2{201_M732}	~				
Consensus	-				

## SEQ ID NO. 5212

STRAIN\_090 frame: 1  
SDTFNFDIDQIADNATTKTDKTTETIISNQTTSQTGQIAFFEKLTPAQKSAISEKTPALVD  
TFVGDQNALLDGQSAVEGVNTTVNHLSEQKKIQIPQVDDLLKNANRELNGFIAKYKDA  
TPAELEKPNLQKLFQSKTSLQEFYFDSQNIIEQKMDMMAANVVKQEDTLARNIVSAEM  
LIEDNTKSIENLVGVIAFIESSQAEANRAHLQOEILALDSQTSEYQIKSNQLARMTEV  
INTLEQQHTVEYVSRLYVAVATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGM  
QQSVKSGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAEISLVAQN  
NGIIAAIDKGRKERAQLESAAVSKAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

## SEQ ID NO. 52013

STRAIN\_A909 frame: 1  
SDTFNFDIDQIADNATTKTDKTTETIISNQTTSQTGQIAFFEKLTPAQKSAISEKTPALVD  
TFVGDQNALLDGQSAVEGVNTTVNHLSEQKKIQIPQVDDLLKNANRELNGFIAKYKDA  
TPAELEKPNLQKLFQSKTSLQEFYFDSQNIIEQKMDMMAANVVKQEDTLARNIVSAEM

Table 52: Comparative Sequences relating to SAG 1823

LIEDNTKSIENLVGVXAFIESSQAEANRASHLQQEILALDSQTSEYQIKSNQLARMTEV  
INTLEQQHTEYVSRLYVAVATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM  
QQSVKSGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN  
NGIIAAIDKGRKERAQLESASAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

## SEQ ID NO. 5214

STRAIN H36B frame: 1

SDTFNFDIDQIADNNAITKTDKTEIISNQTTSTGTGQIAFFFEKLTAPAKSAISEKTPALVD  
TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDA  
TPAELEKKPNLIQKLFQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEM  
LIEDNTKSIENLVGVIAFIESSQAEANRASHLQQEILALDSQTSEYQIKSNQLARMTEV  
INTLEQQHTEYVSRLYVAVATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM  
QQSVKSGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN  
NGIIAAIDKGRKERAQLESASAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

## SEQ ID NO. 5215

STRAIN 18RS21 frame: 2

FDIDQIADNNAITKTDKTEIISNQTTSTGTGQIAFFFEKLTAPAKSAISEKTPALVDTFVGD  
QNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAEL  
EKKPNLIQKLFQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEM  
LIEDNTKSIENLVGVIAFIESSQAEANRASHLQQEILALDSQTSEYQIKSNQLARMTEVINTLE  
QQHPEYVSRLYVAVATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVK  
SGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIA  
AIDKGRKERAQLESASAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

## SEQ ID NO. 5216

STRAIN M732 frame: 1

SDTFNFDIDQIADNNAITKTDKTEIISNQTTSTGTGQIAFFFEKLTAPAKSAISEKTPALVD  
TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDA  
TPAELEKKPNLIQKLFQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEM  
LIEDNTKSIENLVGVIAFIESSQAEANRASHLQQEILALDSQTSEYQIKSNQLARMTEV  
INTLEQQHTEYVSRLYVAVATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM  
QQSVKSGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN  
NGIIAAIDKGRKERAQLESASAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

## SEQ ID NO. 5217

STRAIN COH1 frame: 3

KTDKTEIISNQTTCTGTGQIAFFFEKLTAPAKSAXSEKTPALVDTFVGDQNALLDGQSAV  
EGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAELEKKPNLIQKLFK  
QSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEM  
LIEDNTKSIENLVGVIAFIESSQAEANRASHLQQEILALDSQTSEYQIKSNQLARMTEVINTLEQQHTEYVSRLYV  
AVATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVKSGVTADAIVNAN  
NALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIAAIDKGRKERAQ  
LESASAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

## SEQ ID NO. 5218

STRAIN COH1 frame: 3

KTDKTEIISNQTTCTGTGQIAFFFEKLTAPAKSAXSEKTPALVDTFVGDQNALLDGQSAV  
EGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAELEKKPNLIQKLFK  
QSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEM  
LIEDNTKSIENLVGVIAFIESSQAEANRASHLQQEILALDSQTSEYQIKSNQLARMTEVINTLEQQHTEYVSRLYV  
AVATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVKSGVTADAIVNAN  
NALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIAAIDKGRKERAQ  
LESASAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

## SEQ ID NO. 5219

STRAIN M781 frame: 2

FDIDQIADNNAITKTDKTEIISNQTTSTGTGQIAFFFEKLTAPAKSAISEKTPALVDTFVGD  
QNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAEL  
EKKPNLIQKLFQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEM  
LIEDNTKSIENLVGVIAFIESSQAEANRASHLQQEILALDSQTSEYQIKSNQLARMTEVINTLE  
QQHTEYVSRLYVAVATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVK  
SGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIA  
AIDKGRKERAQLESASAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

## SEQ ID NO. 5220

STRAIN CJB110 frame: 2

FDIDQIADNNAITKTDKTEIISNQTTSTGTGQIAFFFEKLTAPAKSAISEKTPALVDTFVGD  
QNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAEL  
EKKPNLIQKLFQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEM  
LIEDNTKSIENLVGVIAFIESSQAEANRASHLQQEILALDSQTSEYQIKSNQLARMTEVINTLE  
QQHTEYVSRLYVAVATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVK  
SGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIA  
AIDKGRKERAQLESASAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

## SEQ ID NO. 5221

STRAIN 1169NT frame: 1

ADNAITKTDKTEIISNQTTSTGTGQIAFFFEKLTAPAKSAISEKTPALVDTFVGDQNALLD  
FGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAELEKKPNLI  
QKLFQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEM  
LIEDNTKSIENLVGVIAFIESSQAEANRASHLQQEILALDSQTSEYQIKSNQLARMTEVINTLEQQHTEY  
VSRLYVAVATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVKSGVTAD  
AIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIAAIDKGR

Table 52: Comparative Sequences relating to SAG 1823

KERAQLES AVIKSAETINDSVKIRDKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5222

STRAIN JM9130013 frame: 1

SDTFNFDIDQIADNAITKTDKTEIISNQTTSTGTGQIAFFEKLTTPAQKSAISEKTPALVD  
 TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIIPQVDDLLKNANRELNGFIAKYKDA  
 TPAELEKKPNLIQKLFQKSKTSLQEFYFDSQNIQKMDMMANVVKQEDTLARNIVSAEM  
 LIEDNTKSIENLVGVIAFIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEV  
 INTLEQQHPEYVSRLYVAVATTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM  
 QQSVKSGVTADAI VNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN  
 NGIIAAIDKGRKERAQLES AVIKSAETINDSVKIRDKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5223

STRAIN 2603 frame: 1

SDTFNFDIDQIADNAITKTDKTEIISNQTTSTGTGQIAFFEKLTTPAQKSAISEKTPALVD  
 TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIIPQVDDLLKNANRELNGFIAKYKDA  
 TPAELEKKPNLIQKLFQKSKTSLQEFYFDSQNIQKMDMMANVVKQEDTLARNIVSAEM  
 LIEDNTKSIENLVGVIAFIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEV  
 INTLEQQHPEYVSRLYVAVATTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM  
 QQSVKSGVTADAI VNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN  
 NGIIAAIDKGRKERAQLES AVIKSAETINDSVKIRDKIVEALLNEGKSTQEKVDES

PRETTY of: /biotmp/msa28369.2{\*} April 22, 2002 04:27 ..

	1				50
msa28369.2{201_090}	sdtfnfdidq	iadnaitKTD	KTEIISNQTT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_1169NT}	-----	-adnaitKTD	KTEIISNQTT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_A909}	sdtfnfdidq	iadnaitKTD	KTEIISNQTT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_JM9130013}	sdtfnfdidq	iadnaitKTD	KTEIISNQTT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_COH1}	-----	-----KTD	KTEIISNQTT	TcQTGQIAFF	EKLTPAQKSA
msa28369.2{201_CJB110}	-----fdidq	iadnaitKTD	KTEIISNQTT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_M781}	-----fdidq	iadnaitKTD	KTEIISNQTT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_2603}	sdtfnfdidq	iadnaitKTD	KTEIISNQTT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_H36B}	sdtfnfdidq	iadnaitKTD	KTEIISNQTT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_18RS21}	-----fdidq	iadnaitKTD	KTEIISNQTT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_M732}	sdtfnfdidq	iadnaitKTD	KTEIISNQTT	TsQTGQIAFF	EKLTPAQKSA
Consensus	-----	-----*	*****	*-----	*****
	51				100
msa28369.2{201_090}	iSEKTPALVD	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_1169NT}	iSEKTPALVD	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_A909}	iSEKTPALVD	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_JM9130013}	iSEKTPALVD	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_COH1}	xSEKTPALVD	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_CJB110}	iSEKTPALVD	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_M781}	iSEKTPALVD	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_2603}	iSEKTPALVD	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_H36B}	iSEKTPALVD	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_18RS21}	iSEKTPALVD	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_M732}	iSEKTPALVD	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
Consensus	-*****	*****	*****	*****	*****
	101				150
msa28369.2{201_090}	DLLKNANREL	NGFIAKYKDA	TPAELEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_1169NT}	DLLKNANREL	NGFIAKYKDA	TPAELEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_A909}	DLLKNANREL	NGFIAKYKDA	TPAELEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_JM9130013}	DLLKNANREL	NGFIAKYKDA	TPAELEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_COH1}	DLLKNANREL	NGFIAKYKDA	TPAELEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_CJB110}	DLLKNANREL	NGFIAKYKDA	TPAELEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_M781}	DLLKNANREL	NGFIAKYKDA	TPAELEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_2603}	DLLKNANREL	NGFIAKYKDA	TPAELEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_H36B}	DLLKNANREL	NGFIAKYKDA	TPAELEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_18RS21}	DLLKNANREL	NGFIAKYKDA	TPAELEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_M732}	DLLKNANREL	NGFIAKYKDA	TPAELEKKPN	LIQKLFQKSK	TSLQEFYFDS
Consensus	*****	*****	*****	*****	*****
	151				200
msa28369.2{201_090}	QNIQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_1169NT}	QNIQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_A909}	QNIQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_JM9130013}	QNIQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_COH1}	QNIQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_CJB110}	QNIQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_M781}	QNIQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_2603}	QNIQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_H36B}	QNIQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE

Table 52: Comparative Sequences relating to SAG 1823

msa28369.2{201_18RS21}	QNIEQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_M732}	QNIEQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
Consensus	*****	*****	*****	*****	*****
201					
msa28369.2{201_090}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_1169NT}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_A909}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_JM9130013}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_COH1}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_CJB110}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_M781}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_2603}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_H36B}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_18RS21}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_M732}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
Consensus	*****	*****	*****	*****	*****
251					
msa28369.2{201_090}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_1169NT}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_A909}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_JM9130013}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_COH1}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_CJB110}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_M781}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_2603}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_H36B}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_18RS21}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_M732}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
Consensus	*****	*****	*****	*****	*****
301					
msa28369.2{201_090}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_1169NT}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_A909}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_JM9130013}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_COH1}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_CJB110}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_M781}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_2603}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_H36B}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_18RS21}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_M732}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
Consensus	*****	*****	*****	*****	*****
351					
msa28369.2{201_090}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_1169NT}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_A909}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_JM9130013}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_COH1}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_CJB110}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_M781}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_2603}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_H36B}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_18RS21}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_M732}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
Consensus	*****	*****	*****	*****	*****
401					
msa28369.2{201_090}	EALLNEGKST	QEKvdes			
msa28369.2{201_1169NT}	EALLNEGKST	QEKvdes			
msa28369.2{201_A909}	EALLNEGKST	QEKvdes			
msa28369.2{201_JM9130013}	EALLNEGKST	QEKvdes			
msa28369.2{201_COH1}	EALLNEGKST	QEKvdes			
msa28369.2{201_CJB110}	EALLNEGKST	QEKvdes			
msa28369.2{201_M781}	EALLNEGKST	QEKvdes			
msa28369.2{201_2603}	EALLNEGKST	QEKvdes			
msa28369.2{201_H36B}	EALLNEGKST	QEKvdes			
msa28369.2{201_18RS21}	EALLNEGKST	QEKvdes			
msa28369.2{201_M732}	EALLNEGKST	QEKvdes			
Consensus	*****	*****			
417					
msa28369.2{201_090}	EALLNEGKST	QEKvdes			
msa28369.2{201_1169NT}	EALLNEGKST	QEKvdes			
msa28369.2{201_A909}	EALLNEGKST	QEKvdes			
msa28369.2{201_JM9130013}	EALLNEGKST	QEKvdes			
msa28369.2{201_COH1}	EALLNEGKST	QEKvdes			
msa28369.2{201_CJB110}	EALLNEGKST	QEKvdes			
msa28369.2{201_M781}	EALLNEGKST	QEKvdes			
msa28369.2{201_2603}	EALLNEGKST	QEKvdes			
msa28369.2{201_H36B}	EALLNEGKST	QEKvdes			
msa28369.2{201_18RS21}	EALLNEGKST	QEKvdes			
msa28369.2{201_M732}	EALLNEGKST	QEKvdes			
Consensus	*****	*****			

Table 53: Comparative Sequences relating to SAG 0755

## SEQ ID NO. 5301

## STRAIN 2603

acaaataactttgaaaaaagaatttagttgaagctaaaaagacaattccatc  
cgtaaaagcttcaaaagtaccgcaaaaatcaacatcatcgaaagataaag  
agtttgttcttaaacgattatcgatgtctctggttggcaacttcctaag  
gagattgattacgatacgcctttcaaaaaatatttcaggtgtgttattcgt  
tgtctttggtggatcaaagatatctaaagactaataacgctgcttatacaa  
ctggaatcgataaatacgtttaagaccatatacaagaatttcaaaagcga  
aatatcccagtagctgtctacagttatgcacttgggttcaagtggttaaga  
aatgaaagaagaggctcagatatatttataagaatgcagctccttacaac  
caactttttattggattgacgtagaagaggagacaatgtctaactgaat  
aaaggtgtccaagcattccgaaagaattaaaaagacttgggtgctaaaaa  
tggtggtatctacattgggtacttactttatgactgagcaaggcatctctg  
taaaaggatttgacgctgttttggattccaacttatggtagcgattctgga  
tactatgaagcggtccgcaaaactgaacttaaatacgatttacaccaata  
cacctctcaagggttatctaccaggawtcaatcaaccgcttgatttaaatc  
aaattgcagttaataaagacaagaagaaacttatgagaaacttttggga  
aaagtaaaagag

## SEQ ID NO. 5302

## STRAIN 090

ACAAATACTTTGAAAAAAGAATTAG  
TTGAAGCTAAAAAGACAATTCCATCCGTAAAAGCTTCAAAGTACCGCAA  
AAATCAACATCATCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGA  
TGTCTCTGTTGGCAACTTCTTAAGGAGATTGATTACGATACGCTTTCAA  
AAAATATTTCAAGTGTGTATTCTGTCTTTGGTGGATCAAAGATATCT  
AAGACTAATAACGCTGCTTATACAACTGGAATCGATAAATCGTTTAAGAC  
CCATATCAAGAATTTCAAAAGCGAATATCCAGTAGCTGTCTACAGTT  
ATGCACCTTGGTTCAAGTGTAAAGAAATGAAAGAAGAGGCTCAGATATTT  
TATAAAGATGCAGCTCCTTACAAACCAACTTTTATTGGATTGACGTAGA  
AGAGGAGACAATGTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAG  
AATTAAAAAGACTTGGTGCTAAAAATGTTGGTATCTACATTGGTACTTAC  
TTTATGACTGAGCAAGGCATCTCTGTAAAAGGATTGACGCTGTTTGGAT  
TCCAACCTTATGGTAGCGATTCTGGATACTATGAAGCGGCTCCGCAAACTG  
AACTTAAATACGATTACACCAATACACCTCTCAAGGTTATCTACCAGGA  
TTCAATCAACCGCTTGATTAAATCAAATTGCAGTTAATAAAGACAAGAA  
GAAAACCTTATGAGAACTTTTGGAAAAGTAAAAGAG

## SEQ ID NO. 5303

## STRAIN A909

ACAAATACTTTGAAAAAAGAATTAGTTGAAGCTAAAA  
AGACAATTCCATCCGTAAAAGCTTCAAAGTACCGCAAAATCAACATCA  
TCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGTTG  
GCAACTTCTTAAGGAGATTGATTACGATACGCTTTCAAAAATATTTAG  
GTGTTGTATTCTGTCTTTGGTGGATCAAAGATATCTAAGACTAATAAC  
GCTGCTTATACAACTGGAATCGATAAATCGTTTAAGACCCATATCAAAGA  
ATTTCAAAGCGAAATATCCAGTAGCTGTCTACAGTTATGCACTTGGTT  
CAAGTGTAAAGAAATGAAAGAAGAGGCTCAGATATTTTAAAGAAATGCA  
GCTCCTTACAAACCAACTTTTATTGGATTGACGTAGAAGAGGAGACAAT  
GTCTAAGATGAATAAAGGTGTCCAAGCATTCCGAAAAGAAATTAAGAAGAC  
TTGGTGCTAAAAATGTTGGTATCTACATTGGTACTTACTTTATGACTGAG  
CAAGGCATCTCTGTAAAAGGATTGACGCTGTTTGGATTCCAACCTTATGG  
TAGCGATTCTGGATACTATGAAGCGGCTCCGCAAACTGAACTTAAATACG  
ATTACACCAATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACCG  
CTTGATTAAATCAAATTGCAGTTAATAAAGACAAGAAGAAACCTATGA  
GAAACTTTTGGAAAAGTAAAAGAG

## SEQ ID NO. 5304

## STRAIN H36B

ACAAATACTTTGAAAAAAGAATTAG  
TTGAAGCTAAAAAGACAATTCCATCCGTAAAAGCTTCAAAGTACCGCAA  
AAATCAACATCATCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGA  
TGTCTCTGTTGGCAACTTCTTAAGGAGATTGATTACGATACGCTTTCAA  
AAAATATTTCAAGTGTGTATTCTGTCTTTGGTGGATCAAAGATATCT  
AAGACTAATAACGCTGCTTATACAACTGGAATCGATAAATCGTTTAAGAC  
CCATATCAAGAATTTCAAAAGCGAATATCCAGTAGCTGTCTACAGTT  
ATGCACCTTGGTTCAAGTGTAAAGAAATGAAAGAAGAGGCTCAGATATTT  
TATAAAGATGCAGCTCCTTACAAACCAACTTTTATTGGATTGACGTAGA  
AGAGGAGACAATGTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAG  
AATTAAAAAGACTTGGTGCTAAAAATGTTGGTATCTACATTGGTACTTAC  
TTTATGACTGAGCAAGGCATCTCTGTAAAAGGATTGACGCTGTTTGGAT  
TCCAACCTTATGGTAGCGATTCTGGATACTATGAAGCGGCTCCGCAAACTG  
AACTTAAATACGATTACACCAATACACCTCTCAAGGTTATCTACCAGGA  
TTCAATCAACCGCTTGATTAAATCAAATTGCAGTTAATAAAGACAAGAA  
GAAAACCTTATGAGAACTTTTGGAAAAGTAAAAGAG

## SEQ ID NO. 5305

## STRAIN 18R521

ACAAATACTTTGAAAAAAGAATTAGTTGAAGCTAAAA  
GACAAATCCATCCGTAAAAGCTTCAAAGTACCGCAAAATCAACATCAT  
CGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGTTGG  
CAACTTCTTAAGGAGATTGATTACGATACGCTTTCAAAAATATTTTCAGG  
TGTTGTTATTCTGTCTTTGGTGGATCAAAGATATCTAAGACTAATAACG

Table 53: Comparative Sequences relating to SAG 0755

CTGCTTATACAACTGGAATCGATAAATCGTTTAAAGACCCATATCAAAGAA  
 TTTCAAAAGCGAAATATCCAGTAGCTGTCTACAGTTATGCACTTGGTTC  
 AAGTGTAAAGAAATGAAGAAGAGGCTCAGATATTTATAAGAAATGCAG  
 CTCTTACAAACCAACTTTTATTTGGATTGACGTAGAAGAGGAGACAATG  
 TCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAGAAATAAAAAGACT  
 TGGTGTCTAAAAATGTTGGTATCTACATTGGTACTTACTTTATGACTGAGC  
 AAGGCATCTCTGTAAAAGGATTGACGCTGTTGGATTCCAACCTTATGGT  
 AGCGATTCTGGATACTATGAAGCGGCTCCGCAAACTGAACTTAAATACGA  
 TTTACACCAATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACCGC  
 TTGATTTAAATCAAATTGCAGTTAATAAAGACAAGAAGAAAACCTATGAG  
 AAACCTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5306  
 STRAIN M732

ACAAATACTTTGAAAAAAGAATTAGTTGAAGCTAAA  
 AAGACAATTCCATCCGTAAAAGCTTCAAAGTACCGCAAAAATCAACATC  
 ATCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGGTT  
 GGCAACTTCTTAAGGAGATTGATTACGATACGCTTTCAAAAAATATTTCA  
 GGTGTTGTTTATTCGTATCTTGGTGGATCAAAGATATCTAAGACTAATAA  
 CGCTGCTTATACAACTGGAATCGATAAATCGTTTAAAGACCCATATCAAAG  
 AATTTCAAAGCGAAATATCCAGTAGCTGTCTACAGTTATGCACTTGGT  
 TCAAGTGTAAAGAAATGAAAGAAGAGGCTCAGATATTTATAAGAAATGC  
 AGCTCCTTACAAACCAACTTTTATTGGATTGACGTAGAAGAGGAGACAA  
 TGTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAGAGTTAAAAAGA  
 CTGGTGCTAAAAATGTTGGTATCTACATCGGTACTTACTTTATGACTGA  
 GCAAGGTATCTCTGTAAAAGGATTGACGCTGTTGGATTCCAACCTTATG  
 GTAGCGATTCTGGATACTATGAAGCAGCTCCACAACTGAACTTAAATAC  
 GATTTACACCAATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACC  
 GCTTGATTAAATCAAATTGCAGTTAATAAAGACAAGAAGAAAACCTTATG  
 AGAACTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5307  
 STRAIN COH1

ACAAATACTTTGAAAAAAGAATTAGTTGAAGCTAAA  
 AGACAATTCCATCCGTAAAAGCTTCAAAGTACCGCAAAAATCAACATCA  
 TCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGGTTG  
 GCAACTTCTTAAGGAGATTGATTACGATACGCTTTCAAAAAATATTTCA  
 GTGTTGTTTATTCGTATCTTGGTGGATCAAAGATATCTAAGACTAATAAC  
 GCTGCTTATACAACTGGAATCGATAAATCGTTTAAAGACCCATATCAAAGA  
 AITTTCAAAGCGAAATATCCAGTAGCTGTCTACAGTTATGCACTTGGTT  
 CAAGTGTAAAGAAATGAAAGAAGAGGCTCAGATATTTATAAGAAATGCA  
 GCTCCTTACAAACCAACTTTTATTGGATTGACGTAGAAGAGGAGACAAT  
 GTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAGAGTTAAAAAGAC  
 TTGGTGCTAAAAATGTTGGTATCTACATCGGTACTTACTTTATGACTGAG  
 CAAGGTATCTCTGTAAAAGGATTGACGCTGTTGGATTCCAACCTTATGG  
 TAGCGATTCTGGATACTATGAAGCAGCTCCACAACTGAACTTAAATACG  
 AITTTACACCAATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACCG  
 CTTGATTAAATCAAATTGCAGTTAATAAAGACAAGAAGAAAACCTTATGA  
 GAACTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5308  
 STRAIN M781

ACAAATACTTTGAAAAAAGAATTAGTTGAAGCTAAA  
 AAGACAATTCCATCCGTAAAAGCTTCAAAGTACCGCAAAAATCAACATC  
 ATCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGGTT  
 GGCAACTTCTTAAGGAGATTGATTACGATACGCTTTCAAAAAATATTTCA  
 GGTGTTGTTTATTCGTATCTTGGTGGATCAAAGATATCTAAGACTAATAA  
 CGCTGCTTATACAACTGGAATCGATAAATCGTTTAAAGACCCATATCAAAG  
 AATTTCAAAGCGAAATATCCAGTAGCTGTCTACAGTTATGCACTTGGT  
 TCAAGTGTAAAGAAATGAAAGAAGAGGCTCAGATATTTATAAGAAATGC  
 AGCTCCTTACAAACCAACTTTTATTGGATTGACGTAGAAGAGGAGACAA  
 TGTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAGAGTTAAAAAGA  
 CTGGTGCTAAAAATGTTGGTATCTACATCGGTACTTACTTTATGACTGA  
 GCAAGGTATCTCTGTAAAAGGATTGACGCTGTTGGATTCCAACCTTATG  
 GTAGCGATTCTGGATACTATGAAGCAGCTCCACAACTGAACTTAAATAC  
 GATTTACACCAATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACC  
 GCTTGATTAAATCAAATTGCAGTTAATAAAGACAAGAAGAAAACCTTATG  
 AGAACTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5309  
 STRAIN CJB110

AAATACTTTGAAAAAAGAATTAGTTGAAGCTAAAAGACAATTCCATCCG  
 TAAAGCTTCAAAGTACCGCAAAAATCAACATCATCGAAAGATAAAGAG  
 TTTGTTCTTAAACCGATTATCGATGTCTCTGGTTGGCAACTTCTTAAGGA  
 GATTGATTACGATACGCTTTCAAAAAATATTTCAAGGTGTTGTTATTCGTG  
 TCTTTGGTGGATCAAAGATATCTAAGACTAATAACGCTGCTTATACAACT  
 GGAATCGATAAATCGTTTAAAGACCCATATCAAAGAAATTTCAAAGCGAAA  
 TATCCAGTAGCTGTCTACAGTTATGCACTTGGTTCAAGTGTAAAGAAA  
 TGAAGAAGAGGCTCAGATATTTATAAGAAATGCAGCTTCTTACAAACCA  
 ACTTTTATTGGATTGACGTAGAAGAGGAGACAATGTCTAACATGAATAA  
 AGGTGCTCAAGCATTCCGAAAAGAAATTAAGAAGACTTGGTGCTAAAAATG  
 TTGGTATCTACATTTGGTACTTACTTTATGACTGAGCAAGGCATCTCTGTA  
 AAAGGATTGACGCTGTTTGGATTCCAACCTTATGGTAGCGATTCTGGATA



Table 53: Comparative Sequences relating to SAG 0755

CTATGAAGCGGCTCCGCAAACTGAACCTAAATACGATTTACACCAATACA  
CCTCTCAAGGTTATCTACCAGGATTCAATCAACCGCTTGATTTAAATCAA  
ATTACAGTTAATAAGACAAGAAGAAACTTTATGAGAACTTTTGGAAA  
AGTAAAGAG

SEQ ID NO. 5310

STRAIN 1169NT

ACAAATACTTTGAAAAAGAATTAGTTGAAGCTAAAAAGACAATTCC  
ATCCGTAAAGCTTCAAAAGTACCGCAAAATCAACATCATCGAAAGATA  
AAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGGTTGGCACTTCCT  
AAGGAGATTGATTACGATACGCTTTCAAAAAATATTTCAGGTGTGTTAT  
TCGTGTCTTTGGTGGATCAAGATATCTAAGACTAATAACGCTGCTTATA  
CAACTGGAATCGATAAATCCTTTAAGACCCATATCAAGAATTTCAAAAG  
CGAAATATCCAGTAGCTGTCTACAGTTATGCACTTGGTTCAAGTGTAA  
AGAAATGAAAGAGAGGCTCAGATATTTATAAGAAATGCAGCTCCTTACA  
AACCAACTTTTATTGGATTGACGTAGAAGAGGAGACAATGTCTAACATG  
AATAAAGGTGTCCAAGCATTCCGAAAAGAATTAAAAAGACTTGGCGCTAA  
AAATGTTGGTATCTACATCGGTACTTACTTTATGACTGAGCAAGGTATCT  
CTGTAAAGGATTGACGCTGTTTGGATTCCAACTTATGGTAGCGATTCT  
GGATACATGAAAGCAGCTCCGCAAACTGAACTTAAATACGATTTACACCA  
ATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACCGCTTGATTTAA  
ATCAAATTGCAGTTAATAAGACAAGAAGAAACTTTATGAGAACTTTT  
GGAAAAGTAAAGAG

SEQ ID NO. 5311

STRAIN JM9130013

ACAAATACTTTGAAAAAGAATTAG  
TTGAAGCTAAAAAGACAATTCCATCCGTAAAGCTTCAAAAGTACCGCAA  
AAATCAACATCATCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGA  
TGCTCTGGTTGGCACTTCTAAGGAGATTGATTACGATACGCTTTCAA  
AAAATATTTCAAGGTGTGTTATTCTGTCTTTGGTGGATCAAAGATATCT  
AAGACTAATAACGCTGCTTATACAACTGGAATCGATAAATCGTTTAAAGAC  
CCATATCAAAGAATTTCAAAAGCGAAATATCCAGTAGCTGTCTACAGTT  
ATGCACCTTGGTTCAAGTGTAAAGAAATGAAAGAAGAGGCTCAGATATTT  
TATAAGAAATGCAGCTCCTTACAAACCACTTTTATTGGATTGACGTAGA  
AGAGGAGACAATGTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAG  
AATTAAAAAGACTTGGTGTCTAAAAATGTTGGTATCTACATTGGTACTTAC  
TTTATGACTGAGCAAGGCATCTCTGTAAAGGATTGACGCTGTTTGGAT  
TCCAACCTTATGGTAGCGATTCTGGATACTATGAAGCGGCTCCGCAAACTG  
AACTTAAATACGATTACACCAATACACCTCTCAAGGTTATCTACCAGGA  
TTCAATCAACCGCTTGATTTAAATCAAATTGCAGTTAATAAGACAAGAA  
GAAACTTATGAGAACTTTTGGAAAAGTAAAGAG

PRETTY of: /biotmp/msa21441.2{\*} January 20, 2003 03:46 ...

	1				50
msa21441.2{206_090}	acAAATACTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCATC
msa21441.2{206_18RS21}	acAAATACTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCATC
msa21441.2{206_2603}	acAAATACTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCATC
msa21441.2{206_A909}	acAAATACTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCATC
msa21441.2{206_H36B}	acAAATACTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCATC
msa21441.2{206_JM9130013}	acAAATACTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCATC
msa21441.2{206_CJB110}	--AAATACTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCATC
msa21441.2{206_COH1}	acAAATACTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCATC
msa21441.2{206_M732}	acAAATACTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCATC
msa21441.2{206_M781}	acAAATACTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCATC
msa21441.2{206_1169NT}	acAAATACTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCATC
	Consensus	*****	*****	*****	*****
	51				100
msa21441.2{206_090}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_18RS21}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_2603}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_A909}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_H36B}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_JM9130013}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_CJB110}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_COH1}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_M732}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_M781}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_1169NT}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
	Consensus	*****	*****	*****	*****
	101				150
msa21441.2{206_090}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_18RS21}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_2603}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_A909}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_H36B}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_JM9130013}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_CJB110}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_COH1}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_M732}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG

Table 53: Comparative Sequences relating to SAG 0755

msa21441.2{206_M781}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG		
msa21441.2{206_1169NT}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG		
Consensus	*****	*****	*****	*****	*****		
msa21441.2{206_090}	151	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG	200
msa21441.2{206_18RS21}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG	TTGTTATTTCG	
msa21441.2{206_2603}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG	TTGTTATTTCG	
msa21441.2{206_A909}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG	TTGTTATTTCG	
msa21441.2{206_H36B}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG	TTGTTATTTCG	
msa21441.2{206_JM9130013}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG	TTGTTATTTCG	
msa21441.2{206_CJB110}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG	TTGTTATTTCG	
msa21441.2{206_COH1}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG	TTGTTATTTCG	
msa21441.2{206_M732}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG	TTGTTATTTCG	
msa21441.2{206_M781}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG	TTGTTATTTCG	
msa21441.2{206_1169NT}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG	TTGTTATTTCG	
Consensus	*****	*****	*****	*****	*****	*****	
msa21441.2{206_090}	201	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA	250
msa21441.2{206_18RS21}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA	GCTTATACAA	
msa21441.2{206_2603}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA	GCTTATACAA	
msa21441.2{206_A909}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA	GCTTATACAA	
msa21441.2{206_H36B}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA	GCTTATACAA	
msa21441.2{206_JM9130013}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA	GCTTATACAA	
msa21441.2{206_CJB110}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA	GCTTATACAA	
msa21441.2{206_COH1}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA	GCTTATACAA	
msa21441.2{206_M732}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA	GCTTATACAA	
msa21441.2{206_M781}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA	GCTTATACAA	
msa21441.2{206_1169NT}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA	GCTTATACAA	
Consensus	*-*****	*****	*****	*****	*****	*****	
msa21441.2{206_090}	251	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA	300
msa21441.2{206_18RS21}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA	TCAAAAGCGA	
msa21441.2{206_2603}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA	TCAAAAGCGA	
msa21441.2{206_A909}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA	TCAAAAGCGA	
msa21441.2{206_H36B}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA	TCAAAAGCGA	
msa21441.2{206_JM9130013}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA	TCAAAAGCGA	
msa21441.2{206_CJB110}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA	TCAAAAGCGA	
msa21441.2{206_COH1}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA	TCAAAAGCGA	
msa21441.2{206_M732}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA	TCAAAAGCGA	
msa21441.2{206_M781}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA	TCAAAAGCGA	
msa21441.2{206_1169NT}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA	TCAAAAGCGA	
Consensus	*****	*****	*****	*****	*****	*****	
msa21441.2{206_090}	301	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA	350
msa21441.2{206_18RS21}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA	GTGTTAAAGA	
msa21441.2{206_2603}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA	GTGTTAAAGA	
msa21441.2{206_A909}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA	GTGTTAAAGA	
msa21441.2{206_H36B}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA	GTGTTAAAGA	
msa21441.2{206_JM9130013}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA	GTGTTAAAGA	
msa21441.2{206_CJB110}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA	GTGTTAAAGA	
msa21441.2{206_COH1}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA	GTGTTAAAGA	
msa21441.2{206_M732}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA	GTGTTAAAGA	
msa21441.2{206_M781}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA	GTGTTAAAGA	
msa21441.2{206_1169NT}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA	GTGTTAAAGA	
Consensus	*****	*****	*****	*****	*****	*****	
msa21441.2{206_090}	351	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC	400
msa21441.2{206_18RS21}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC	CCTTACAAAC	
msa21441.2{206_2603}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC	CCTTACAAAC	
msa21441.2{206_A909}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC	CCTTACAAAC	
msa21441.2{206_H36B}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC	CCTTACAAAC	
msa21441.2{206_JM9130013}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC	CCTTACAAAC	
msa21441.2{206_CJB110}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC	CCTTACAAAC	
msa21441.2{206_COH1}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC	CCTTACAAAC	
msa21441.2{206_M732}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC	CCTTACAAAC	
msa21441.2{206_M781}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC	CCTTACAAAC	
msa21441.2{206_1169NT}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC	CCTTACAAAC	
Consensus	*****	*****	*****	*****	*****	*****	
msa21441.2{206_090}	401	CAACTTTTAA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT	450
msa21441.2{206_18RS21}	CAACTTTTAA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT	TAACATGAAT	
msa21441.2{206_2603}	CAACTTTTAA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT	TAACATGAAT	
msa21441.2{206_A909}	CAACTTTTAA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT	TAACATGAAT	
msa21441.2{206_H36B}	CAACTTTTAA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT	TAACATGAAT	
msa21441.2{206_JM9130013}	CAACTTTTAA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT	TAACATGAAT	
msa21441.2{206_CJB110}	CAACTTTTAA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT	TAACATGAAT	
msa21441.2{206_COH1}	CAACTTTTAA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT	TAACATGAAT	

Table 53: Comparative Sequences relating to SAG 0755

msa21441.2{206_M732}	CAACTTTT	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
msa21441.2{206_M781}	CAACTTTT	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
msa21441.2{206_1169NT}	CAACTTTT	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
Consensus	*****	*****	*****	*****	*****
msa21441.2{206_090}	AAAGGTGTCC	AAGCATTCCG	AAAAGAAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_18RS21}	AAAGGTGTCC	AAGCATTCCG	AAAAGAAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_2603}	AAAGGTGTCC	AAGCATTCCG	AAAAGAAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_A909}	AAAGGTGTCC	AAGCATTCCG	AAAAGAAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_H36B}	AAAGGTGTCC	AAGCATTCCG	AAAAGAAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_JM9130013}	AAAGGTGTCC	AAGCATTCCG	AAAAGAAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_CJB110}	AAAGGTGTCC	AAGCATTCCG	AAAAGAAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_COH1}	AAAGGTGTCC	AAGCATTCCG	AAAAGAAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_M732}	AAAGGTGTCC	AAGCATTCCG	AAAAGAAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_M781}	AAAGGTGTCC	AAGCATTCCG	AAAAGAAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_1169NT}	AAAGGTGTCC	AAGCATTCCG	AAAAGAAaTTA	AAAAGACTTG	GtGCTAAAAA
Consensus	*****	*****	*****	*****	*****
msa21441.2{206_090}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_18RS21}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_2603}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_A909}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_H36B}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_JM9130013}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_CJB110}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_COH1}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_M732}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_M781}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_1169NT}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
Consensus	*****	*****	*****	*****	*****
msa21441.2{206_090}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_18RS21}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_2603}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_A909}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_H36B}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_JM9130013}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_CJB110}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_COH1}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_M732}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_M781}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_1169NT}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
Consensus	*****	*****	*****	*****	*****
msa21441.2{206_090}	TACTATGAAG	CgGCTCCgCA	AACTGAACIT	AAATACGATT	TACACCAATA
msa21441.2{206_18RS21}	TACTATGAAG	CgGCTCCgCA	AACTGAACIT	AAATACGATT	TACACCAATA
msa21441.2{206_2603}	TACTATGAAG	CgGCTCCgCA	AACTGAACIT	AAATACGATT	TACACCAATA
msa21441.2{206_A909}	TACTATGAAG	CgGCTCCgCA	AACTGAACIT	AAATACGATT	TACACCAATA
msa21441.2{206_H36B}	TACTATGAAG	CgGCTCCgCA	AACTGAACIT	AAATACGATT	TACACCAATA
msa21441.2{206_JM9130013}	TACTATGAAG	CgGCTCCgCA	AACTGAACIT	AAATACGATT	TACACCAATA
msa21441.2{206_CJB110}	TACTATGAAG	CgGCTCCgCA	AACTGAACIT	AAATACGATT	TACACCAATA
msa21441.2{206_COH1}	TACTATGAAG	CgGCTCCgCA	AACTGAACIT	AAATACGATT	TACACCAATA
msa21441.2{206_M732}	TACTATGAAG	CgGCTCCgCA	AACTGAACIT	AAATACGATT	TACACCAATA
msa21441.2{206_M781}	TACTATGAAG	CgGCTCCgCA	AACTGAACIT	AAATACGATT	TACACCAATA
msa21441.2{206_1169NT}	TACTATGAAG	CgGCTCCgCA	AACTGAACIT	AAATACGATT	TACACCAATA
Consensus	*****	*****	*****	*****	*****
msa21441.2{206_090}	CACCTCTCAA	GGTTATCTAC	CAGGATTCaA	TCAACCGCTT	GATTAAATC
msa21441.2{206_18RS21}	CACCTCTCAA	GGTTATCTAC	CAGGATTCaA	TCAACCGCTT	GATTAAATC
msa21441.2{206_2603}	CACCTCTCAA	GGTTATCTAC	CAGGATTCaA	TCAACCGCTT	GATTAAATC
msa21441.2{206_A909}	CACCTCTCAA	GGTTATCTAC	CAGGATTCaA	TCAACCGCTT	GATTAAATC
msa21441.2{206_H36B}	CACCTCTCAA	GGTTATCTAC	CAGGATTCaA	TCAACCGCTT	GATTAAATC
msa21441.2{206_JM9130013}	CACCTCTCAA	GGTTATCTAC	CAGGATTCaA	TCAACCGCTT	GATTAAATC
msa21441.2{206_CJB110}	CACCTCTCAA	GGTTATCTAC	CAGGATTCaA	TCAACCGCTT	GATTAAATC
msa21441.2{206_COH1}	CACCTCTCAA	GGTTATCTAC	CAGGATTCaA	TCAACCGCTT	GATTAAATC
msa21441.2{206_M732}	CACCTCTCAA	GGTTATCTAC	CAGGATTCaA	TCAACCGCTT	GATTAAATC
msa21441.2{206_M781}	CACCTCTCAA	GGTTATCTAC	CAGGATTCaA	TCAACCGCTT	GATTAAATC
msa21441.2{206_1169NT}	CACCTCTCAA	GGTTATCTAC	CAGGATTCaA	TCAACCGCTT	GATTAAATC
Consensus	*****	*****	*****	*****	*****
msa21441.2{206_090}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTGGGA
msa21441.2{206_18RS21}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTGGGA
msa21441.2{206_2603}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTGGGA
msa21441.2{206_A909}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTGGGA
msa21441.2{206_H36B}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTGGGA
msa21441.2{206_JM9130013}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTGGGA
msa21441.2{206_CJB110}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTGGGA

Table 53: Comparative Sequences relating to SAG 0755

msa21441.2{206_COH1}	AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACTTTTGGGA
msa21441.2{206_M732}	AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACTTTTGGGA
msa21441.2{206_M781}	AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACTTTTGGGA
msa21441.2{206_1169NT}	AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACTTTTGGGA
Consensus	*****-**** ***** ***** ***** ***** *****

  

	751	762
msa21441.2{206_090}	AAAGTAAAAG AG	
msa21441.2{206_18RS21}	AAAGTAAAAG AG	
msa21441.2{206_2603}	AAAGTAAAAG AG	
msa21441.2{206_A909}	AAAGTAAAAG AG	
msa21441.2{206_H36B}	AAAGTAAAAG AG	
msa21441.2{206_JM9130013}	AAAGTAAAAG AG	
msa21441.2{206_CJB110}	AAAGTAAAAG AG	
msa21441.2{206_COH1}	AAAGTAAAAG AG	
msa21441.2{206_M732}	AAAGTAAAAG AG	
msa21441.2{206_M781}	AAAGTAAAAG AG	
msa21441.2{206_1169NT}	AAAGTAAAAG AG	
Consensus	***** **	

**SEQ ID NO. 5312**

STRAIN 2603 frame: 1

TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKN  
 ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PVAVYSYALGSSVKEMKE  
 EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ  
 GISVKGFDVAVWIPTYGSDSGYYEAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD  
 KKKTYEKLFGKVKE

**SEQ ID NO. 5313**

STRAIN 090 frame: 1

TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKN  
 ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PVAVYSYALGSSVKEMKE  
 EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ  
 GISVKGFDVAVWIPTYGSDSGYYEAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD  
 KKKTYEKLFGKVKE

**SEQ ID NO. 5314**

STRAIN A909 frame: 1

TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKN  
 ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PVAVYSYALGSSVKEMKE  
 EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ  
 GISVKGFDVAVWIPTYGSDSGYYEAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD  
 KKKTYEKLFGKVKE

**SEQ ID NO. 5315**

STRAIN H36B frame: 1

TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKN  
 ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PVAVYSYALGSSVKEMKE  
 EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ  
 GISVKGFDVAVWIPTYGSDSGYYEAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD  
 KKKTYEKLFGKVKE

**SEQ ID NO. 5316**

STRAIN 18RS21 frame: 1

TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKN  
 ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PVAVYSYALGSSVKEMKE  
 EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ  
 GISVKGFDVAVWIPTYGSDSGYYEAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD  
 KKKTYEKLFGKVKE

**SEQ ID NO. 5317**

STRAIN M732 frame: 1

TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKN  
 ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PVAVYSYALGSSVKEMKE  
 EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ  
 GISVKGFDVAVWIPTYGSDSGYYEAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD  
 KKKTYEKLFGKVKE

**SEQ ID NO. 5318**

STRAIN COH1 frame: 1

TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKN  
 ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PVAVYSYALGSSVKEMKE  
 EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ  
 GISVKGFDVAVWIPTYGSDSGYYEAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD  
 KKKTYEKLFGKVKE

**SEQ ID NO. 5319**

STRAIN M781 frame: 1

TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKEFVLKPIIDVSGWQLPKEIDYDTLSKN  
 ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PVAVYSYALGSSVKEMKE  
 EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ  
 GISVKGFDVAVWIPTYGSDSGYYEAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD  
 KKKTYEKLFGKVKE

Table 53: Comparative Sequences relating to SAG 0755

## SEQ ID NO. 5320

STRAIN CJB110 frame: 2

NTLKKELVEAKKTIIPSVKASKVPQKSTSSKDKFVLKPIIDVSGWQLPKEIDYDTLSKN  
 ISGVVIRVFGGSKISKTNNAAYTTGIDKSFKTHIKEFQKRNIIPVAVYSYALGSSVKEMKEE  
 AQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQG  
 ISVKGFDVAVWIPTYGSDSGYEAAPQTELKYDLHQYTSQGYLPGFNQPLDLNQITVNNKD  
 KKTYEKLFGKVKE

## SEQ ID NO. 5321

STRAIN 1169NT frame: 1

TNTLKKELVEAKKTIIPSVKASKVPQKSTSSKDKFVLKPIIDVSGWQLPKEIDYDTLSKN  
 ISGVVIRVFGGSKISKTNNAAYTTGIDKSFKTHIKEFQKRNIIPVAVYSYALGSSVKEMKEE  
 EAQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ  
 GISVKGFDVAVWIPTYGSDSGYEAAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNNK  
 KKTYEKLFGKVKE

## SEQ ID NO. 5322

STRAIN JM9130013 frame: 1

TNTLKKELVEAKKTIIPSVKASKVPQKSTSSKDKFVLKPIIDVSGWQLPKEIDYDTLSKN  
 ISGVVIRVFGGSKISKTNNAAYTTGIDKSFKTHIKEFQKRNIIPVAVYSYALGSSVKEMKEE  
 EAQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ  
 GISVKGFDVAVWIPTYGSDSGYEAAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNNK  
 KKTYEKLFGKVKE

PRETTY of: /biotmp/msa21641.2{\*} January 20, 2003 03:59 ..

	1		50
msa21641.2{206_090}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_1169NT}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_18RS21}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_2603}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_A909}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_H36B}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_JM9130013}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_COH1}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_M732}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_M781}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_CJB110}	-NTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
Consensus	*****	*****	*****
	51		100
msa21641.2{206_090}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_1169NT}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_18RS21}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_2603}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_A909}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_H36B}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_JM9130013}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_COH1}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_M732}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_M781}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_CJB110}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
Consensus	*****	*****	*****
	101		150
msa21641.2{206_090}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_1169NT}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_18RS21}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_2603}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_A909}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_H36B}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_JM9130013}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_COH1}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_M732}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_M781}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_CJB110}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
Consensus	*****	*****	*****
	151		200
msa21641.2{206_090}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_1169NT}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_18RS21}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_2603}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_A909}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_H36B}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_JM9130013}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_COH1}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_M732}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_M781}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_CJB110}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
Consensus	*****	*****	*****

Table 53: Comparative Sequences relating to SAG 0755

	201		250
msa21641.2{206_090}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_1169NT}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_18RS21}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_2603}	YYEAAPQTEL KYDLHQYTSQ GYLPGxNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_A909}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_H36B}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_JM9130013}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_COH1}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_M732}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_M781}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_CJB110}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
Consensus	*****	*****	*****
	251		
msa21641.2{206_090}	KVKE		
msa21641.2{206_1169NT}	KVKE		
msa21641.2{206_18RS21}	KVKE		
msa21641.2{206_2603}	KVKE		
msa21641.2{206_A909}	KVKE		
msa21641.2{206_H36B}	KVKE		
msa21641.2{206_JM9130013}	KVKE		
msa21641.2{206_COH1}	KVKE		
msa21641.2{206_M732}	KVKE		
msa21641.2{206_M781}	KVKE		
msa21641.2{206_CJB110}	KVKE		
Consensus	****		

Table 54: Comparative Sequences relating to SAG0949

## SEQ ID NO. 5401

## STRAIN 2603

TTGACTCACAAAAATATATTATTAACCATTATATTGGATTATTT  
 ATGATTATATTATCAGCATGTGGTATGCTTAATAAGGAAATGGCTGGTATTGATAATTGG  
 GAACATTATCAAAGGAAAGAAAAATTACTATTGGATTGATAATACTTTTGTTCCTATG  
 GGATTGAAAGTCGTTCTGGTGACTATACCGGCTTGATATTGATTTAGCTAATGCTGTT  
 TTTAAAGAATACGGTATTTCACTGAAATGGCAGCCTATTAAGTGGGATATGAAAGAACT  
 GAACCTTAATAATGGTAATATAGACCTTATTGGAAATGGTATTCAAAAACGGCAGAACGT  
 GCTAAAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTTGTACTAAA  
 ACTTCATCAGATATTAAAGTATTAAGGATATGAAGGGGAAAAAACTAGGAGCCCAGTCG  
 GGTTTCATCTGGTTTGTATGCTTTTAAACGCTAAACCTGATATTTTAAAAAAGTTTGTAAAA  
 GGAAAAGAAGCAGTTCAATACGATACCTTCACTCAGGCTTTGATTGATTTAAAAAATAAC  
 CGTATTGATGGTCTTTTGTATGATGAAGTTTATGCTAACTATTATTTAAAGCAAGAAGGA  
 AATATAAAAGCTTATTATTTTGTAAAACTGCTTATCAAGGAGAAAAATTTGTAGTAGGA  
 GCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAAACAAAGCTTTCAAACAGCTTCAT  
 AATAAGGGGAGATTTCAAAAAATCTCTTACAAATGGTTTGGTGAAGATGTTTATAGTAAA  
 GAA

## SEQ ID NO. 5402

## STRAIN 090

## ATTGGGaaCATTATC

AAAAGGAAAAGAAAATTACTATTGGATTGATAATACTTTTGTTCCTATG  
 GGATTGAAAGCCGTTCTGGTGACTATACCGGCTTGATATTGATTTAGC  
 TAATGCTGTTTAAAGAATACGGTATTTCACTGAAATGGCAGCCTATTA  
 ACTGGGATATGAAAGAACTGAACCTTAATAATGGTAATATAGACCTTATT  
 TGGAAATGGTATTCAAAAACGGCAGAACGTGCTAAAAAAGTCGCTTTTAC  
 AAACCCATATATGAATAATCATCAAGTAATTTGTACTAAAACCTCATCAC  
 ATATTAAATAGTATTAAAGGATATGAAGGGGAAAAAACTAGGAGCCCAGTCG  
 GGTTTCATCTGGTTTGTATGCTTTTAAATGCTAAACCTGATATTTTAAAAAA  
 GTTTGTAAAGGAAAAGAAGCAGTTCAATACGATACCTTCACTCAGGCTT  
 TGATTGATTTAAAAAATAACCGTATTGATGGTCTTTTGTATGATGAAGTT  
 TATGCTAACTATTATTAAAGCAAGAAGGAATATAAAAGCTTATTATT  
 TGTAAAACTGCTTATCAAGGAGAAAAATTTGTAGTAGGAGCTCGCAAAG  
 TTGATCGTAGACTAATTGAAAAGATTAAACAAAGCTTTCAAACAGCTTCAT  
 AATAAGGGAATAATTTCAAAAAATCTCTTACAAATGGTTTGGTGAAGATGT  
 TTATAGTAAAGAA

## SEQ ID NO. 5403

## STRAIN A909

## ATTGGG

aACATTATCAAAGGAAAAGAAAATTACTATTGGATTGATAATACTTTT  
 GTTCCTATGGGATTGAAAGTCGTTCTGGTGACTATACCGGCTTGATAT  
 TGATTAGCTAATGCTGTTTAAAGAATACGGTATTTCACTGAAATGGC  
 AGCCTATTAACTGGGATATgAAAGAACTGAACCTTAATAATGGTAATATA  
 GACCTTATTGGAAATGGTTATTCAAAAACGGCAGAACGTGCTAAAAAAGT  
 CGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTTGTACTAAAA  
 CTTCATCAGATATTAAAGTATTAAAGGATATGAAGGGGAAAAAACTAGGA  
 GCCCAGTCGGGTTTCATCTGGTTTGTATGCTTTTAAACGCTAAACCTGATAT  
 TTTAAAAAAGTTTGTAAAGGAAAAGAAGCAGTCAATACGATACCTTCA  
 CTGAGGCTTTGATTGATTTAAAAAATAACCGTATTGATGGTCTTTTGTAT  
 GATGAAGTTTATGCTAACTATTATTAAAGCAAGAAGGAATATAAAAGC  
 TTATTATTTTGTAAAACTGCTTATCAAGGAGAAAAATTTGTAGTAGGAG  
 CTGCTAAAGTTGATCGTAGACTAATTGAAAAGATTAAACAAAGCTTTCAA  
 CAGCTTCATAATAAGGGGAGATTTCAAAAAATCTCTTACAAATGGTTTGG  
 TGAAGATGTTTATAGTAAAGaa

## SEQ ID NO. 5404

## STRAIN H36B

ATTGGGAACATTATCAAAGGAAAAGAAAATTACTATTGGATT  
 TGATAATACTTTTGTTCCTATGGGATTGAAAGTCGTTCTGGTGACTATA  
 CCGGCTTTGATATTGATTTAGCTAATGCTGTTTAAAGAATACGGTATT  
 TCAGTGAATGGCAGCCTATTAAGTGGGATATGAAAGAACTGAACCTAA  
 TAATGGTAATATAGACCTTATTGGAAATGGTTATTCAAAAACGGCAGAAC  
 GTGCTAAAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTA  
 ATTGTTACTAAAACCTCATCAGATATTAAAGTATTAAGGATATGAAGGG  
 GAAAAAAGTGGAGCCAGTCGGGTTTCATCTGGTTTGTATGCTTTTAAACG  
 CTAACCTGATATTTTAAAAAAGTTTGTAAAGGAAAAGAAGCAGTCAA  
 TACGATACCTTCACTCAGGCTTTGATTGATTTAAAAAATAACCGTATTGA  
 TGGTCTTTTGTATGATGAAGTATGCTAACTATTATTAAAGCAAGAAG  
 GAAATATAAAAGCTTATTATTGTGTAAAACTGCTTATCAAGGAGAAAAT  
 TTTGTAGTAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAA  
 CAAAGCTTTCAAACAGCTTCATAATAAGGGGAGATTTCAAAAAATCTCTT  
 ACAATATGTTTGGTGAAGATGTTTATAGTAAAGAA

## SEQ ID NO. 5405

## STRAIN 18RS21

## ATTGGGAACATTA

TCAAAGGAAAAGAAAATTACTATTGGATTGATAATACTTTTGTTCCTA  
 TGGGATTGAAAGTCGTTCTGGTGACTATACCGGCTTGATATTGATTTA  
 GCTAATGCTGTTTAAAGAATACGGTATTTCACTGAAATGGCAGCCTAT  
 TAAGTGGGATATGAAAGAACTGAACCTTAATAATGGTAATATAGACCTTA  
 TTTGGAAATGGTTATTCAAAAACGGCAGAACGTGCTAAAAAAGTCGCTTT  
 ACAACCCATATATGAATAATCATCAAGTAATTTGTACTAAAACCTCATC

Table 54: Comparative Sequences relating to SAG0949

ACATATTAAATAGTATTAAAGGATATGAAGGGGAAAAAACTAGGAGCCAGT  
CGGGTTCATCTGGTTTGTGATGCTTTAAAGCTAAACCTGATATTTAAAA  
AAGTTTGTAAAGGAAAAGAAGCAGTTCAATACGATACCTTCACTCAGGC  
TTTGATTGATTTAAAAAATAACCGTATTGATGGTCTTTGATTGATGAAG  
TTTATGCTAACTATTATTTAAAGCAAGAAGGAAATATAAAAGCTTATTAT  
TTTGTTAAACCTGCTTATCAAGGAGAAAAATTTGTAGTAGGAGCTCGTAA  
AGTTGATCGTAGACTAATTGAAAAGATTACAAAGCTTTCAAACAGCTTC  
ATAATAAGGGGAGATTTCAAAAAATCTCTTACAAATGGTTTGGTGAAGAT  
GTTTATAGTAAAGAA

## SEQ ID NO. 5406

STRAIN M732

ATTGGGAACATTATCAAAAGGAAAAAGAAATTACTATTGGATTGATAA  
TACITTTTGTTCCTATGGGATTTGAAAGTCGTTCTGGTGACTATACCGGCT  
TTGATATTGATTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCACTG  
AAATGGCAGCCTATTAACTGGGATATGAAAGAACTGAACCTTAATAATGG  
TAATATAGACCTTATTGGAATGGTTATTCAAAAACGGCAGAACCGTGCTA  
AAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTT  
ACTAAAACCTTCATCACATATTAAATAGTATTAAAGGATATGAAGGGGAAAA  
CTAGGAGCCAGTCGGGTTTCATCTGGTTTGTGATGCTTTTAAAGCTAAAC  
CTGATATTTTAAAAAAGTTTGTAAAGGAAAAAGAGCAGTTCAATACGAT  
ACTTTCACTCAGGCTTTGATTGATTAAAAAATAACCGTATTGATGGTCT  
TTTGATTGATGAAGTTTATGCTAACTATTATTAAAGCAAGAAGGAAATA  
TAAAGCTTATTATTGTTTAAAGCTGCTTATCAAGGAGAAAAATTTGTGTA  
GTAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAAACAAAGC  
TTTCAAACAGCTTCATAATAAGGGGAGATTTCAAAAAATCTCTTACAAAT  
GGTTTGGTGAAGATGTTTATAGTAAAGAA

## SEQ ID NO. 5407

STRAIN COH1

ATTGGGAACATTATCAAAAGGAAAAAGAAATTACTATTGGATTGATAA  
TACITTTTGTTCCTATGGGATTTGAAAGTCGTTCTGGTGACTATACCGGCT  
TTGATATTGATTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCACTG  
AAATGGCAGCCTATTAACTGGGATATGAAAGAACTGAACCTTAATAATGG  
TAATATAGACCTTATTGGAATGGTTATTCAAAAACGGCAGAACCGTGCTA  
AAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTT  
ACTAAAACCTTCATCACATATTAAATAGTATTAAAGGATATGAAGGGGAAAA  
CTAGGAGCCAGTCGGGTTTCATCTGGTTTGTGATGCTTTTAAAGCTAAAC  
CTGATATTTTAAAAAAGTTTGTAAAGGAAAAAGAGCAGTTCAATACGAT  
ACTTTCACTCAGGCTTTGATTGATTAAAAAATAACCGTATTGATGGTCT  
TTTGATTGATGAAGTTTATGCTAACTATTATTAAAGCAAGAAGGAAATA  
TAAAGCTTATTATTGTTTAAAGCTGCTTATCAAGGAGAAAAATTTGTGTA  
GTAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAAACAAAGC  
TTTCAAACAGCTTCATAATAAGGGGAGATTTCAAAAAATCTCTTACAAAT  
GGTTTGGTGAAGATGTTTATAGTAAAGAA

## SEQ ID NO. 5408

STRAIN M781

ATTGGGAACATTATCAAAAGGAAAAAGAAATTACTATTGGATTGATAA  
ATACITTTTGTTCCTATGGGATTTGAAAGTCGTTCTGGTGACTATACCGGC  
TTTGATATTGATTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCACTG  
GAAATGGCAGCCTATTAACTGGGATATGAAAGAACTGAACCTTAATAATGG  
GTAATATAGACCTTATTGGAATGGTTATTCAAAAACGGCAGAACCGTGCT  
AAAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGT  
TACTAAAACTTCATCACATATTAAATAGTATTAAAGGATATGAAGGGGAAAA  
AACTAGGAGCCAGTCGGGTTTCATCTGGTTTGTGATGCTTTTAAAGCTAAAC  
CTGATATTTTAAAAAAGTTTGTAAAGGAAAAAGAGCAGTTCAATACGA  
TACTTTCACTCAGGCTTTGATTGATTAAAAAATAACCGTATTGATGGTC  
TTTGATTGATGAAGTTTATGCTAACTATTATTAAAGCAAGAAGGAAAT  
ATAAAAGCTTATTATTGTTTAAAGCTGCTTATCAAGGAGAAAAATTTGT  
AGTAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAAACAAAG  
CTTTCAAACAGCTTCATAATAAGGGGAGATTTCAAAAAATCTCTTACAAA  
TGGTTTGGTGAAGATGTTTATAGTAAAGAA

## SEQ ID NO. 5409

STRAIN CJB110

ATTGGGAACATTATCAAAAGGAAAAAGAAATTACTATTGGATTGATAA  
ACTTTTGTTCCTATGGGATTTGAAAGTCGTTCTGGTGACTATACCGGCTT  
TGATATTGATTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCACTG  
AATGGCAGCCTATTAACTGGGATATGAAAGAACTGAACCTTAATAATGGT  
AATATAGACCTTATTGGAATGGTTATTCAAAAACGGCAGAACCGTGCTAA  
AAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTTA  
CTAAAACCTTCATCACATATTAAATAGTATTAAAGGATATGAAGGGGAAAA  
CTAGGAGCCAGTCGGGTTTCATCTGGTTTGTGATGCTTTTAAAGCTAAAC  
TGATATTTTAAAAAAGTTTGTAAAGGAAAAAGAGCAGTTCAATACGATA  
CTTTCACTCAGGCTTTGATTGATTAAAAAATAACCGTATTGATGGTCTT  
TTGATTGATGAAGTTTATGCTAACTATTATTAAAGCAAGAAGGAAATAT  
AAAAGCTTATTATTGTTTAAAGCTGCTTATCAAGGAGAAAAATTTGTGTA  
TAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAAACAAAGCT  
TTCAAACAGCTTCATAATAAGGGGAGATTTCAAAAAATCTCTTACAAATG  
GTTTGGTGAAGATGTTTATAGTAAAGAA

## SEQ ID NO. 5410



Table 54: Comparative Sequences relating to SAG0949

STRAIN 1169NT  
 ATTGGGAACATTATCAAAAGGAAAAGAAAATTACTATTGGATTGGATAA  
 TACTTTTGTTCCTATGGGATTGAAAAGTCGTTCTGGTGACTATACCGGCT  
 TTGATATTGATTTAGCTAATGCTGTTTTTAAAGAAATACGGTATTTCAAGT  
 AAATGGCAGCCTATTAACTGGGATATGAAAGAACTGAACTCAATAATGG  
 TAATATAGACCTTATTTGGAATGGTTATTCAAAAACGGCAGAACGTCCTA  
 AAAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTT  
 ACTAAACTTCATCACATATTAAATAGTATTAAAGGATATGAAGGGGAAAAA  
 ACTAGGAGCCAGTCGGGTTTCATCTGGTTTTGATGCTTTTAATGCTAAAC  
 CTGACATTTTAAAAAAGTTTGTAAAGGAAAAGAGCAGTTCAATACGAT  
 ACTTTCACTCAGGCTTTGATTGATTAAAAAATAACCGTATTGATGGTCT  
 TTTGATTGATGAAGTTTATGCTAATATTATTAAAGCAAGAGGAAATA  
 TAAAAGCTTATTATTGTTAAACTGCTTATCAAGGAGAAAAATTTTGTA  
 GTAGGAGCTCGCAAAGTTGATCGTAGACTAATTGAAAAGATTAAACAAAGC  
 TTTCAAACAGCTTCATAATAAGGGGAAATTTCAAAAAATCTCTACAAAT  
 GGTTCGTTGAAGATGTTTATAGTAAAGAA

SEQ ID NO. 5411  
 STRAIN JM9130013

ATTGGGAACATTATC  
 AAAAGGAAAAGAAAATTACTATTTGGATTGGATAATACTTTGTTCCTATG  
 GGATTGAAAAGTCGTTCTGGTGACTATACCGGCTTTGATATTGATTTAGC  
 TAATGCTGTTTTTAAAGAAATACGGTATTTCAAGTAAATGGCAGCCTATTA  
 ACTGGGATATGAAAAGAACTGAACTTAATAATGGTAATATAGACCTTATT  
 TGGAAATGGTTATTCAAAAACGGCAGAACGTCGCTAAAAAAGTCGCTTTTAC  
 AAACCCATATATGAATAATCATCAAGTAATTGTTACTAAAACTTCATCAC  
 ATATTAAATAGTATTAAAGGATATGAAGGGGAAAAAACTAGGAGCCAGTCG  
 GGTTTCATCTGGTTTTGATGCTTTTAAACGCTAAACCTGATATTTAAAAA  
 GTTTGTAAAAGGAAAAGAGCAGTTCAATACGATACCTTCACTCAGGCCT  
 TGATTGATTTAAAAAATAACCGTATTGATGCTTTTGTATTGATGAAGTT  
 TATGCTAACTATTATTAAAGCAAGAGGAAATATAAAAGCTTATTATT  
 TGTATAAAGCTGCTTATCAAGGAGAAAAATTTGTAGTAGGAGCTCGTAAAG  
 TTGATCGTAGACTAATTGAAAAGATTAAACAAAGCTTTCAAACAGCTTCAT  
 AATAAGGGGAGATTTCAAAAATCTCTTACAAATGGTTTGGTGAAGATGT  
 TTATAGTAAAGAA

PRETTY of: /biotmp/msa39314.2{\*} February 18, 2003 11:01 ..

	1				50
msa39314.2{225_18RS21}	-----	-----	-----	-----	-----
msa39314.2{225_2603}	ttgactcaca	aaaatatatt	attaaccatt	atatttggat	tatttatgat
msa39314.2{225_A909}	-----	-----	-----	-----	-----
msa39314.2{225_CJB110}	-----	-----	-----	-----	-----
msa39314.2{225_COH1}	-----	-----	-----	-----	-----
msa39314.2{225_H36B}	-----	-----	-----	-----	-----
msa39314.2{225_KM9130013}	-----	-----	-----	-----	-----
msa39314.2{225_M732}	-----	-----	-----	-----	-----
msa39314.2{225_M781}	-----	-----	-----	-----	-----
msa39314.2{225_090}	-----	-----	-----	-----	-----
msa39314.2{225_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa39314.2{225_18RS21}	-----	-----	-----	-----	-----
msa39314.2{225_2603}	tatatattatca	gcatgtggta	tgtctaataa	ggaaatggct	ggtattgata
msa39314.2{225_A909}	-----	-----	-----	-----	-----
msa39314.2{225_CJB110}	-----	-----	-----	-----	-----
msa39314.2{225_COH1}	-----	-----	-----	-----	-----
msa39314.2{225_H36B}	-----	-----	-----	-----	-----
msa39314.2{225_KM9130013}	-----	-----	-----	-----	-----
msa39314.2{225_M732}	-----	-----	-----	-----	-----
msa39314.2{225_M781}	-----	-----	-----	-----	-----
msa39314.2{225_090}	-----	-----	-----	-----	-----
msa39314.2{225_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	101				150
msa39314.2{225_18RS21}	ATTGGGAACA	TTATCAAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAT
msa39314.2{225_2603}	ATTGGGAACA	TTATCAAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAT
msa39314.2{225_A909}	ATTGGGAACA	TTATCAAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAT
msa39314.2{225_CJB110}	ATTGGGAACA	TTATCAAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAT
msa39314.2{225_COH1}	ATTGGGAACA	TTATCAAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAT
msa39314.2{225_H36B}	ATTGGGAACA	TTATCAAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAT
msa39314.2{225_KM9130013}	ATTGGGAACA	TTATCAAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAT
msa39314.2{225_M732}	ATTGGGAACA	TTATCAAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAT
msa39314.2{225_M781}	ATTGGGAACA	TTATCAAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAT
msa39314.2{225_090}	ATTGGGAACA	TTATCAAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAT
msa39314.2{225_1169NT}	ATTGGGAACA	TTATCAAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAT
Consensus	*****	*****	*****	*****	*****
	151				200
msa39314.2{225_18RS21}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGACT	ATACCGGCTT
msa39314.2{225_2603}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGACT	ATACCGGCTT

Table 54: Comparative Sequences relating to SAG0949

msa39314.2{225_A909}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGA	ATACCGGCTT
msa39314.2{225_CJB110}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGA	ATACCGGCTT
msa39314.2{225_COH1}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGA	ATACCGGCTT
msa39314.2{225_H36B}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGA	ATACCGGCTT
msa39314.2{225_KM9130013}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGA	ATACCGGCTT
msa39314.2{225_M732}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGA	ATACCGGCTT
msa39314.2{225_M781}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGA	ATACCGGCTT
msa39314.2{225_090}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGA	ATACCGGCTT
msa39314.2{225_1169NT}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGA	ATACCGGCTT
Consensus	*****	*****	*****	*****	*****
msa39314.2{225_18RS21}	201	250			
msa39314.2{225_2603}	TCATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
msa39314.2{225_A909}	TCATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
msa39314.2{225_CJB110}	TCATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
msa39314.2{225_COH1}	TCATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
msa39314.2{225_H36B}	TCATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
msa39314.2{225_KM9130013}	TCATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
msa39314.2{225_M732}	TCATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
msa39314.2{225_M781}	TCATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
msa39314.2{225_090}	TCATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
msa39314.2{225_1169NT}	TCATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
Consensus	*****	*****	*****	*****	*****
msa39314.2{225_18RS21}	251	300			
msa39314.2{225_2603}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
msa39314.2{225_A909}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
msa39314.2{225_CJB110}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
msa39314.2{225_COH1}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
msa39314.2{225_H36B}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
msa39314.2{225_KM9130013}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
msa39314.2{225_M732}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
msa39314.2{225_M781}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
msa39314.2{225_090}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
msa39314.2{225_1169NT}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
Consensus	*****	*****	*****	*****	*****
msa39314.2{225_18RS21}	301	350			
msa39314.2{225_2603}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_A909}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_CJB110}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_COH1}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_H36B}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_KM9130013}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_M732}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_M781}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_090}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_1169NT}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
Consensus	*****	*****	*****	*****	*****
msa39314.2{225_18RS21}	351	400			
msa39314.2{225_2603}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_A909}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_CJB110}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_COH1}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_H36B}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_KM9130013}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_M732}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_M781}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_090}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_1169NT}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
Consensus	*****	*****	*****	*****	*****
msa39314.2{225_18RS21}	401	450			
msa39314.2{225_2603}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_A909}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_CJB110}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_COH1}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_H36B}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_KM9130013}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_M732}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_M781}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_090}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_1169NT}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
Consensus	*****	*****	*****	*****	*****
msa39314.2{225_18RS21}	451	500			
msa39314.2{225_2603}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTTT	GATGCTTTTA	AcGCTAAACC

Table 54: Comparative Sequences relating to SAG0949

msa39314.2{225_2603}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_A909}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_CJB110}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_COH1}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_H36B}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_KM9130013}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_M732}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_M781}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_090}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_1169NT}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
Consensus	*****	*****	*****	*****	*****
501					550
msa39314.2{225_18RS21}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_2603}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_A909}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_CJB110}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_COH1}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_H36B}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_KM9130013}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_M732}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_M781}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_090}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_1169NT}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
Consensus	***-*****	*****	*****	*****	*****
551					600
msa39314.2{225_18RS21}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_2603}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_A909}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_CJB110}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_COH1}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_H36B}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_KM9130013}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_M732}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_M781}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_090}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_1169NT}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
Consensus	*****	*****	*****	*****	*****
601					650
msa39314.2{225_18RS21}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_2603}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_A909}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_CJB110}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_COH1}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_H36B}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_KM9130013}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_M732}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_M781}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_090}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_1169NT}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
Consensus	*****	*****	*****	*****	*****
651					700
msa39314.2{225_18RS21}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_2603}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_A909}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_CJB110}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_COH1}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_H36B}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_KM9130013}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_M732}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_M781}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_090}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_1169NT}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
Consensus	*****	*****	*****	*****	*****
701					750
msa39314.2{225_18RS21}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_2603}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_A909}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_CJB110}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_COH1}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_H36B}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_KM9130013}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_M732}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_M781}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_090}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_1169NT}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
Consensus	*****	*****	*****	*****	*****
751					800

Table 54: Comparative Sequences relating to SAG0949

msa39314.2{225_18RS21}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_2603}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_A909}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_CJB110}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_COH1}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_H36B}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_KM9130013}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_M732}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_M781}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_090}	TTCAAACAGC	TTCATAATAA	GGGgAaATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_1169NT}	TTCAAACAGC	TTCATAATAA	GGGgAaATTT	CAAAAAATCT	CTTACAAATG
Consensus	*****	*****	***-**-****	*****	*****

	801	828
msa39314.2{225_18RS21}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_2603}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_A909}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_CJB110}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_COH1}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_H36B}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_KM9130013}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_M732}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_M781}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_090}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_1169NT}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
Consensus	*****	*****

## SEQ ID NO. 5412

STRAIN 2603 frame: 1

LTHKNILLTIIFGLFMIISACGSMNKEMAGIDNWEHYQKEKKITIGFDNTFVPMGFESR  
SGDYTGFDIDLAVFKEYGISVKWQPINWDMKETLNNGNIDLIWNGYSKTAERAKKVA  
FTNPYMNHHQVIVTKTSSHINSIKDMKGKGLGAQSGSSGFDFAFNAPDILKKFVKGKEAV  
QYDTFTQALIDLKNNRIDGLLIDEVYANYLKEGNIKAYYFVKITAYQGENFVVGARKVD  
RRLEIKINKAFKQLHNKGRFQKISYKWFGEDEVYSKE

## SEQ ID NO. 5413

STRAIN 090 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLAVFKEYGISVKWQPINWDMKE  
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHHQVIVTKTSSHINSIKDMKGKGLGAQ  
SGSSGFDFAFNAPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLKEG  
NIKAYYFVKITAYQGENFVVGARKVDRLLEIKINKAFKQLHNKGRFQKISYKWFGEDEVYS  
KE

## SEQ ID NO. 5414

STRAIN A909 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLAVFKEYGISVKWQPINWDMKE  
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHHQVIVTKTSSHINSIKDMKGKGLGAQ  
SGSSGFDFAFNAPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLKEG  
NIKAYYFVKITAYQGENFVVGARKVDRLLEIKINKAFKQLHNKGRFQKISYKWFGEDEVYS  
KE

## SEQ ID NO. 5415

STRAIN H36B frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLAVFKEYGISVKWQPINWDMKE  
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHHQVIVTKTSSHINSIKDMKGKGLGAQ  
SGSSGFDFAFNAPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLKEG  
NIKAYYFVKITAYQGENFVVGARKVDRLLEIKINKAFKQLHNKGRFQKISYKWFGEDEVYS  
KE

## SEQ ID NO. 5416

STRAIN 18RS21 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLAVFKEYGISVKWQPINWDMKE  
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHHQVIVTKTSSHINSIKDMKGKGLGAQ  
SGSSGFDFAFNAPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLKEG  
NIKAYYFVKITAYQGENFVVGARKVDRLLEIKINKAFKQLHNKGRFQKISYKWFGEDEVYS  
KE

## SEQ ID NO. 5417

STRAIN M732 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLAVFKEYGISVKWQPINWDMKE  
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHHQVIVTKTSSHINSIKDMKGKGLGAQ  
SGSSGFDFAFNAPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLKEG  
NIKAYYFVKITAYQGENFVVGARKVDRLLEIKINKAFKQLHNKGRFQKISYKWFGEDEVYS  
KE

## SEQ ID NO. 5418

STRAIN COH1 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLAVFKEYGISVKWQPINWDMKE  
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHHQVIVTKTSSHINSIKDMKGKGLGAQ  
SGSSGFDFAFNAPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLKEG  
NIKAYYFVKITAYQGENFVVGARKVDRLLEIKINKAFKQLHNKGRFQKISYKWFGEDEVYS  
KE

Table 54: Comparative Sequences relating to SAG0949

## SEQ ID NO. 5419

STRAIN M781 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE  
 TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHNQVIVTKTSSHINSIKDMKGKGLGAQ  
 SGSSGDFAFNAKPDILKKFVKGEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLQKE  
 GNIKAYYFVKTAQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYS  
 KE

## SEQ ID NO. 5420

STRAIN CJB110 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE  
 TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHNQVIVTKTSSHINSIKDMKGKGLGAQ  
 SGSSGDFAFNAKPDILKKFVKGEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLQKE  
 GNIKAYYFVKTAQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYS  
 KE

## SEQ ID NO. 5421

STRAIN 1169NT frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE  
 TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHNQVIVTKTSSHINSIKDMKGKGLGAQ  
 SGSSGDFAFNAKPDILKKFVKGEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLQKE  
 GNIKAYYFVKTAQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYS  
 KE

## SEQ ID NO. 5422

STRAIN JM9130013 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE  
 TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHNQVIVTKTSSHINSIKDMKGKGLGAQ  
 SGSSGDFAFNAKPDILKKFVKGEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLQKE  
 GNIKAYYFVKTAQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYS  
 KE

PRETTY of: /biotmp/msa45901.2(\*) February 19, 2003 03:09 ..

	1				50
msa45901.2{225_090}	-----	-----	-----	-----WEHYQK	EKKITIGFDN
msa45901.2{225_1169NT}	-----	-----	-----	-----WEHYQK	EKKITIGFDN
msa45901.2{225_18RS21}	-----	-----	-----	-----WEHYQK	EKKITIGFDN
msa45901.2{225_2603}	lthknillti	ifglfmiils	acgmsnkema	gidnWEHYQK	EKKITIGFDN
msa45901.2{225_A909}	-----	-----	-----	-----WEHYQK	EKKITIGFDN
msa45901.2{225_CJB110}	-----	-----	-----	-----WEHYQK	EKKITIGFDN
msa45901.2{225_COH1}	-----	-----	-----	-----WEHYQK	EKKITIGFDN
msa45901.2{225_H36B}	-----	-----	-----	-----WEHYQK	EKKITIGFDN
msa45901.2{225_JM9130013}	-----	-----	-----	-----WEHYQK	EKKITIGFDN
msa45901.2{225_M732}	-----	-----	-----	-----WEHYQK	EKKITIGFDN
msa45901.2{225_M781}	-----	-----	-----	-----WEHYQK	EKKITIGFDN
Consensus	*****	*****	*****	*****	*****
	51				100
msa45901.2{225_090}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_1169NT}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_18RS21}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_2603}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_A909}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_CJB110}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_COH1}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_H36B}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_JM9130013}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_M732}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_M781}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
Consensus	*****	*****	*****	*****	*****
	101				150
msa45901.2{225_090}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_1169NT}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_18RS21}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_2603}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_A909}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_CJB110}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_COH1}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_H36B}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_JM9130013}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_M732}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_M781}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
Consensus	*****	*****	*****	*****	*****
	151				200
msa45901.2{225_090}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_1169NT}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_18RS21}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_2603}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_A909}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_CJB110}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGEAV	QYDTFTQALI	DLKNNRIDGL

Table 54: Comparative Sequences relating to SAG0949

msa45901.2{225_COH1}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_H36B}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_JM9130013}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_M732}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_M781}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
Consensus	*****	*****	*****	*****	*****
201					
msa45901.2{225_090}	LIDEVYANY	LKQEGNIKAY	YFVKTAHQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_1169NT}	LIDEVYANY	LKQEGNIKAY	YFVKTAHQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_18RS21}	LIDEVYANY	LKQEGNIKAY	YFVKTAHQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_2603}	LIDEVYANY	LKQEGNIKAY	YFVKTAHQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_A909}	LIDEVYANY	LKQEGNIKAY	YFVKTAHQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_CJB110}	LIDEVYANY	LKQEGNIKAY	YFVKTAHQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_COH1}	LIDEVYANY	LKQEGNIKAY	YFVKTAHQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_H36B}	LIDEVYANY	LKQEGNIKAY	YFVKTAHQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_JM9130013}	LIDEVYANY	LKQEGNIKAY	YFVKTAHQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_M732}	LIDEVYANY	LKQEGNIKAY	YFVKTAHQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_M781}	LIDEVYANY	LKQEGNIKAY	YFVKTAHQGE	NFVVGARKVD	RRLIEKINKA
Consensus	*****	*****	*****	*****	*****
251					
msa45901.2{225_090}	FKQLHNKGKf	QKISYKWFGE	DVYSKE		
msa45901.2{225_1169NT}	FKQLHNKGKf	QKISYKWFGE	DVYSKE		
msa45901.2{225_18RS21}	FKQLHNKGKf	QKISYKWFGE	DVYSKE		
msa45901.2{225_2603}	FKQLHNKGKf	QKISYKWFGE	DVYSKE		
msa45901.2{225_A909}	FKQLHNKGKf	QKISYKWFGE	DVYSKE		
msa45901.2{225_CJB110}	FKQLHNKGKf	QKISYKWFGE	DVYSKE		
msa45901.2{225_COH1}	FKQLHNKGKf	QKISYKWFGE	DVYSKE		
msa45901.2{225_H36B}	FKQLHNKGKf	QKISYKWFGE	DVYSKE		
msa45901.2{225_JM9130013}	FKQLHNKGKf	QKISYKWFGE	DVYSKE		
msa45901.2{225_M732}	FKQLHNKGKf	QKISYKWFGE	DVYSKE		
msa45901.2{225_M781}	FKQLHNKGKf	QKISYKWFGE	DVYSKE		
Consensus	*****	*****	*****		
276					
msa45901.2{225_090}	FKQLHNKGKf	QKISYKWFGE	DVYSKE		
msa45901.2{225_1169NT}	FKQLHNKGKf	QKISYKWFGE	DVYSKE		
msa45901.2{225_18RS21}	FKQLHNKGKf	QKISYKWFGE	DVYSKE		
msa45901.2{225_2603}	FKQLHNKGKf	QKISYKWFGE	DVYSKE		
msa45901.2{225_A909}	FKQLHNKGKf	QKISYKWFGE	DVYSKE		
msa45901.2{225_CJB110}	FKQLHNKGKf	QKISYKWFGE	DVYSKE		
msa45901.2{225_COH1}	FKQLHNKGKf	QKISYKWFGE	DVYSKE		
msa45901.2{225_H36B}	FKQLHNKGKf	QKISYKWFGE	DVYSKE		
msa45901.2{225_JM9130013}	FKQLHNKGKf	QKISYKWFGE	DVYSKE		
msa45901.2{225_M732}	FKQLHNKGKf	QKISYKWFGE	DVYSKE		
msa45901.2{225_M781}	FKQLHNKGKf	QKISYKWFGE	DVYSKE		
Consensus	*****	*****	*****		

Table 55: Comparative Sequences relating to SAG1592

SEQ ID NO. 5501  
STRAIN 2603  
ATGCTTAAATCTTTTGTGATTTCCTTAGTTCGCTTTTACCAAAAAATATTTCTCCAGCT  
TTCCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGAAGCTATTCAA  
AAACATGCTCTAAAAGGTGTGTGATGGGGATTGCACGTAATTTGCGATGTCATCCCTTA  
GCCACGGAGGAAATGATCCTGTCCCTGATCAITTTAGCTTAAGACGTAATAAACGGAT  
ATATCAGAT

SEQ ID NO. 5502  
STRAIN 090  
TTCCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGA  
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA  
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT  
CATTTTAGCTT

SEQ ID NO. 5503  
STRAIN A909  
TTCCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGA  
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA  
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT  
CATTTTAGCTTAAGACGTAATAAACGGATATA

SEQ ID NO. 5504  
STRAIN H36B  
TTCCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGA  
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA  
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT  
CATTTTAGCTTAAGACGTAATAAACGGATATATCAGAT

SEQ ID NO. 5505  
STRAIN 18RS21  
TTCCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGA  
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA  
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT  
CATTTTAGCTTAAGACGTAATAAACGGATATATCAGAT

SEQ ID NO. 5506  
STRAIN M732  
TTCCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGA  
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA  
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT  
CATTTTAGCTTAAGACGTAATAAACGGATATATCAGAT

SEQ ID NO. 5507  
STRAIN COH1  
TTCCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGAAGCTATTCAA  
AAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTAATTTGCGATGTCATCCCTTA  
GCCACGGAGGAAATGATCCTGTCCCTGATCAITTTAGCT

SEQ ID NO. 5508  
STRAIN M781  
TTCCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGA  
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA  
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT  
CATTTTAGCTTAAGACGTAATAAACGGATATATCAGAT

SEQ ID NO. 5509  
STRAIN CJB110  
TTCCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGA  
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA  
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT  
CATTTTAGCTTAAGACGTAATAAACGGATATATCAGAT

SEQ ID NO. 5510  
STRAIN 1169NT  
TTCCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGA  
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA  
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT  
TAITTTAGCTTAAGACGTAATAAACGGATATATCAGAT

SEQ ID NO. 5511  
STRAIN JM9130013  
TTCCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGA  
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA  
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT  
CATTTTAGCTTAAGACGTAATAAACGGATATATCAGAT

PRETTY of: /biotmp/msa119306.2{\*} April 29, 2003 06:23 ..

	1	50
msa119306.2{233_H36B}	-----	-----
msa119306.2{233_JM9130013}	-----	-----

Table 55: Comparative Sequences relating to SAG1592

msa119306.2{233_090}	-----	-----	-----	-----	-----
msa119306.2{233_18RS21}	-----	-----	-----	-----	-----
msa119306.2{233_2603}	atgcttaaat	cttttttgat	tttcttagtt	cgcttttacc	aaaaaaatat
msa119306.2{233_A909}	-----	-----	-----	-----	-----
msa119306.2{233_CJB110}	-----	-----	-----	-----	-----
msa119306.2{233_COH1}	-----	-----	-----	-----	-----
msa119306.2{233_M732}	-----	-----	-----	-----	-----
msa119306.2{233_M781}	-----	-----	-----	-----	-----
msa119306.2{233_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
51					
msa119306.2{233_H36B}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_JM9130013}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_090}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_18RS21}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_2603}	ttctccagct	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_A909}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_CJB110}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_COH1}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_M732}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_M781}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_1169NT}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
Consensus	*****	*****	*****	*****	*****
101					
msa119306.2{233_H36B}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	tctGATGGGG
msa119306.2{233_JM9130013}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	tctGATGGGG
msa119306.2{233_090}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_18RS21}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_2603}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_A909}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_CJB110}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_COH1}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_M732}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_M781}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_1169NT}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	ggTGATGGGG
Consensus	*****	*****	*****	*****	-----
151					
msa119306.2{233_H36B}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_JM9130013}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_090}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_18RS21}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_2603}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_A909}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_CJB110}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_COH1}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_M732}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_M781}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_1169NT}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
Consensus	*****	*****	*****	*****	*****
201					
msa119306.2{233_H36B}	TGTCCTTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_JM9130013}	TGTCCTTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_090}	TGTCCTTGAT	cATTTTAGCT	t-----	-----	-----
msa119306.2{233_18RS21}	TGTCCTTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_2603}	TGTCCTTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_A909}	TGTCCTTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	ata-----
msa119306.2{233_CJB110}	TGTCCTTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_COH1}	TGTCCTTGAT	cATTTTAGCT	-----	-----	-----
msa119306.2{233_M732}	TGTCCTTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_M781}	TGTCCTTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_1169NT}	TGTCCTTGAT	tATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
Consensus	*****	*****	-----	-----	-----
249					
SEQ ID NO. 5512					
STRAIN 2603 frame: 1					
MLKSFLI FLVRFYQKNISPAFPASCRRYPTCSTYMI EAIQKHGLKGVL MGIARILRCHPL					
AHGNDPVPDHFSLRRNKTDISD					
SEQ ID NO. 5513					
STRAIN 090 frame: 1					
FPASCRRYPTCSTYMI EAIQKHGLKGVL MGIARILRCHPLAHGGNDPVPDHFSLRRNKTD					
I					
SEQ ID NO. 5514					
STRAIN A909 frame: 1					
FPASCRRYPTCSTYMI EAIQKHGLKGVL MGIARILRCHPLAHGGNDPVPDHFSLRRNKTD					
I					
SEQ ID NO. 5515					
STRAIN H36B frame: 1					



Table 55: Comparative Sequences relating to SAG1592

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD  
ISD

SEQ ID NO. 5516

STRAIN 18RS21 frame: 1

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD  
ISD

SEQ ID NO. 5517

STRAIN M732 frame: 1

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD  
ISD

SEQ ID NO. 5518

STRAIN COH1 frame: 1

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFS

SEQ ID NO. 5519

STRAIN M781 frame: 1

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD  
ISD

SEQ ID NO. 5520

STRAIN CJB110 frame: 1

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD  
ISD

SEQ ID NO. 5521

STRAIN 1169NT frame: 1

FPASCRYRPTCSTYMIEAIQKHGLKGVVMGIARILRCHPLAHGGNDPVPDYFSLRRNKTD  
ISD

SEQ ID NO. 5522

STRAIN JM9130013 frame: 1

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD  
ISD

PRETTY of: /biotmp/msa119415.2{\*} April 29, 2003 06:25 ..

	1		50
msa119415.2{233_090}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_18RS21}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_COH1}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_A909}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_2603}	mlksfliflv rfyqknispa	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_CJB110}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_H36B}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_JM9130013}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_M732}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_M781}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_1169NT}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVVMG
Consensus	*****	*****	*****-*
	51		83
msa119415.2{233_090}	IARILRCHPL AHGGNDPVPD	hFS-----	---
msa119415.2{233_18RS21}	IARILRCHPL AHGGNDPVPD	hFSLRNKT	ISD
msa119415.2{233_COH1}	IARILRCHPL AHGGNDPVPD	hFS-----	---
msa119415.2{233_A909}	IARILRCHPL AHGGNDPVPD	hFSLRNKT	I--
msa119415.2{233_2603}	IARILRCHPL AHGGNDPVPD	hFSLRNKT	ISD
msa119415.2{233_CJB110}	IARILRCHPL AHGGNDPVPD	hFSLRNKT	ISD
msa119415.2{233_H36B}	IARILRCHPL AHGGNDPVPD	hFSLRNKT	ISD
msa119415.2{233_JM9130013}	IARILRCHPL AHGGNDPVPD	hFSLRNKT	ISD
msa119415.2{233_M732}	IARILRCHPL AHGGNDPVPD	hFSLRNKT	ISD
msa119415.2{233_M781}	IARILRCHPL AHGGNDPVPD	hFSLRNKT	ISD
msa119415.2{233_1169NT}	IARILRCHPL AHGGNDPVPD	yFSLRNKT	ISD
Consensus	*****	*****	*****

Table 56: Comparative Sequences relating to SAG0806

## SEQ ID NO. 5601

## STRAIN 2603

aagaagcttacttttatttgggatttagatgggacattaatagattcgta  
 tgtaccaattatggaagctcttgaagaaacctatcgctcatttttggtttaa  
 tatttgataaagaattaatccatgaatatattttacaggaatcagtgggg  
 aaattatttggttaacctttcagaggaagagcaaatacctcatgaaaaact  
 gaaagcatattttacaaaagaacaagaaagtcgagattctaaaaatcatt  
 taatgccatattgcaaaagagattttagaatggaccaagaacaagatatc  
 cccaattttatgtatacacataaaggagcaagtacgcattcagtggtgga  
 aaccttgagatctctcattattttgatgaaattttaactggtgtttcgg  
 gattcgagcgaaaaccacatccacaagggattaaatttttagttaaacga  
 tattcttttagataaatcaatgacttattacataggagatcgccactaga  
 tttggaggttgctcaaaatgctggtataaaatccataaacttaaggttag  
 agaattccaaagaaaactataatatttcaagctcacaagatataatatca  
 cttgatttcactcgtttggat

## SEQ ID NO. 5602

## STRAIN COH1

AAGAAGCTTACTTTTATTGGGATTAGATGGGACATTAA  
 TAGATTCTGATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCAT  
 TTTGGCTTAATATTGATAAAGAATTAATCCATGAATATATTTTACAGGA  
 ATCAGTGGGGCAATTATTTGGTAAACCTTTTACAGGGAAGAGCAAATACCTC  
 ATGAAAAAAGTGAAGCATATTTTACAAAAGAACAAGAAAGTCGAGATTCT  
 AAAATACATTAAATGCCATATGCAAAAGAGATTTTGAATGGACCAAGA  
 ACAAGATATTCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATT  
 CAGTGTGGAAACCTTGCGAGATCTCTCATTATTTTGAATGAAATTTTAACT  
 GGTGTTCGGGATTCGAGCGAAAACCATCCACAAGGGATTAAATTTATTT  
 AGTTAAACGATATTCTTTAGATAAATCAATGACTTATTACATAGGAGATC  
 GTCCACTAGATTTCGGAGGTTGCTCAAAATGCTGGTATAAAATCCATAAAC  
 TTAAGGTTAGAGAATTCCAAAGAAAACATAATATTCAAGTCTCAAAGA  
 TATAATATCACTTGATTTCACCTCGTTTGGAT

## SEQ ID NO. 5603

## STRAIN A909

AAGAAGCTTACTTTTATTGGGATTAGATGGGACATTAAAT  
 AGATTCTGATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATT  
 TTTGGTTTAAATATTGATAAAGAATTAATCCATGAATATATTTTACAGGAAT  
 CAGTGGGGAAATTTATTTGGTAAACCTTTTACAGGGAAGAGCAAATACCTC  
 ATGAAAAAAGTGAAGCATATTTTACAAAAGAACAAGAAAGTCGAGATTCT  
 AAAATACATTAAATGCCATATGCAAAAGAGATTTTGAATGGACCAAGA  
 ACAAGATATTCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATT  
 CAGTGTGGAAACCTTGCGAGATCTCTCATTATTTTGAATGAAATTTTAACT  
 GGTGTTCGGGATTCGAGCGAAAACCATCCACAAGGGATTAAATTTATTTAG  
 TAAATCAATGACTTATTACATAGGAGATCGTCCACTAGATTTCGGAGGTTGCT  
 CAAAATGCTGGTATAAATCCATAAACTTAAGGTTAGAGAATTCCAAAGAAAAC  
 TATAATATTTCAGGATTTCACTCGTTTGGAT

## SEQ ID NO. 5604

## STRAIN H3B6

AAGAAGCTTACTTTTATTGGGATTAGATGGGACATTAAATAGATTCTG  
 TAGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGTTTAAAT  
 TTTGATTAAGAAATTAATCCATGAATATATTTTACAGGAATCAGTGGGGAAAT  
 TTTGGTAAACCTTTTACAGGGAAGAGCAAATACCTCATGAAAAAAGTGAAGCA  
 TATTTTACAAAAGAACAAGAAAGTTCGAGATTCTTAAATACATTAAATGCCAT  
 ATGCAAAAGAGATTTTGAATGGACCAAGAAAGATATATCCCAATTTTATGTAT  
 ACACATAAAGGAGCAAGTACGCATTTCAGTGTGGAACCTTGCGAGATCTCTC  
 ATTATTTTGAATGAAATTTTAACTGGTGTTCGGGATTCGAGCGAAAACCATCC  
 ACAAGGGATTAAATTTATTTAGTTAAACGATATTCTTTAGATAAATCAATGAC  
 TTTATTACATAGGAGATCGTCCACTAGATTTCGGAGGTTGCTCAAAATGCTGG  
 TATAAATCCATAAACTTAAGGTTAGAGAATTCCAAAGAAAACATAATATTTCAG  
 TCTCAAGATATAATATCACTTGATTTCACCTCGTTTGGAT

## SEQ ID NO. 5605

## STRAIN 18RS21

AAGAAGCTTACTTTTATTGGGATTAGATGGGACATTAAATAGATTCTG  
 CGTATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGTTTAA  
 TTTGATTAAGAAATTAATCCATGAATATATTTTACAGGAATCAGTGGGGAAAT  
 TTTGGTAAACCTTTTACAGGGAAGAGCAAATACCTCATGAAAAAAGTGAAGCA  
 TATTTTACAAAAGAACAAGAAAGTTCGAGATTCTTAAATACATTAAATGCCAT  
 ATGCAAAAGAGATTTTGAATGGACCAAGAAAGATATATCCCAATTTTATGTAT  
 ACACATAAAGGAGCAAGTACGCATTTCAGTGTGGAACCTTGCGAGATCTCTC  
 ATTATTTTGAATGAAATTTTAACTGGTGTTCGGGATTCGAGCGAAAACCATCC  
 ACAAGGGATTAAATTTATTTAGTTAAACGATATTCTTTAGATAAATCAATGAC  
 TTTATTACATAGGAGATCGTCCACTAGATTTCGGAGGTTGCTCAAAATGCTGG  
 TATAAATCCATAAACTTAAGGTTAGAGAATTCCAAAGAAAACATAATATTTCAG  
 TCTCAAGATATAATATCACTTGATTTCACCTCGTTTGGAT

## SEQ ID NO. 5606

## STRAIN M732

AAGAAGCTTACTTTTATTGGGATTAGATGGGACATTAAATAGAT  
 TCGTATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGCTTAA  
 TTTGATTAAGAAATTAATCCATGAATATATTTTACAGGAATCAGTGGGGCAAT  
 TTTGGTAAACCTTTTACAGGGAAGAGCAAATACCTCATGAAAAAAGTGAAGCA  
 TATTTTACAAAAGAACAAGAAAGTTCGAGATTCTTAAATACATTAAATGCCAT  
 ATGCAAAAGAGATTTTGAATGGACCAAGAAAGATATATCCCAATTTTATGTAT  
 ACACATAAAGGAGCAAGTACGCATTTCAGTGTGGAACCTTGCGAGATCTCTC  
 ATTATTTTGAATGAAATTTTAACTGGTGTTCGGGATTCGAGCGAAAACCATCC  
 ACAAGGGATTAAATTTATTTAGTTAAACGATATTCTTTAGATAAATCAATGAC  
 TTTATTACATAGGAGATCGTCCACTAGATTTCGGAGGTTGCTCAAAATGCTGG  
 TATAAATCCATAAACTTAAGGTTAGAGAATTCCAAAGAAAACATAATATTTCAG  
 TCTCAAGATATAATATCACTTGATTTCACCTCGTTTGGAT

Table 56: Comparative Sequences relating to SAG0806

TTGGAAACCTTGCAGATCTCTCATTATTTTGTGATAAAATTTAACTGGTGTTCGGGATTTC  
GAGCGAAAACCCACATCCACAAGGGATTAAATATTTAGTTAAACGATATCTTTAGATAAA  
TCAATGACTTATTACATAGGAGATCGTCCACTAGATTTGGAGGTTGCTCAAATGCTGGT  
ATAAAATCCATAAACTTAAGGTTAGAGAATTCCAAAGAAAACATAATATTTCAAGTCTC  
AAGATATAATATCACTTGATTTCACCTCGTTTGGAT

SEQ ID NO. 5607

STRAIN CJB110

AAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATT  
AATAGATTCGTATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGCTT  
AATATTTGATAAAGAATTAAATCCATGAATATATTTTACAGGAATCAGTGGGGCAATTATT  
GGTAAACCTTTTCAGAGGAAGAGCAAATACCTCATGAAAACTGAAAGCATAATTTTACAAA  
AGAACAAGAAAGTCGAGATTCTAAAATACATTTAATGCCATATGCAAAAGAGATTTTAGA  
ATGGACCAAGAACAAGATATCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCA  
TTCAGTGTGGAAACCTTGCAGATCTCTCATTTATTTGATGAAATTTTAACTGGTGTTC  
TGGATTTCGAGCGAAAACCATCCACAAGGGATTAAATATTTAGTTAAACGATATCTTT  
AGATAAATCAATGACTTATTTACATAGGAGATCGTCCCTAGATTGGAGGTTGCTCAA  
TGCTGGTATAAAATCCATAAACCTTAAGGTTAGAGAATTCCAAAGAAAACATAATATTT  
AAGTCTCAAGGATATAATATCACTTGATTTCACCTCGT

SEQ ID NO. 5608

STRAIN 1169NT

aAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAATAGATTCGTATGTACCAATTA  
TAGAAGCTCTTGAAGAAACCTATCGTCATTTTGGCTTAATATTTGATAAAGAATTAAATCC  
ATGAATATATTTTACAGGAATCAGTGGGGAAATTATTTGGTAAACCTTTTCAGAGGAAGAGC  
AAATACCTCATGAAAACTGAAAGCATATTTTACAAAAGAACAAAGTTCGAGATTCTA  
AAATACATTTTAAATGCCATACGCAAAAGAGATTTAGAATGGACCAAGAACAGATATCC  
CCAAATTTTATGTATACACATAAAGGAGCAAGTACGCATTGAGTGTGGAAACCTTGCAGA  
TCTCTCATTTTGTGATAAATTTAACTGGTGTTCGGGATTTCGAGCGAAAACCCACATC  
CACAAGGGATTAAATATTTAGTTAAACGATATCTTTAGATAAATCAATGACTTATTACA  
TAGGAGATCGTCCCTAGATTGGAGGTTGCTCAAATGCTGGTATAAAATCCATAAACT  
TAAGGTTAGAGAATTCCAAAGAAAACATAATATTTCAAGTCTCAAGGATATAATATCAC  
TTGATTTCACTCGTTTGGAT

SEQ ID NO. 5609

STRAIN JM9130013

AAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAATAGA  
TTGATGTATACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGTTTAAATATT  
TGATAAAGAATTAAATCCATGAATATATTTTACAGGAATCAGTGGGGAAATTATTTGGTAAA  
CCCTTTTCAGAGGAAGAGCAAATACCTCATGAAAACTGAAAGCATATTTTACAAAAGAAC  
AGAAAGTCGAGATTCTAAAATACATTTAATGCCATATGCAAAAGAGATTTAGAATGGAC  
CAAAGAACAAGATATCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATTGAGT  
GTTGGAACCTTGCAGATCTCTCATTTATTTGATGAAATTTAACTGGTGTTCGGGATT  
CGAGCGAAAACCATCCACAAGGGATTAAATATTTAGTTAAACGATATCTTTAGATAA  
ATCAATGACTTATTACATAGGAGATCGTCCACTAGATTTGGAGGTTGCTCAAATGCTGG  
TATAAAATCCATAAACTTAAGGTTAGAGAATTCCAAAGAAAACATAATATTTCAAGTCT  
CAAAGATATAATATCACTTGATTTCACCTCGT

SEQ ID NO. 5610

STRAIN 090

AAGAAGCTTACTTTTATTTGG  
GATTTAGATGGGACATTAATAGATTCGTATGTACCAATTATGGAAGCTCT  
TGAAGAAACCTATCGTCATTTTGGCTTAATATTTGATAAAGAATTAAATCC  
ATGAATATATTTTACAGGAATCAGTGGGGCAATTATTTGGTAAACCTTTCA  
GAGGAAGAGCAAATACCTCATGAAAACTGAAAGCATATTTTACAAAAGA  
ACAAAGAAAGTCGAGATTCTAAAATACATTTAATGCCATATGCAAAAGAGA  
TTTTAGAAATGGACCAAGAACAAAGATATCCCAATTTTATGTATACACAT  
AAAGGAGCAAGTACGCATTGAGTGTGGAAACCTTGCAGATCTCTCATTA  
TTTTGATGAAATTTTAACTGGTGTTCGAGTTCGAGCGAAAACCATC  
CACAAGGGATTAAATATTTAGTTAAACGATATCTTTAGATAAATCAATG  
ACTTATTACATAGGAGATCGTCCCTAGATTGGAGGTTGCTCAAATGCT  
TGGTATAAAATCCATAAACTTAAGGTTAGAGAATTCCAAAGAAAACATA  
ATATTTCAAGTCTCAAGGATATAATATCACTTGATTTCACCTCGT

SEQ ID NO. 5611

STRAIN M781

AAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAATAGATTCGT  
ATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGCTTA  
ATATTTGATAAAGAATTAAATCCATGAATATATTTTACAGGAATCAGTGGG  
GCAATTTATTTGGTAAACCTTTTCAGAGGAAGAGCAAATACCTCATGAAAAAC  
TGAAAGCATATTTTACAAAAGAACAAAGTTCGAGATTyTAAAATACAT  
TTAATGCCATATGCAAAAGAGATTTAGAATGGACCAAGAACAAAGATAT  
TCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATTGAGTGTGG  
AAACCTTGCAGATCTCTCATTTATTTGATGAAATTTTAACTGGTGTTCG  
GGATTTCGAGCGAAAACCATCCACAAGGGATTAAATATTTAGTTAAACG  
ATATTTCTTAGATAAATCAATGACTTATTACATAGGAGATCGTCCACTAG  
ATTTGGAGGTTGCTCAAATGCTGGTATAAAATCCATAAACTTAAGGTTA  
GAGAATTCCAAAGAAAACATAATATTTCAAGTCTCAAGATATAATATC  
ACTTGATTTCACTCGT

PRETTY of: /biotmp/msa45163.2{\*} January 21, 2003 06:53 ..

Table 56: Comparative Sequences relating to SAG0806

	1				50
msa45163.2{240_18RS21}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_2603}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_A909}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_H36B}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_JM9130013}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_COH1}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_M732}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_M781}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_090}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_CJB110}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_1169NT}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
Consensus	*****	*****	*****	*****	*****
	51				100
msa45163.2{240_18RS21}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGTTTAA
msa45163.2{240_2603}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGTTTAA
msa45163.2{240_A909}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGTTTAA
msa45163.2{240_H36B}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGTTTAA
msa45163.2{240_JM9130013}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGTTTAA
msa45163.2{240_COH1}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGTTTAA
msa45163.2{240_M732}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGTTTAA
msa45163.2{240_M781}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGTTTAA
msa45163.2{240_090}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGTTTAA
msa45163.2{240_CJB110}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGTTTAA
msa45163.2{240_1169NT}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGTTTAA
Consensus	*****	*****	*****	*****	*****
	101				150
msa45163.2{240_18RS21}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_2603}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_A909}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_H36B}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_JM9130013}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_COH1}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_M732}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_M781}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_090}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_CJB110}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_1169NT}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
Consensus	*****	*****	*****	*****	*****
	151				200
msa45163.2{240_18RS21}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_2603}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_A909}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_H36B}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_JM9130013}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_COH1}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_M732}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_M781}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_090}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_CJB110}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_1169NT}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
Consensus	*****	*****	*****	*****	*****
	201				250
msa45163.2{240_18RS21}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_2603}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_A909}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_H36B}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_JM9130013}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_COH1}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_M732}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_M781}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTyT	AAAATACATT
msa45163.2{240_090}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_CJB110}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_1169NT}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
Consensus	*****	*****	*****	*****	*****
	251				300
msa45163.2{240_18RS21}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_2603}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_A909}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_H36B}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_JM9130013}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_COH1}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_M732}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_M781}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_090}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_CJB110}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_1169NT}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
Consensus	*****	*****	*****	*****	*****

Table 56: Comparative Sequences relating to SAG0806

301						350					
msa45163.2{240_18RS21}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA						
msa45163.2{240_2603}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA						
msa45163.2{240_A909}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA						
msa45163.2{240_H36B}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA						
msa45163.2{240_JM9130013}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA						
msa45163.2{240_COH1}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA						
msa45163.2{240_M732}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA						
msa45163.2{240_M781}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA						
msa45163.2{240_090}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA						
msa45163.2{240_CJB110}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA						
msa45163.2{240_1169NT}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA						
Consensus	*****	*****	*****	*****	*****						
351						400					
msa45163.2{240_18RS21}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTAACT	GGTGTTCGg						
msa45163.2{240_2603}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTAACT	GGTGTTCGg						
msa45163.2{240_A909}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTAACT	GGTGTTCGg						
msa45163.2{240_H36B}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTAACT	GGTGTTCGg						
msa45163.2{240_JM9130013}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTAACT	GGTGTTCGg						
msa45163.2{240_COH1}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTAACT	GGTGTTCGg						
msa45163.2{240_M732}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTAACT	GGTGTTCGg						
msa45163.2{240_M781}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTAACT	GGTGTTCGg						
msa45163.2{240_090}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTAACT	GGTGTTCGg						
msa45163.2{240_CJB110}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTAACT	GGTGTTCGg						
msa45163.2{240_1169NT}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AATTTAACT	GGTGTTCGg						
Consensus	*****	*****	*****	*****	*****						
401						450					
msa45163.2{240_18RS21}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA						
msa45163.2{240_2603}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA						
msa45163.2{240_A909}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA						
msa45163.2{240_H36B}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA						
msa45163.2{240_JM9130013}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA						
msa45163.2{240_COH1}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA						
msa45163.2{240_M732}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA						
msa45163.2{240_M781}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA						
msa45163.2{240_090}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA						
msa45163.2{240_CJB110}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA						
msa45163.2{240_1169NT}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA						
Consensus	*****	*****	*****	*****	*****						
451						500					
msa45163.2{240_18RS21}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCaCTAGA						
msa45163.2{240_2603}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCaCTAGA						
msa45163.2{240_A909}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCaCTAGA						
msa45163.2{240_H36B}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCaCTAGA						
msa45163.2{240_JM9130013}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCaCTAGA						
msa45163.2{240_COH1}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCaCTAGA						
msa45163.2{240_M732}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCaCTAGA						
msa45163.2{240_M781}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCaCTAGA						
msa45163.2{240_090}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCcCTAGA						
msa45163.2{240_CJB110}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCcCTAGA						
msa45163.2{240_1169NT}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCcCTAGA						
Consensus	*****	*****	*****	*****	*****						
501						550					
msa45163.2{240_18RS21}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG						
msa45163.2{240_2603}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG						
msa45163.2{240_A909}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG						
msa45163.2{240_H36B}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG						
msa45163.2{240_JM9130013}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG						
msa45163.2{240_COH1}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG						
msa45163.2{240_M732}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG						
msa45163.2{240_M781}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG						
msa45163.2{240_090}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG						
msa45163.2{240_CJB110}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG						
msa45163.2{240_1169NT}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG						
Consensus	*****	*****	*****	*****	*****						
551						600					
msa45163.2{240_18RS21}	AGAATTCCAA	AGAAAACAT	AATATTTC	GTCTCAAaGA	TATAATATCA						
msa45163.2{240_2603}	AGAATTCCAA	AGAAAACAT	AATATTTC	GTCTCAAaGA	TATAATATCA						
msa45163.2{240_A909}	AGAATTCCAA	AGAAAACAT	AATATTTC	GTCTCAAaGA	TATAATATCA						
msa45163.2{240_H36B}	AGAATTCCAA	AGAAAACAT	AATATTTC	GTCTCAAaGA	TATAATATCA						
msa45163.2{240_JM9130013}	AGAATTCCAA	AGAAAACAT	AATATTTC	GTCTCAAaGA	TATAATATCA						
msa45163.2{240_COH1}	AGAATTCCAA	AGAAAACAT	AATATTTC	GTCTCAAaGA	TATAATATCA						
msa45163.2{240_M732}	AGAATTCCAA	AGAAAACAT	AATATTTC	GTCTCAAaGA	TATAATATCA						
msa45163.2{240_M781}	AGAATTCCAA	AGAAAACAT	AATATTTC	GTCTCAAaGA	TATAATATCA						
msa45163.2{240_090}	AGAATTCCAA	AGAAAACAT	AATATTTC	GTCTCAAaGA	TATAATATCA						
msa45163.2{240_CJB110}	AGAATTCCAA	AGAAAACAT	AATATTTC	GTCTCAAaGA	TATAATATCA						
msa45163.2{240_1169NT}	AGAATTCCAA	AGAAAACAT	AATATTTC	GTCTCAAaGA	TATAATATCA						

Table 56: Comparative Sequences relating to SAG0806

```

Consensus      *****
msa45163.2{240_18RS21} 601          621
msa45163.2{240_2603}  CTTGATTTCa CTCGTttgga t
msa45163.2{240_A909}  CTTGATTTCa CTCGT-----
msa45163.2{240_H36B}  CTTGATTTCa CTCGTttgga t
msa45163.2{240_JM9130013} CTTGATTTCa CTCGT-----
msa45163.2{240_COH1}  CTTGATTTCa CTCGTttgga t
msa45163.2{240_M732}  CTTGATTTCa CTCGTttgga t
msa45163.2{240_M781}  CTTGATTTCa CTCGT-----
msa45163.2{240_090}  CTTGATTTCa CTCGT-----
msa45163.2{240_CJB110} CTTGATTTCa CTCGTt-----
msa45163.2{240_1169NT} CTTGATTTCa CTCGTttgga t
Consensus      *****

```

## SEQ ID NO. 5612

STRAIN 2603 frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGKLLVNLSEEE  
 QIPHEKLYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ  
 ISHYFDEILTGVSGFERKPHPGQGINYLVKRYSLDKSMYYIGDRPLDLEVAQNAGIKSIN  
 LRLENSKENYNISLKDIIISLDFTRLD

## SEQ ID NO. 5613

STRAIN A909 frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGKLLVNLSEEE  
 QIPHEKLYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ  
 ISHYFDEILTGVSGFERKPHPGQGINYLVKRYSLDKSMYYIGDRPLDLEVAQNAGIKSIN  
 LRLENSKENYNISLKDIIISLDFTR

## SEQ ID NO. 5614

STRAIN H36B frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGKLLVNLSEEE  
 QIPHEKLYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ  
 ISHYFDEILTGVSGFERKPHPGQGINYLVKRYSLDKSMYYIGDRPLDLEVAQNAGIKSIN  
 LRLENSKENYNISLKDIIISLDFTRLD

## SEQ ID NO. 5615

STRAIN 18RS21 frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGKLLVNLSEEE  
 QIPHEKLYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ  
 ISHYFDEILTGVSGFERKPHPGQGINYLVKRYSLDKSMYYIGDRPLDLEVAQNAGIKSIN  
 LRLENSKENYNISLKDIIISLDFTRLD

## SEQ ID NO. 5616

STRAIN M732 frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGQLLVNLSEEE  
 QIPHEKLYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ  
 ISHYFDEILTGVSGFERKPHPGQGINYLVKRYSLDKSMYYIGDRPLDLEVAQNAGIKSIN  
 LRLENSKENYNISLKDIIISLDFTRLD

## SEQ ID NO. 5617

STRAIN COH1 frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGQLLVNLSEEE  
 QIPHEKLYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ  
 ISHYFDEILTGVSGFERKPHPGQGINYLVKRYSLDKSMYYIGDRPLDLEVAQNAGIKSIN  
 LRLENSKENYNISLKDIIISLDFTRLD

## SEQ ID NO. 5618

STRAIN CJB110 frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGQLLVNLSEEE  
 QIPHEKLYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ  
 ISHYFDEILTGVSGFERKPHPGQGINYLVKRYSLDKSMYYIGDRPLDLEVAQNAGIKSIN  
 LRLENSKENYNISLKDIIISLDFTR

## SEQ ID NO. 5619

STRAIN 1169NT frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGKLLVNLSEEE  
 QIPHEKLYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ  
 ISHYFDEILTGVSGFERKPHPGQGINYLVKRYSLDKSMYYIGDRPLDLEVAQNAGIKSIN  
 LRLENSKENYNISLKDIIISLDFTRLD

## SEQ ID NO. 5620

STRAIN JM9130013 frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGKLLVNLSEEE  
 QIPHEKLYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ  
 ISHYFDEILTGVSGFERKPHPGQGINYLVKRYSLDKSMYYIGDRPLDLEVAQNAGIKSIN  
 LRLENSKENYNISLKDIIISLDFTR

## SEQ ID NO. 5621

STRAIN 090 frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGQLLVNLSEEE  
 QIPHEKLYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ

Table 56: Comparative Sequences relating to SAG0806

ISHYFDEILTGVSGFERKPHPGQGINYLVKRYSLDKSMTYYIGDRPLDLEVAQNAGIKSIN  
LRLNSKENYNISSLKDIISLDFTR

SEQ ID NO. 5622

STRAIN M781 frame: 1

KKLTFIWDLDGTLIDSYPVIMEALEETRYRHFGFLIFDKELIHEYILQESVQGQLLVNLSEEE  
QIPHEKLKAYFTKEQESRDXXKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ  
ISHYFDEILTGVSGFERKPHPGQGINYLVKRYSLDKSMTYYIGDRPLDLEVAQNAGIKSIN  
LRLNSKENYNISSLKDIISLDFTR

PRETTY of: /biotmp/msa45645.2(\*) January 21, 2003 06:57 ..

	1				50
msa45645.2{240_18RS21}	KKLTFIWDLD	GTLDISYVPI	mEAL EETRYH	FGLIFDKELI	HEYILQESVG
msa45645.2{240_A909}	KKLTFIWDLD	GTLDISYVPI	mEAL EETRYH	FGLIFDKELI	HEYILQESVG
msa45645.2{240_JM9130013}	KKLTFIWDLD	GTLDISYVPI	mEAL EETRYH	FGLIFDKELI	HEYILQESVG
msa45645.2{240_2603}	KKLTFIWDLD	GTLDISYVPI	mEAL EETRYH	FGLIFDKELI	HEYILQESVG
msa45645.2{240_H36B}	KKLTFIWDLD	GTLDISYVPI	mEAL EETRYH	FGLIFDKELI	HEYILQESVG
msa45645.2{240_090}	KKLTFIWDLD	GTLDISYVPI	mEAL EETRYH	FGLIFDKELI	HEYILQESVG
msa45645.2{240_CJB110}	KKLTFIWDLD	GTLDISYVPI	mEAL EETRYH	FGLIFDKELI	HEYILQESVG
msa45645.2{240_M781}	KKLTFIWDLD	GTLDISYVPI	mEAL EETRYH	FGLIFDKELI	HEYILQESVG
msa45645.2{240_COH1}	KKLTFIWDLD	GTLDISYVPI	mEAL EETRYH	FGLIFDKELI	HEYILQESVG
msa45645.2{240_M732}	KKLTFIWDLD	GTLDISYVPI	mEAL EETRYH	FGLIFDKELI	HEYILQESVG
msa45645.2{240_1169NT}	KKLTFIWDLD	GTLDISYVPI	iEAL EETRYH	FGLIFDKELI	HEYILQESVG
Consensus	*****	*****	-*****	*****	*****
	51				100
msa45645.2{240_18RS21}	KLLVNLSEEE	QIPHEKLKAY	FTKEQESRDs	KIHLMPYAKE	ILEWTKEQDI
msa45645.2{240_A909}	KLLVNLSEEE	QIPHEKLKAY	FTKEQESRDs	KIHLMPYAKE	ILEWTKEQDI
msa45645.2{240_JM9130013}	KLLVNLSEEE	QIPHEKLKAY	FTKEQESRDs	KIHLMPYAKE	ILEWTKEQDI
msa45645.2{240_2603}	KLLVNLSEEE	QIPHEKLKAY	FTKEQESRDs	KIHLMPYAKE	ILEWTKEQDI
msa45645.2{240_H36B}	KLLVNLSEEE	QIPHEKLKAY	FTKEQESRDs	KIHLMPYAKE	ILEWTKEQDI
msa45645.2{240_090}	qLLVNLSEEE	QIPHEKLKAY	FTKEQESRDs	KIHLMPYAKE	ILEWTKEQDI
msa45645.2{240_CJB110}	qLLVNLSEEE	QIPHEKLKAY	FTKEQESRDs	KIHLMPYAKE	ILEWTKEQDI
msa45645.2{240_M781}	qLLVNLSEEE	QIPHEKLKAY	FTKEQESRDx	KIHLMPYAKE	ILEWTKEQDI
msa45645.2{240_COH1}	qLLVNLSEEE	QIPHEKLKAY	FTKEQESRDs	KIHLMPYAKE	ILEWTKEQDI
msa45645.2{240_M732}	qLLVNLSEEE	QIPHEKLKAY	FTKEQESRDs	KIHLMPYAKE	ILEWTKEQDI
msa45645.2{240_1169NT}	KLLVNLSEEE	QIPHEKLKAY	FTKEQESRDs	KIHLMPYAKE	ILEWTKEQDI
Consensus	-*****	*****	*****	*****	*****
	101				150
msa45645.2{240_18RS21}	PNFMYTHKGA	STHSVLETLQ	ISHYFDEILT	GVSGFERKPH	PQGINYLVKR
msa45645.2{240_A909}	PNFMYTHKGA	STHSVLETLQ	ISHYFDEILT	GVSGFERKPH	PQGINYLVKR
msa45645.2{240_JM9130013}	PNFMYTHKGA	STHSVLETLQ	ISHYFDEILT	GVSGFERKPH	PQGINYLVKR
msa45645.2{240_2603}	PNFMYTHKGA	STHSVLETLQ	ISHYFDEILT	GVSGFERKPH	PQGINYLVKR
msa45645.2{240_H36B}	PNFMYTHKGA	STHSVLETLQ	ISHYFDEILT	GVSGFERKPH	PQGINYLVKR
msa45645.2{240_090}	PNFMYTHKGA	STHSVLETLQ	ISHYFDEILT	GVSGFERKPH	PQGINYLVKR
msa45645.2{240_CJB110}	PNFMYTHKGA	STHSVLETLQ	ISHYFDEILT	GVSGFERKPH	PQGINYLVKR
msa45645.2{240_M781}	PNFMYTHKGA	STHSVLETLQ	ISHYFDEILT	GVSGFERKPH	PQGINYLVKR
msa45645.2{240_COH1}	PNFMYTHKGA	STHSVLETLQ	ISHYFDEILT	GVSGFERKPH	PQGINYLVKR
msa45645.2{240_M732}	PNFMYTHKGA	STHSVLETLQ	ISHYFDEILT	GVSGFERKPH	PQGINYLVKR
msa45645.2{240_1169NT}	PNFMYTHKGA	STHSVLETLQ	ISHYFDEILT	GVSGFERKPH	PQGINYLVKR
Consensus	*****	*****	*****	*****	*****
	151				200
msa45645.2{240_18RS21}	YSLDKSMTYY	IGDRPLDLEV	AQNAGIKSIN	LRLNSKENY	NISSLKDIIS
msa45645.2{240_A909}	YSLDKSMTYY	IGDRPLDLEV	AQNAGIKSIN	LRLNSKENY	NISSLKDIIS
msa45645.2{240_JM9130013}	YSLDKSMTYY	IGDRPLDLEV	AQNAGIKSIN	LRLNSKENY	NISSLKDIIS
msa45645.2{240_2603}	YSLDKSMTYY	IGDRPLDLEV	AQNAGIKSIN	LRLNSKENY	NISSLKDIIS
msa45645.2{240_H36B}	YSLDKSMTYY	IGDRPLDLEV	AQNAGIKSIN	LRLNSKENY	NISSLKDIIS
msa45645.2{240_090}	YSLDKSMTYY	IGDRPLDLEV	AQNAGIKSIN	LRLNSKENY	NISSLKDIIS
msa45645.2{240_CJB110}	YSLDKSMTYY	IGDRPLDLEV	AQNAGIKSIN	LRLNSKENY	NISSLKDIIS
msa45645.2{240_M781}	YSLDKSMTYY	IGDRPLDLEV	AQNAGIKSIN	LRLNSKENY	NISSLKDIIS
msa45645.2{240_COH1}	YSLDKSMTYY	IGDRPLDLEV	AQNAGIKSIN	LRLNSKENY	NISSLKDIIS
msa45645.2{240_M732}	YSLDKSMTYY	IGDRPLDLEV	AQNAGIKSIN	LRLNSKENY	NISSLKDIIS
msa45645.2{240_1169NT}	YSLDKSMTYY	IGDRPLDLEV	AQNAGIKSIN	LRLNSKENY	NISSLKDIIS
Consensus	*****	*****	*****	*****	*****
	201				
msa45645.2{240_18RS21}	LDFTRLd				
msa45645.2{240_A909}	LDFTTR--				
msa45645.2{240_JM9130013}	LDFTTR--				
msa45645.2{240_2603}	LDFTRLd				
msa45645.2{240_H36B}	LDFTRLd				
msa45645.2{240_090}	LDFTTR--				
msa45645.2{240_CJB110}	LDFTTR--				
msa45645.2{240_M781}	LDFTTR--				
msa45645.2{240_COH1}	LDFTRLd				
msa45645.2{240_M732}	LDFTRLd				
msa45645.2{240_1169NT}	LDFTRLd				
Consensus	*****				

Table 57: Comparative Sequences relating to SAG 1488

SEQ ID NO: 5701

STRAIN 2603

ATGCTTATGACAAAAATAATAGGACTGACAGGAGGGATAGCTTCT  
 GGAAGTCAACGGTAACAAAAATAATACGAGAATCAGGTTTAAAGTCATAGATGCGGAT  
 CAAGTGGTTTCATAAATTGCAAGCTAAGGGTGGGAACTTTACCAAGCTTTATTAGAATGG  
 TTGGGTCCCGAGATACCTGATGCTGATGGTGGAGTTGGATAGACCAAAGCTTTCTCAAATG  
 ATTTTTGGCTAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTGCT  
 CAAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAAACAGAAGAGATATTTTCATGGAT  
 ATTCCCTTTATTGATTGAAGAAAAGTATATAAAATGGTTTGGATGAGATTGGTTGGTATT  
 GTTGATAAAGAAAAACAATTACAAACGATTAAATGGCCCGTAACAACTACAGTCGAGAAGAA  
 GCAGAAATACGACTTTACACCAAAATGCCCTTTAACAGATAAAAAAGTTTCGCTAGTCTT  
 ATTATTGACAATAATGGTGATTATAAATCTTTAAAGAGCAAATATTGGATGCTCTTCAA  
 CGTTTA

SEQ ID NO: 5702

STRAIN 090

AAGTCAACGGTAACAAAAATAATACGAGAATCAG  
 GTTTTAAAGTCATAGATGCGGATCAAGTGGTTTCATAAATTGCAAGCTAAG  
 GGTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACCT  
 TGATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTGG  
 CTAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATT  
 CGTCAAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAAACAGAAGAGAT  
 ATTTTTCGTGGATATTCCCTTTATTGATTGAAGAAAAGTATATAAAATGGT  
 TTGATGAGATTGGTTGGTATTGTTGATAAAGAAAAACAATTACAAACGA  
 TTAATGGCCCGTAACAACTACAGTCGAGAAGAAGCAGAATTACGACTTTC  
 ACACCAAATGCCCTTTAACAGATAAAAAAGTTTCGCTAGTCTTATTATTA  
 ATAATAATGGTGATTATAAATCTTTAAAGAGCAAATATTGGATGCTCTT  
 CAACGTTTA

SEQ ID NO: 5703

STRAIN A909

AAGTCAACGGTAACAAAAATAATACGAGAATCAG  
 GTTTTAAAGTCATAGATGCGGATCAAGTGGTTTCATAAATTGCAAGCTAAG  
 GGTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACCT  
 TGATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTGG  
 CTAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATT  
 CGTCAAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAAACAGAAGAGAT  
 ATTTTTCATGGATATTCCCTTTATTGATTGAAGAAAAGTATATAAAATGGT  
 TTGATGAGATTGGTTGGTATTGTTGATAAAGAAAAACAATTACAAACGA  
 TTAATGGCCCGTAACAACTACAGTCGAGAAGAAGCAGAATTACGACTTTC  
 ACACCAAATGCCCTTTAACAGATAAAAAAGTTTCGCTAGTCTTATTATTA  
 ACAATAATGGTGATTATAAATCTTTAAAGAGCAAATATTGGATGCTCTT  
 CAACGTTTA

SEQ ID NO: 5704

STRAIN H36B

AAGTCAACGGTAACAAAAATAATACGAGAATCAGG  
 TTTTAAAGTCATAGATGCGGATCAAGTGGTTTCATAAATTGCAAGCTAAGG  
 GTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACCT  
 GATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTGG  
 TAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATT  
 GTCAAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAAACAGAAGAGATA  
 TTTTTCATGGATATTCCCTTTATTGATTGAAGAAAAGTATATAAAATGGT  
 TGATGAGATTGGTTGGTATTGTTGATAAAGAAAAACAATTACAAACGAT  
 TAATGGCCCGTAACAACTACAGTCGAGAAGAAGCGGAATTACGACTTTC  
 CACCAAATACCTTTAACAGATAAAAAAGTTTCGCTAGTCTTATTATTGA  
 TAATAATGGTGATTATAAATCTTTAAAGAGCAAATATTGGATGCTCTTC  
 AACGTTTA

SEQ ID NO: 5705

STRAIN 18RS21

AAGTCAACGGTAACAAAAATAATACGAGAATCAGG  
 TTTTAAAGTCATAGATGCGGATCAAGTGGTTTCATAAATTGCAAGCTAAGG  
 GTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACCT  
 GATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTGG  
 TAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATT  
 GTCAAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAAACAGAAGAGATA  
 TTTTTCATGGATATTCCCTTTATTGATTGAAGAAAAGTATATAAAATGGT  
 TGATGAGATTGGTTGGTATTGTTGATAAAGAAAAACAATTACAAACGAT  
 TAATGGCCCGTAACAACTACAGTCGAGAAGAAGCAGAATTACGACTTTC  
 CACCAAATACCTTTAACAGATAAAAAAGTTTCGCTAGTCTTATTATTGA  
 CAATAATGGTGATTATAAATCTTTAAAGAGCAAATATTGGATGCTCTTC  
 AACGTTTA

SEQ ID NO: 5706

STRAIN M732

AAGTCAACGGTAACAAAAATAATACGAGAATCAGGTT  
 TTTAAAGTCATAGATGCGGATCAAGTGGTTTCATAAATTGCAAGCTAAGGGT  
 GGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACCTGA  
 TGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTGGCTA  
 ATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTGCT  
 CAAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAAACAGAAGAGATATT



Table 57: Comparative Sequences relating to SAG 1488

TTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTTTG  
 ATGAGATTTGGTTGGTATTGTTGATAAAGAAAAACAATTACAACGATTA  
 ATGGCCCGTAACAACACTACAGTCGAGAAGAAGCAGAATTACGACTTTCACA  
 CCAAATGCCCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTGACA  
 ATAATGGTGATTTAATAACTTTAAAAAGAGCAAATATTGGATGCTCTTCAA  
 CGTTTA

SEQ ID NO: 5707

STRAIN COH1

AAGTCAACGGTAACAAAAATAATACGAGAATCAGGT  
 TTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAGGG  
 TGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTTG  
 ATGCTGATGGTGAGTTGGATAGACCAAGCTTTCTCAAATGATTTTGGCT  
 AATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTG  
 TCAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAACAGAAGAGATAT  
 TTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTTT  
 GATGAGATTTGGTTGGTATTGTTGATAAAGAAAAACAATTACAACGATT  
 AATGGCCCGTAAACAACACTACAGTCGAGAAGAAGCAGAATTACGACTTTCAC  
 ACCAAATGCCCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTGAC  
 AATAATGGTGATTTAATAACTTTAAAAAGAGCAAATATTGGATGCTCTTCA  
 ACGTTTA

SEQ ID NO: 5708

STRAIN M781

AAGTCAACGGTAACAAAAATAATACGAGAATCAGG  
 TTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAGG  
 GTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTT  
 GATGCTGATGGTGAGTTGGATAGACCAAGCTTTCTCAAATGATTTTGGC  
 TAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTG  
 GTCAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAACAGAAGAGATA  
 TTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTT  
 TGATGAGATTTGGTTGGTATTGTTGATAAAGAAAAACAATTACAACGAT  
 TAATGGCCCGTAACAACACTACAGTCGAGAAGAAGCAGAATTACGACTTTCAC  
 ACCAAATGCCCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTGA  
 CAATAATGGTGATTTAATAACTTTAAAAAGAGCAAATATTGGATGCTCTTC  
 AACGTTTA

SEQ ID NO: 5709

STRAIN CJB110

AAGTCAACGGTAACAAAAATAATACGAGAA  
 TCAGGTTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGC  
 TAAGGGTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGA  
 TACTTGATGCTGATGGTGAGTTGGATAGACCAAGCTTTCTCAAATGATT  
 TTTGCTAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTAT  
 CATTGCTCAAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAACAGAAG  
 AGATATTTTTCGTTGGATATTCCTTTATTGATTGAAGAAAAGTATATAAA  
 TGGTTTGATGAGATTTGGTTGGTATTGTTGATAAAGAAAAACAATTACA  
 ACGATTAAATGGCCCGTAAACAACACTACAGTCGAGAAGAAGCAGAATTACGAC  
 TTTTACACCAAATGCCCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATT  
 ATTAATAATAATGGTGATTTAATAACTTTAAAAAGAGCAAATATTGGATGCTCTTC  
 TCTTCAACGTTTA

SEQ ID NO: 5710

STRAIN 1169NT

AAGTCAACGGTAACAAAAATAATACGAGAATCAGG  
 TTTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAGG  
 GTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTT  
 GATGCTGATGGTGAGTTGGATAGACCAAGCTTTCTCAAATGATTTTGGC  
 TAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTG  
 GTCAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAACAGAAGAGATA  
 TTTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTT  
 TGATGAGATTTGGTTGGTATTGTTGATAAAGAAAAACAATTACAACGAT  
 TAATGGCCCGTAACAACACTACAGTCGAGAAGAAGCAGAATTACGACTTTCAC  
 CACCAAATACCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTGA  
 TAATAATGGTGATTTAATAACTTTAAAAAGAGCAAATGTTGGATGCTCTTC  
 AACGTTTA

SEQ ID NO: 5711

STRAIN JM9130013

AAGTCAACGGTAACAAAAATAATACGAGAATCAGGT  
 TTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAGGG  
 TGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTTG  
 ATGCTGATGGTGAGTTGGATAGACCAAGCTTTCTCAAATGATTTTGGCT  
 AATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTG  
 TCAAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAACAGAAGAGATAT  
 TTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTTT  
 GATGAGATTTGGTTGGTATTGTTGATAAAGAAAAACAATTACAACGATT  
 AATGGCCCGTAACAACACTACAGTCGAGAAGAAGCGGAATTACGACTTTCAC  
 ACCAAATACCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTGA  
 AATAATGGTGATTTAATAACTTTAAAAAGAGCAAATGTTGGATGCTCTTCA  
 ACGTTTA

Table 57: Comparative Sequences relating to SAG 1488

PRETTY of: /biotmp/msa221059.2{\*} February 10, 2003 07:07 ..

	1				50
msa221059.2{245_H36B}	-----	-----	-----	-----	-----AA
msa221059.2{245_JM9130013}	-----	-----	-----	-----	-----AA
msa221059.2{245_1169NT}	-----	-----	-----	-----	-----AA
msa221059.2{245_090}	-----	-----	-----	-----	-----AA
msa221059.2{245_CJB110}	-----	-----	-----	-----	-----AA
msa221059.2{245_18RS21}	-----	-----	-----	-----	-----AA
msa221059.2{245_2603}	atgctttatga	caaaaataat	aggactgaca	ggaggggatag	cttcttggaAA
msa221059.2{245_A909}	-----	-----	-----	-----	-----AA
msa221059.2{245_COH1}	-----	-----	-----	-----	-----AA
msa221059.2{245_M732}	-----	-----	-----	-----	-----AA
msa221059.2{245_M781}	-----	-----	-----	-----	-----AA
Consensus	*****	*****	*****	*****	*****
	51				100
msa221059.2{245_H36B}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTAAAA	GTCATAGATG
msa221059.2{245_JM9130013}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTAAAA	GTCATAGATG
msa221059.2{245_1169NT}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTAAAA	GTCATAGATG
msa221059.2{245_090}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTAAAA	GTCATAGATG
msa221059.2{245_CJB110}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTAAAA	GTCATAGATG
msa221059.2{245_18RS21}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTAAAA	GTCATAGATG
msa221059.2{245_2603}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTAAAA	GTCATAGATG
msa221059.2{245_A909}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTAAAA	GTCATAGATG
msa221059.2{245_COH1}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTAAAA	GTCATAGATG
msa221059.2{245_M732}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTAAAA	GTCATAGATG
msa221059.2{245_M781}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTAAAA	GTCATAGATG
Consensus	*****	*****	*****	*****	*****
	101				150
msa221059.2{245_H36B}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_JM9130013}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_1169NT}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_090}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_CJB110}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_18RS21}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_2603}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_A909}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_COH1}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_M732}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_M781}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
Consensus	*****	*****	*****	*****	*****
	151				200
msa221059.2{245_H36B}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_JM9130013}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_1169NT}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_090}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_CJB110}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_18RS21}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_2603}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_A909}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_COH1}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_M732}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_M781}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
Consensus	*****	*****	*****	*****	*****
	201				250
msa221059.2{245_H36B}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_JM9130013}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_1169NT}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_090}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_CJB110}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_18RS21}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_2603}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_A909}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_COH1}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_M732}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_M781}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
Consensus	*****	*****	*****	*****	*****
	251				300
msa221059.2{245_H36B}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_JM9130013}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_1169NT}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_090}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_CJB110}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_18RS21}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_2603}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_A909}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_COH1}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_M732}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT

Table 57: Comparative Sequences relating to SAG 1488

msa221059.2{245_M781}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
Consensus	*****	*****	*****	*****	*****
msa221059.2{245_H36B}	301				350
msa221059.2{245_JM9130013}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_1169NT}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_090}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCg	TGGATATTCC
msa221059.2{245_CJB110}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCg	TGGATATTCC
msa221059.2{245_18RS21}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_2603}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_A909}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_COH1}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_M732}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_M781}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
Consensus	*****	*****	*****	*****	*****
msa221059.2{245_H36B}	351				400
msa221059.2{245_JM9130013}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
msa221059.2{245_1169NT}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
msa221059.2{245_090}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
msa221059.2{245_CJB110}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
msa221059.2{245_18RS21}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
msa221059.2{245_2603}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
msa221059.2{245_A909}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
msa221059.2{245_COH1}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
msa221059.2{245_M732}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
msa221059.2{245_M781}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
Consensus	*****	*****	*****	*****	*****
msa221059.2{245_H36B}	401				450
msa221059.2{245_JM9130013}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_1169NT}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_090}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_CJB110}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_18RS21}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_2603}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_A909}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_COH1}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_M732}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_M781}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
Consensus	*****	*****	*****	*****	*****
msa221059.2{245_H36B}	451				500
msa221059.2{245_JM9130013}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TaCCTTTAAC
msa221059.2{245_1169NT}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TaCCTTTAAC
msa221059.2{245_090}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_CJB110}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_18RS21}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_2603}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_A909}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_COH1}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_M732}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_M781}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
Consensus	*****	*****	*****	*****	*-*****
msa221059.2{245_H36B}	501				550
msa221059.2{245_JM9130013}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAtAATAAT	GGTGATTTAA
msa221059.2{245_1169NT}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAtAATAAT	GGTGATTTAA
msa221059.2{245_090}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TaAtAATAAT	GGTGATTTAA
msa221059.2{245_CJB110}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TaAtAATAAT	GGTGATTTAA
msa221059.2{245_18RS21}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAcAATAAT	GGTGATTTAA
msa221059.2{245_2603}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAcAATAAT	GGTGATTTAA
msa221059.2{245_A909}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAcAATAAT	GGTGATTTAA
msa221059.2{245_COH1}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAcAATAAT	GGTGATTTAA
msa221059.2{245_M732}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAcAATAAT	GGTGATTTAA
msa221059.2{245_M781}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAcAATAAT	GGTGATTTAA
Consensus	*****	*****	*****	*-*****	*****
msa221059.2{245_H36B}	551				591
msa221059.2{245_JM9130013}	TAACTTTAAA	AGAGCAAATg	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_1169NT}	TAACTTTAAA	AGAGCAAATg	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_090}	TAACTTTAAA	AGAGCAAATa	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_CJB110}	TAACTTTAAA	AGAGCAAATa	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_18RS21}	TAACTTTAAA	AGAGCAAATa	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_2603}	TAACTTTAAA	AGAGCAAATa	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_A909}	TAACTTTAAA	AGAGCAAATa	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_COH1}	TAACTTTAAA	AGAGCAAATa	TTGGATGCTC	TTCAACGTTT	A

Table 57: Comparative Sequences relating to SAG 1488

```

msa221059.2{245_M732} TAACTTTAAA AGAGCAAATA TTGGATGCTC TTCAACGTTT A
msa221059.2{245_M781} TAACTTTAAA AGAGCAAATA TTGGATGCTC TTCAACGTTT A
Consensus *****- *****

```

## SEQ ID NO: 5712

STRAIN 2603 frame: 1

```

MLMTKIIIGLTGGIASGKSTVTTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPET
LDADGELDRPKLSQMI FANPDNMKTSARLQNSI IRQELACQDQLKQTEEFFMDIPLLI
EEKYIKWFDEIWLWVFDKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI IDNN
GDLITLKEQILDALQRL

```

## SEQ ID NO: 5713

STRAIN 090 frame: 1

```

KSTVTTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI
FANPDNMKTSARLQNSI IRQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI INNNGDLITLKEQILDALQ
L

```

## SEQ ID NO: 5714

STRAIN A909 frame: 1

```

KSTVTTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI
FANPDNMKTSARLQNSI IRQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI IDNNNGDLITLKEQILDALQ
L

```

## SEQ ID NO: 5715

STRAIN H36B frame: 1

```

KSTVTTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI
FANPDNMKTSARLQNSI IRQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD
DKEKQLQRLMARNNYSREEAELRLSHQIPLTDKKS FASLI IDNNNGDLITLKEQMLDALQ
L

```

## SEQ ID NO: 5716

STRAIN 18RS21 frame: 1

```

KSTVTTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI
FANPDNMKTSARLQNSI IRQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI IDNNNGDLITLKEQILDALQ
L

```

## SEQ ID NO: 5717

STRAIN M732 frame: 1

```

KSTVTTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI
FANPDNMKTSARLQNSI IRQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI IDNNNGDLITLKEQILDALQ
L

```

## SEQ ID NO: 5718

STRAIN COH1 frame: 1

```

KSTVTTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI
FANPDNMKTSARLQNSI IRQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI IDNNNGDLITLKEQILDALQ
L

```

## SEQ ID NO: 5719

STRAIN M781 frame: 1

```

KSTVTTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI
FANPDNMKTSARLQNSI IRQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI IDNNNGDLITLKEQILDALQ
L

```

## SEQ ID NO: 5720

STRAIN CJB110 frame: 1

```

KSTVTTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI
FANPDNMKTSARLQNSI IRQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI INNNGDLITLKEQILDALQ
L

```

## SEQ ID NO: 5721

STRAIN 1169NT frame: 1

```

KSTVTTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI
FANPDNMKTSARLQNSI IRQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD
DKEKQLQRLMARNNYSREEAELRLSHQIPLTDKKS FASLI IDNNNGDLITLKEQMLDALQ
L

```

## SEQ ID NO: 5722

STRAIN JM9130013 frame: 1

```

KSTVTTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI
FANPDNMKTSARLQNSI IRQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD
DKEKQLQRLMARNNYSREEAELRLSHQIPLTDKKS FASLI IDNNNGDLITLKEQMLDALQ
L

```

Table 57: Comparative Sequences relating to SAG 1488

PRETTY of: /biotmp/msa221398.2(\*) February 10, 2003 07:15 ..

```

1
msa221398.2{245_090} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_CJB110} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_1169NT} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_H36B} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_JM9130013} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_18RS21} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_2603} mlmtkiiglt ggiasgKSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_A909} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_COH1} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_M732} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_M781} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
Consensus *****

51
msa221398.2{245_090} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_CJB110} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_1169NT} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_H36B} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_JM9130013} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_18RS21} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_2603} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_A909} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_COH1} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_M732} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_M781} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
Consensus *****

101
msa221398.2{245_090} QRDQLKQTEE IFFvDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_CJB110} QRDQLKQTEE IFFvDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_1169NT} QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_H36B} QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_JM9130013} QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_18RS21} QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_2603} QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_A909} QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_COH1} QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_M732} QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_M781} QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
Consensus *****

151
msa221398.2{245_090} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
msa221398.2{245_CJB110} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
msa221398.2{245_1169NT} YSREEAELRL SHQiPLTDKK SFASLIIdNN GDLITLKEQm LDALQRL
msa221398.2{245_H36B} YSREEAELRL SHQiPLTDKK SFASLIIdNN GDLITLKEQm LDALQRL
msa221398.2{245_JM9130013} YSREEAELRL SHQiPLTDKK SFASLIIdNN GDLITLKEQm LDALQRL
msa221398.2{245_18RS21} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
msa221398.2{245_2603} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
msa221398.2{245_A909} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
msa221398.2{245_COH1} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
msa221398.2{245_M732} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
msa221398.2{245_M781} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
Consensus *****

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Table 58: Comparative Sequences relating to SAG0182

SEQ ID NO. 5801

STRAIN 2603

ATGTTGATGGTGTGTTATTCCAAAGGCTAGGAATTATTATGATTTTAGCCCTTTTATTG  
 GTAATAATAGTTATTTTAGACAGTTAATTGAAGAGCGGTCTAAACGTGAAACGGTAGTC  
 CTTGTTCATCATTTTCGGCTGTGTTGTTATATATCTAATATAACAGGAATTGAATAAAAA  
 GGGGATCGAAGTTTGGTCGAGCGCCCTTTCTAACAACGATTCTCATTCTGACTCACTT  
 GCTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCTCTGGTTGGA  
 TCAATTGTTGGTTTATTTGGAGGAGTTTCATCGCTTTTTCAGGAAGCTTTTCAGGTTCT  
 TTCTATATTGTTCAGTTTCAGTTCTAGTCGGCATTGTTAGCGGAAAGATTGGTGATAAGCTT  
 AAGGAAAACCATCTCTACCCCTTCAACAAGCCAAGTTATTTAATTAGTATTAATTGCCGAA  
 AGTATCCAGATGCTATTTGTTGGCATTTTTACAGGATGGGAACCTGTCAAATGATTGTC  
 ATTTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCCCTTGCAGTTTGTAAACT  
 TATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAGAGATGTTCTGAATTGACT  
 CGACAGACTCTGCCCTACCTTAGACAAGGTTTGACACCGCAATCTGCTAGGAGCGTTTGC  
 GAAATTATAAAGAGGCATACTAAGTTGATGCTGTGGGATTAAACAGATCGGTCAAACGTA  
 TTAGCTCATATTGGTGTGGCCATGATCACCATTATGTCAGGACAACCGGTCAAACAGAC  
 TTATCTAAAGTGTGTTATTTTGTATGGCGAACCAGAAATGCGCAAGATAAAGCGCGATT  
 TCTTGTCCAGATCACAACCTGTTCAGTTAAATCTGCTATTTGTAGTTCCTCTAAAAATAAAT  
 GATAAACTGTGGGTGCCCTTAAATGTACTTTGTCAGGAGATAAGCAATGTCTGAGGTG  
 GAGGAAAACCTAGTCTTGGTTTAGCGCAAATATTTTTCAGGACAACCTGGCAATGGGGATA  
 ACAGAGGAACAAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCAAAAATC  
 AACCTCATTTCTCTTTTAAATGCCATTAAACACAATTAGTGCAATTAATCCGTATTGATTCT  
 GATAAAGCAGTTATGCTAGTGCAGTTAAGTACTTTTGAAGCAAGTTTTCAGGGT  
 GGTTCAGGATCGTGAGGTAAAGCTTGAGCAAGAAAATCACATGTGGATGCTTATATGAAT  
 GTTGAAAAATTAAGTTTCCCTGATAAATATCAGTTATCTTATGATATTAGTGACCCAGAA  
 AAAATGAAGTTACCACTTTTGGTTTACAGGTACTGGTAGAGAAATGCAGTTTCGACATGCT  
 TTAAGAAACGTAAGACGGAACAACCATATATTGGTTCAAATAAAGCCAGATGGTCATTAT  
 TATTGTTGTTCTGTAGTGACAATGGACAAGGAATCTCAGATACTATCATTTGATAAATTA  
 GGTCAAGAAACAGTTGCAGAGAGTAAGGGTACAGGTACTGCTCTAGTTAATCTAAATAAC  
 AGGCTGAATTTATTATATGTTAGTGTAAAGTTGCCCTTCATTTTCAGCGCAAGAATGGT  
 ACAAAAGTTTGGTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAAT  
 TCT

SEQ ID NO. 5802

STRAIN 090

TTGATGGTGTGTTATTCCAAAGGCTAGGAATTATTAT  
 GATTTTAGCCCTTTTATTGGTAAATAATAGTTATTTTCAGACAGTTAATTG  
 AAGAGCGGTCTAAACGTGAAACGGTAGTACTTGTTCATCATTTTCGGCTTG  
 TTTGTTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAAG  
 TTTGGTCGAGCGCCCTTTCTAACAACGATTTCCTATTCTGACTCACTTG  
 CTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCT  
 CTGGTTGGATCAATTGTTGGTTTATTGGAGGAGTTTCATCGCTTTTTC  
 AGGAAGCTTTTCAGGTTCTTTCTATATTGTTCAGTTTCAGTTCTAGTCGGCA  
 TTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCCT  
 TCAACAAGCCAAGTTATTTAATTAGTATTATTGCCGAAAGTATCCAGAT  
 GCTATTGTTGGTATTTTACAGGATGGGAACCTGTCAAATGATTGTCA  
 TTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCCCTTGCAGATT  
 TTGAAAACCTTATTGTTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAG  
 AGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTCAGACAAGGTT  
 TGACACCGCAATCTGCTAGGAGCGTTTGCAGAAATTATAAAGAGGCATACT  
 AACTTTGATGCTGTAGGATTAAACAGATCGGTCAAACGTATTAGCTCATAT  
 TGGTGTGGCCATGATCACCATTATGTCAGGACAACAGTCAAACAGACC  
 TATCTAAAGTGTGTTATTTTGTATGGCGAACCAGAAATGCGCAAGATAAA  
 GCGGCGATTCTTGTCCAGATCACAACGTTCAGTTAAATCTGCTATTGTT  
 AGTTCCCTCTAAATAAATAAGATAAAACTGTGGGTGCCCTTAAATGTTACT  
 TTGAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTTGGT  
 TTAGCGCAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAACA  
 AATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAATCA  
 ACCCTCATTTCTCTTAAATGCCATTAAACCAATTAGTGCAATTAATCCGT  
 ATTGATTCTGATAAAGCAGTTATGTCAGTTCAGTTAAGTACTTTT  
 TAGAACAAGTTTTCAGGTTGGTCAGGATCGTGAGGTAACGCTTGAGCAAG  
 AAAATCACATGTGGATGCTTATATGAATGTTGAAAATTAAGTTTCCCT  
 GATAAATATCAGTTATCTTATGATATTAGTGACCCAGAAAAATGAAGTT  
 ACCGCTTTTGGTTTACAGGTAAGTTAGGAGAAATGCAAGTTAGACATGCTT  
 TCAAGAACGTAAGACGGAACAACCATATATTGGTTCAAATAAAGCCAGAT  
 GGTCAATTATTATGTTCTTCTGTTAGTGACAATGGACAAGGAATCTCAGA  
 TACTATCATTTGATAAATTAGGTCAAGAAACAGTTGTCAGAGAGTAAGGGTA  
 CAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGT  
 AGTGTAAAGTTGCCCTTCATTTTCAGGCGACAAGAAATGGTACAAAGTTTG  
 GTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAATT  
 CT

SEQ ID NO. 5803

STRAIN A909

TTGATGGTGTGTTATTCCAAAGGCTAGGAATTATTAT  
 GATTTTAGCCCTTTTATTGGTAAATAATAGTTATTTTCAGACAGTTAATTG  
 AAGAGCGGTCTAAACGTGAAACGGTAGTCTTGTTCATCATTTTCGGCTTG  
 TTTGTTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAAG  
 TTTGGTCGAGCGCCCTTTCTAACAACGATTTCCTATTCTGACTCACTTG  
 CTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCT  
 CTGGTTGGATCAATTGTTGGTTTATTGGAGGAGTTTCATCGCTTTTTC  
 AGGAAGCTTTTCAGGTTCTTTCTATATTGTTCAGTTTCAGTTCTAGTCGGCA  
 TTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCCT

Table 58: Comparative Sequences relating to SAG0182

TCAACAAGCCAAGTTATTTTAATTAGTATTATGCGGAAAGTATCCAGAT  
 GCTATTTGTTGGCAATTTTACAGGATGGGAACCTTGTCAAAATGATTGTCA  
 TTCCAAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCCTTGGGATT  
 TTGAAAACCTTATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAG  
 AGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGGTT  
 TGACACCGCAATCTGTAGGAGCGTTTTCGAAATTATAAAGAGGCATACT  
 AACCTTTGATGCTGTGGGATTAACAGATCGGTCAAACGTATTAGCTCATAT  
 TGGTGTGGCCATGATCACCATATTGCAGGACAACCGGTCAAACAGACT  
 TATCTAAAAGTGTATTTTGTATGGCGAACCAAGAATTGCGCAAGATAAA  
 GCGCGCATTTCTGTCCAGATCACAACTGTCAAGTTAAATTCGTATTGT  
 AGTTCTCTAAAAATAAATGATAAACTGTGGGTGCCCTTAAAAATGTACT  
 TTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTTGGT  
 TTAGCGCAAAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAACA  
 AAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAATCA  
 ACCCTCATTTCTTCTTAATGCCATTAAACACAATTAGTGCATTAAATCCGT  
 ATTGATTCTGATAAAGCACGTTATGCACCTGATGCAGTTAAGTACTTTTTT  
 TAGAACCAAGTTTGCAGGGTGGTCAAGGATCGTGAGGTAACGCTTGAGCAAG  
 AAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCT  
 GATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAATGAAGTT  
 ACCACCTTTTGGTTTACAGGTAAGTGTAGAGAATGCAGTTGCACATGCTT  
 TCAAAGAGACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGAT  
 GGTCAATTATTATGTGTTCTGTAGTGACAATGGACAAGGAATCTCAGA  
 TACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGGTAAGGGTA  
 CAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGT  
 AGTGTAAGTTGCCCTTCAATTTTTCGAGCGACAAGAAATGGTACAAAAGTTTG  
 GTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAAATTTTAATT  
 CT

SEQ ID NO. 5804

STRAIN H36B

TTGATGGTGTGTTTATTTCCAAAGGCTAGGAATTATTATG  
 ATTTTAGCCCTTTTATTTGGTAAATAATAGTTATTTTCAGACAGTTAATTGA  
 AGAGCGGTCTAAACGTTGAAACGGTAGTCTTGTCTCATCTTTTCGGCTTGT  
 TTGTTATTTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAAGT  
 TTGGTTCGAGCGCCCTTTTCTAACACGATTTCTCATTTCTGACTCACTTGC  
 TAATACAAGGACTTTAGTTATTACAAACGGCAAGTTTGGTTGGTGGACCTC  
 TGGTTGGATCAATTTGTTGGTTTATTTGGAGGAGTTTCATCGCTTTTTTCAA  
 GGAAGCTTTTCAGGTTCTTTCTATATTGTCTAGTTTCTAGTCTCGGCAT  
 TGGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCCT  
 CAACAAGCCAAGTTATTTTAATTAGTATTATTGCCGAAAGTATCCAGATG  
 CTATTTGTTGGCAATTTTACAGGATGGGAACTTGTCAAAATGATTGTCTAT  
 TCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTGGCATT  
 TGAAAACCTTATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAGA  
 GATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGGTTT  
 GACACCGCAATCTGCTAGGAGCGTTTTCGAAATTATAAAGAGGCATACTA  
 ACTTTGATGCTGTGGGATTAAACAGATCGGTCAAACGTATTAGCTCATATT  
 GGTGTTGGCCATGATCACCATATTGCAGGACAACCGGTCAAACAGACTT  
 ATCTAAAAGTGTATTTTGTATGGCGAACCAAGAATTGCGCAAGATAAAG  
 CGGCGATTTCTTGTCCAGATCACAACTGTCAAGTTAAATTCGTCTATTGTA  
 GTTCTCTAAAAATAAATGATAAACTGTGGGTGCCCTTAAAAATGTACTT  
 TGCAAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTTGGTT  
 TAGCGCAAAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAACA  
 AATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAATCAA  
 CCCTCATTTCTTCTTAAATGCCATTAAACACAATTAGTGCATTAAATCCGTA  
 TTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTTTT  
 AGAACCAAGTTTGCAGGGTGGTCAAGGATCGTGAGGTAACGCTTGAGCAAGA  
 AAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCTG  
 ATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAATGAAGTTA  
 CCACCTTTTGGTTTACAGGTAAGTGTAGAGAATGCAGTTTCGACATGCTTT  
 CAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGATG  
 GTCATTATTATTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAGAT  
 ACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGGTAC  
 AGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGTA  
 GTGTAAGTTGCCCTTCAATTTTTCGAGCGACAAGAAATGGTACAAAAGTTTG  
 TATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAAATTTTAATTC  
 T

SEQ ID NO. 5805

STRAIN 18RS21

TTGATGGTGTGTTTATTTCCAAAGGCTAGGAATTATTATG  
 ATTTTAGCCCTTTTATTTGGTAAATAATAGTTATTTTACAGGTTAATTGA  
 AGAGCGGTCTAAACGTTGAAACGGTAGTCTTGTCTCATCTTTTCGGCTTGT  
 TTGTTATTTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAAGT  
 TTGGTTCGAGCGCCCTTTTCTAACACGATTTCTCATTTCTGACTCACTTGC  
 TAATACAAGGACTTTAGTTATTACAAACGGCAAGTTTGGTTGGTGGACCTC  
 TGGTTGGATCAATTTGTTGGTTTATTTGGAGGAGTTTCATCGCTTTTTTCAA  
 GGAAGCTTTTTCAGGTTCTTTCTATATTGTCTAGTTTCTAGTCTCGGCAT  
 TGTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCCT  
 CAACAAGCCAAGTTATTTTAATTAGTATTATTGCCGAAAGTATCCAGATG  
 CTATTTGTTGGCAATTTTACAGGATGGGAACTTGTCAAATGATTGTCTAT  
 TCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTGGCATT  
 TGAAAACCTTATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAGA  
 GATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGGTTT

Table 58: Comparative Sequences relating to SAG0182

GACACCGCAATCTGCTAGGAGCGTTTGCAGAAATTATAAGAGGCATACTA  
 ACTTTTGATGCTGTGGGATTAAACAGATCGGTCAAACGTATTAGCTCATATT  
 GGTGTTGGCCATGATCACCATATTGCAGGACAACCGGTCAAAACAGACTT  
 ATCTAAAAGTGTATTATTTTGTATGGCGAACCAAGATTGCGCAAGATAAAG  
 CGGCGATTCTTGTCCAGATCACAACTGT CAGTTAAATTCTGCTATTGTA  
 GTTCCTCTAAAAATAAATGATAAACTGTGGTGCCTTAAAAATGTACTT  
 TGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTTGGTT  
 TAGCGCAAAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAACAA  
 AATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCAAAATCAA  
 CCTCATTTCTTCTTAATGCCATTAAACAAATTAGTGCATTATCCGTA  
 TTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTTTT  
 AGAACCAAGTTTGCAGGGTGGTCAGGATCGTGAGGTAAACGCTTGAGCAAGA  
 AAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCTG  
 ATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAAATGAAGTTA  
 CCACCTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTCGACATGCTTT  
 CAAAGAACGTAAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGATG  
 GTCATTATTATTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAGAT  
 ACTATCATTTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGGTAC  
 AGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGTA  
 GTGTAAGTTGCTTCTATTTTTCGAGCGACAAGATGGTACAAAAGTTTGG  
 TATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAATTC  
 T

SEQ ID NO. 5806

STRAIN M732

TTGATGGTGTGTTATTCCAAAGGCTAGGAATTATTATGAT  
 TTTAGCCTTTTATTGGTAAATAATAGTTAATTCAGACAGTTAATTGAAG  
 AGCGGTCTAAACGTGAAACGGTAGTCTTGTTCATCATTTTCGGCTTGT  
 GTTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAAGTTT  
 GGTGCGAGCGCCCTTTTCTAACACAGATTCCCATTTCTGACTCAGTTGCTA  
 ATCAAGGACITTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCTCTG  
 GTTGGATCAATTGTTGGTTTATTGGAGGAGTTTATCGCTTTTTTCAAGG  
 AAGCTTTTCAGGTTCTTTCTATATTGT CAGTTCAAGTTCTAGTGGCATTG  
 TTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAAACCATCTCTACCTTCA  
 ACAAGCCAAGTTATTTTAATTAGTATTATTGCGGAAAGTATCCAGATGCT  
 ATTTGTTGGCATTTTTTACAGGATGGGAACCTTGTCAAATGATTGTCAATC  
 CAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTGGCATTG  
 AAAACTTATTGTTCAATGAAAGTCAGTTACGCGCAGTTCAAACGAGAGA  
 TGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGGTTTGA  
 CACCGCAATCTGCTAGGAGCGTTTGCAGAAATTATAAGAGGCATACTAAC  
 TTTGATGCTGTGGGATTAAACAGATCGGTCAAACGTATTAGCTCATATTGG  
 TATTGGCCATGATCACCATTATGCAGGACAACCGGTCAAACAGACTTAT  
 CTAAAAAGTGTATTTTTGTATGGCGAACCAAGAATTGCGCAAGATAAAGCG  
 GCGAATTCTTGTCCAGATCACAACTGT CAGTTAAATTCTGCTATTGTAGT  
 TCCCTCTAAAAATAAATGATAAACTGTGTGTGCCCTTAAAAATGTACTTTG  
 CAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTTGGTTTA  
 GCGCAAAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAACAAA  
 TAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCAAAATCAACC  
 CTCATTTCTTCTTAATGCCATTAAACAAATTAGTGCATTATCCGTATT  
 GATTCTGATAAAGCAGTTATGCACTGATGCAGTTAAGTACTTTTTTTAG  
 AACAGTTTGCAGGTGGTCAGGATCGTGAGGTAAACGCTTGAGCAAGAAA  
 AATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCTGAT  
 AAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAAATGAAGTTACC  
 GCCTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTCGACATGCTTTCA  
 AAGAACGTAAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGATGGT  
 CATATTATTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAGATAC  
 TATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGGACAG  
 GTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGTAGT  
 GTAAAGTTGCCCTTCATTTTTCGAGCGACAAGAAATGGTACAAAAGTTTGGTA  
 TCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAATTC

SEQ ID NO. 5807

STRAIN COH1

TTGATGGTGTGTTATTCCAAAGGCTAGGAATTAT  
 TATGATTTTAGCCTTTTATTGGTAAATAATAGTTAATTCAGACAGTTAA  
 TTGAAGAGCGGTCTAAACGTGAAACGGTAGTCTTGTTCATCATTTTCGGC  
 TTGTTTGTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCG  
 AAGTTTGGTTCGAGCGCCCTTTTCTAACACAGATTCCCATTTCTGACTCAC  
 TTGCTAATACAAGGACITTAGTTATTACAACGGCAAGTTTGGTTGGTGGGA  
 CCTCTGGTTGGATCAATTGTTGGTTTATTGGAGGAGTTTATCGCTTTTTT  
 TCAAGGAAGCTTTTCAGGTTCTTTCTATATTGT CAGTTCAAGTTCTAGTGG  
 GCATTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAAACCATCTCTAC  
 CCTTCAACAGCAAGTTAATTTAATTAGTATTATTGCCGAAAGTATCCA  
 GATGCTATTGTTGGCATTTTTACAGGATGGGAACCTTGTCAAATGATTG  
 TCAATTCGAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTGGC  
 ATTTTGAACCTTATTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAAC  
 GAGAGATGTTCTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAG  
 GTTTGACACCGCAATCTGCTAGGAGCGTTTGCAGAAATTATAAAGAGGCAT  
 ACTAATCTTGATGCTGTGGGATTAAACAGATCGGTCAAACGTATTAGCTCA  
 TATTGGTGTGGCCATGATCACCATTATGCAGGACAACCGGTCAAACAG  
 ACTTATCTAAAAGTGTATTTTTGTATGGCGAACCAAGAATTGCGCAAGAT  
 AAAGCGCGGATTCTTGTCCAGATCACAACTGT CAGTTAAATTCTGCTAT  
 TGTAGTTCTCTAAAAATAAATGATAAACTGTGTGTGCCCTTAAAAATGT



Table 58: Comparative Sequences relating to SAG0182

ACTTTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCCTT  
GGTTTAGCGCAAAATATTTTCAGGACCACTGGCAATGGGGATAACAGAGGA  
ACAAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAA  
TCAACCCCTCATTTCTTCTTTAATGCCATTAAACACAATTAGTGCATTAAATC  
CGTATTGATTCTGATAAAGCACGTTATGCACGTGATGCAGTTAAGTACTTT  
TTTTAGAACAAGTTTGCAAGGTGGTCAGGATCGTGAGGTAACGCTTGAGC  
AAGAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTC  
CCTGATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAATGAA  
GTTACCGCCTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTTCGACATG  
CTTTCAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCA  
GATGGTCATTATTATGTGTTTCTGTTAGTGACAATGGACAAGGAATCTC  
AGATACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGG  
GGACAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATAT  
GGTAGTGTAAAGTTGCCTTCATTTTCGAGCGACAAGAATGGTACAAAAGT  
TTGGTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAAATTTA  
ATTCT

SEQ ID NO. 5808

STRAIN M781

TTGATGGTGTGTTATTCCAAAGGCTAGGAATTATTA  
TGATTTAGCCTTTTATTGGTAAATAATAGTTATTTTCAGACAGTTAATT  
GAAGAGCGGTCTAAACGTGAAACGGTAGTCCCTGTGTCATCATTTTCGGCTT  
GTTTGTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAA  
GTTTGGTCGAGCGCCCTTTTCTAACAACGATTTCCTATTCTGACTCACTT  
GCTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACC  
TCTGGTTGGATCAATTGTTGGTTTATTGGAGGAGTTTCATCGCTTTTTC  
AAGGAAGCTTTTCAGGTTCTTTCTATATGTCAGTTTCAGTTCTAGTCGGC  
ATTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCC  
TTCAACAAGCCAAAGTTATTTAATTAGTATTATTGCCGAAAGTATCCAGA  
TGCATATTGTTGGCATTTTACAGGATGGGAACCTGTCAAATGATTGTC  
ATTCCAATGATGATTTAATAAGTTTAGGTTCCACACTTTTCCTTGCGAT  
TTTGAAAACCTTATTGTCAAATGAAAGTCAGTTACGCGCAGTCAAAACGA  
GAGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGGT  
TTGACACCGCAATCTGCTAGGAGCGTTTGGGAAATATAAAGAGGCATAC  
TAACTTTGATGCTGTGGGATTAACAGATCGGTCAAACGTATTAGTCTATA  
TTGGTGTGGCCATGATCACCATATTGCGAGCAACCGGTCAAACAGAC  
TTATCTAAAAGTGTATTTTTGATGGCGAACCAGAAATTGCGCAAGATAA  
AGCGGCGATTCTTGTCCAGATCACAACTGTCAGTTAAATCTGCTATTG  
TAGTTCCTCTAAAAATAAATGATAAACTGTGTGTCCTTAAAAATGTAC  
TTTGCAAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTTGG  
TTTAGCGCAAAATATTTTCAGGACAACCTGGCAATGGGATAACAGAGGAAC  
AAAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAATC  
AACCCTCATTTCTTCTTTAATGCCATTAAACACAATTAGTGCATTAAATCG  
TATTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTT  
TTAGAACAAGTTTGCAAGGTGGTCAGGATCGTGAGGTAACGCTTGAGCAA  
GAAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCC  
TGATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAATGAAGT  
TACCGCCTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTTCGACATGCT  
TTCAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGA  
TGGTCATTATTATTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAG  
ATACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGGG  
ACAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGG  
TAGTGTAAAGTTGCCCTTCATTTTCGAGCGACAAGAATGGTACAAAAGTTT  
GGTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAAATTTAAT  
TCT

SEQ ID NO. 5809

STRAIN CJB110

TTGATGGTGTGTTATTCCAAAGGCTAGGAATTATTAT  
GATTTTAGCCTTTTATTGGTAAATAATAGTTATTTTCAGACAGTTAATTG  
AAGAGCGGTCTAAACGTGAAACGGTAGTACTTGTGTCATCATTTTCGGCTTG  
TTTGTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAAG  
TTTGGTCGAGCGCCCTTTTCTAACAACGATTTCCTATTCTGACTCACTTG  
CTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCT  
CTGGTTGGATCAATTGTTGGTTTATTGGAGGAGTTTCATCGCTTTTTC  
AGGAAGCTTTTCAGGTTCTTTCTATATTGTGAGTTTCAGTTCTAGTCGGCA  
TTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCCT  
TCAACAAGCCAAAGTTATTTAATTAGTATTATTGCCGAAAGTATCCAGAT  
GCTATTGTTGGTATTTTTACAGGATGGGAACCTGTCAAATGATTGTCA  
TTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCCTTGCGATT  
TTGAAAACCTTATTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAG  
AGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTCAGACAAGGTT  
TGACACCGCAATCTGCTAGGAGCGTTTGGGAAATATAAAGAGGCATAC  
AACTTTGATGCTGTAGGATTAACAGATCGGTCAAACGTATTAGCTCATAT  
TGGTGTGGCCCATGATCACCATATTGCAGGACAACCACTCAAACAGACC  
TATCTAAAAGTGTATTTTTGTGCGCAACCAAGAATTGCGCAAGATAAA  
CGGCGGATTTCTGTCCAGATCACAACTGTCAAGTTAAATCTGCTATTGT  
AGTTCTCTAAAAATAAATGATAAACTGTGGGTGCCCTTAAAAATGTACT  
TTGCAAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTTGGT  
TTAGCGCAAAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAACA  
AAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAATCA  
ACCTCATTTTTTCTTTAATGCCATTAAACACAATTAGTGCATTAAATCCGT  
ATTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTTT

Table 58: Comparative Sequences relating to SAG0182

TAGAACAAGTTTTCGAAGGTGGTCAGGATCGTGAGGTAACGCTTGAGCAAG  
 AAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCT  
 GATAAATATCAGTTATCTTATGATATTAGTGACCCAGAAAAAATGAAGTT  
 ACCGCCCTTTGGTTTACAGGTAAGTGGTAGAATGCAGTTAGACATGCTT  
 TCAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGAT  
 GGTCAATTATTTATGTTTCTGTTAGTGACAATGGACAAGGAATCTCAGA  
 TACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGGTA  
 CAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATATATGTT  
 AGTGTAAAGTTGCCCTTCATTTTTCGAGCGACAAGAATGTTACAAAAGTTTG  
 GTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAAATTTTAAAT  
 CT

SEQ ID NO. 5810

STRAIN 1169NT

TTGATGGTGTGTTATTCCAAAGGCTAGGAATTATT  
 ATGATTTTAGCCCTTTTATTGGTAATAATAGTTATTTCAGACAGTTAAT  
 TGAAGAGCGGTCTAAACGTGAAACGGTAGTACTTGTATCATTTTCGGCT  
 TGTTTGTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGA  
 AGTTTGGTCGAGCGCCCTTTTCTAACAACGATTTCTCATTTCTGACTCACT  
 TGCTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGAC  
 CTCTGGTTGGATCAATTGTTGGTTTTATTGGAGGAGTTTCATCGCTTTTT  
 CAAGGAAGCTTTTCAGGTTCTTTCTATATTGTCAAGTTCAAGTTCTAGTCGG  
 CATTTGTGAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACC  
 CTTCAACAAGCCAAGTTATTTTAATTAGTATTATTGCGGAAAGTATCCAG  
 ATGCTATTTGTTGGCATTTTTACAGGATGGGAACCTGTCAAATGATTGT  
 CATTTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTTCGCA  
 TTTTGAAAACTTATTGTTCAAAATGAAAGTCAGTTACGCGCAGTTCAAACG  
 AGAGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGG  
 TTTGACACCGCAATCTGCTAGGAGCGTTTGCAGAAATTATAAAGAGGCATA  
 CTAATTTTGATGCTGTGGGATTAAACAGATCGGTCAAACGTATTAGCTCAT  
 ATTGGTGTGGCCATGATCACCATATTGCAGGACAACCAAGTCAAAACAGA  
 CCTATCTAAAGTGTATTATTGATGGCGAACCAGAAATTGCGCAAGATA  
 AAGCGGCGATTCTTGTCCAGATCACAACTGTCAAGTTAAATTCTGCTATT  
 GTAGTTCTCTAAAAATAAATGATAAACTGTGGGTGCCCTAAAAATGTA  
 CTTTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTCTTG  
 GTTTAGCGCAAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAA  
 CAAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAAT  
 CAACCTCATTTCTCTTTAATGCCATTAAACAATTAGTGCATTATATCC  
 GTATTGATTTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTT  
 TTTAGAACCAAGTTTGCAGGTGGTCAGGATCGTGAGGTAAACGCTTGAGCA  
 AGAAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCC  
 CTGATAAATATCAGTTATCTTATGATATTAGTGACCCAGAAAAAATGAAG  
 TTACCGCCCTTTTGGTTTACAGGTAAGTGGTAGAATGCAGTTTCGACATGC  
 TTTTAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAG  
 ATGGTCATTATTATTTGTTTCTGTTAGTGACAATGGACAAGGAATCTCA  
 GATACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGG  
 TACAGGTAAGTCTCTAGTTAATCTAAATAACAGGCTGAATTTATATATG  
 GTAGTGTAAAGTTGCCCTTCATTTTTCGAGCGACAAGAATGGTACAAAAGTT  
 TGGTATCGAATACCTAATAGAATAAAGGGAGGATGAGCATGAAAAATTTTAA  
 TTCT

SEQ ID NO. 5810

STRAIN JM9130013

TTGATGGTGTGTTATTCCAAAGGCTAGGAATTATT  
 ATGATTTTAGCCCTTTTATTGGTAATAATAGTTATTTCAGACAGTTAAT  
 TGAAGAGCGGTCTAAACGTGAAACGGTAGTCTTGTATCATTTTCGGCT  
 TGTTTGTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGA  
 AGTTTGGTCGAGCGCCCTTTTCTAACAACGATTTCTCATTTCTGACTCACT  
 TGCTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGAC  
 CTCTGGTTGGATCAATTGTTGGTTTTATTGGAGGAGTTTCATCGCTTTTT  
 CAAGGAAGCTTTTCAGGTTCTTTCTATATTGTCAAGTTCAAGTTCTAGTCGG  
 CATTTGTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACC  
 CTTCAACAAGCCAAGTTATTTTAATTAGTATTATTGCGGAAAGTATCCAG  
 ATGCTATTGTTGGCATTTTTACAGGATGGGAACCTGTCAAATGATTGT  
 CATTTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTTCGCA  
 TTTTGAAAACTTATTGTTCAAAATGAAAGTCAGTTACGCGCAGTTCAAACG  
 AGAGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGG  
 TTTGACACCGCAATCTGCTAGGAGCGTTTGCAGAAATTATAAAGAGGCATA  
 CTAACCTTTGATGCTGTGGGATTAAACAGATCGGTCAAACGTATTAGCTCAT  
 ATTGGTGTGGCCATGATCACCATATTGCAGGACAACCGGTCAAAACAGA  
 CTTATCTAAAGTGTATTATTGATGGCGAACCAGAAATTGCGCAAGATA  
 AAGCGGCGATTCTTGTCCAGATCACAACTGTCAAGTTAAATTCTGCTATT  
 GTAGTTCTCTAAAAATAAATGATAAACTGTGGGTGCCCTAAAAATGTA  
 CTTTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTCTTG  
 GTTTAGCGCAAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAA  
 CAAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAAT  
 CAACCTCATTTCTCTTTAATGCCATTAAACAATTAGTGCATTATATCC  
 GTATTGATTTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTT  
 TTTAGAACCAAGTTTGCAGGTGGTCAGGATCGTGAGGTAAACGCTTGAGCA  
 agAAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCC  
 CTGATAAATATCAGTTATCTTATGATATTAGTGACCCAGAAAAAATGAAG  
 TTACCACTTTTGGTTTACAGGTAAGTGGTAGAATGCAGTTTCGACATGC  
 TTTCAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAG

Table 58: Comparative Sequences relating to SAG0182

ATGGTCATTATTATTGTTCTGTTAGTGACAATGGACAAGGAATCTCA  
 GATACATCATTCATTGATAAATTAGGCTCAAGAAACAGTTGCGAGAGTAGGAGG  
 TACAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATG  
 GTAGTGTAAAGTTGCTTCTATTTTCGAGCGACAAGAAATGGTACAAAAGTT  
 TGGTATCGAATACCTAATAGAATAAGGAGGATGAGCATGAAAATTTTAA  
 TTCT

## MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa442667.2{\*} January 13, 2003 06:34 ..

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1                                     50
msa442667.2{248_18RS21} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_2603} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_A909} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_H36B} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_JM9130013} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_COH1} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_M781} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_M732} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_090} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_CJB110} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_1169NT} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
Consensus *****

51                                     100
msa442667.2{248_18RS21} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_2603} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_A909} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_H36B} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_JM9130013} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_COH1} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_M781} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_M732} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_090} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_CJB110} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_1169NT} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
Consensus *****

101                                    150
msa442667.2{248_18RS21} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_2603} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_A909} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_H36B} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_JM9130013} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_COH1} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_M781} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_M732} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_090} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_CJB110} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_1169NT} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
Consensus *****

151                                    200
msa442667.2{248_18RS21} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_2603} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_A909} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_H36B} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_JM9130013} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_COH1} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_M781} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_M732} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_090} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_CJB110} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_1169NT} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
Consensus *****

201                                    250
msa442667.2{248_18RS21} CCCTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_2603} CCCTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_A909} CCCTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_H36B} CCCTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_JM9130013} CCCTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_COH1} CCCTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_M781} CCCTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_M732} CCCTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_090} CCCTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_CJB110} CCCTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_1169NT} CCCTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
Consensus *****

251                                    300
msa442667.2{248_18RS21} CTTTAGTTAT TACAACGGCA AGTTTGGTTG GTGGACCTCT GGTGGATCA
msa442667.2{248_2603} CTTTAGTTAT TACAACGGCA AGTTTGGTTG GTGGACCTCT GGTGGATCA

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Table 58: Comparative Sequences relating to SAG0182

msa442667.2{248_A909}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_H36B}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_JM9130013}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_COH1}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_M781}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_M732}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_090}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_CJB110}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_1169NT}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_2603}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_A909}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_H36B}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_JM9130013}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_COH1}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_M781}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_M732}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_090}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_CJB110}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_1169NT}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTAGCGGAA
msa442667.2{248_2603}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTAGCGGAA
msa442667.2{248_A909}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTAGCGGAA
msa442667.2{248_H36B}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTAGCGGAA
msa442667.2{248_JM9130013}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTAGCGGAA
msa442667.2{248_COH1}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTAGCGGAA
msa442667.2{248_M781}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTAGCGGAA
msa442667.2{248_M732}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTAGCGGAA
msa442667.2{248_090}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTAGCGGAA
msa442667.2{248_CJB110}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTAGCGGAA
msa442667.2{248_1169NT}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTAGCGGAA
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCCTC	AACAAGCCAA
msa442667.2{248_2603}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCCTC	AACAAGCCAA
msa442667.2{248_A909}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCCTC	AACAAGCCAA
msa442667.2{248_H36B}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCCTC	AACAAGCCAA
msa442667.2{248_JM9130013}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCCTC	AACAAGCCAA
msa442667.2{248_COH1}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCCTC	AACAAGCCAA
msa442667.2{248_M781}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCCTC	AACAAGCCAA
msa442667.2{248_M732}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCCTC	AACAAGCCAA
msa442667.2{248_090}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCCTC	AACAAGCCAA
msa442667.2{248_CJB110}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCCTC	AACAAGCCAA
msa442667.2{248_1169NT}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCCTC	AACAAGCCAA
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_2603}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_A909}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_H36B}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_JM9130013}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_COH1}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_M781}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_M732}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_090}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_CJB110}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_1169NT}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_2603}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_A909}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_H36B}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_JM9130013}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_COH1}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_M781}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_M732}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_090}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_CJB110}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_1169NT}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	TTTTAAATAG	TTTAGTTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACITAT

Table 58: Comparative Sequences relating to SAG0182

msa442667.2{248_2603}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_A909}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_H36B}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_JM9130013}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_COH1}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_M781}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_M732}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_090}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_CJB110}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_1169NT}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_2603}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_A909}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_H36B}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_JM9130013}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_COH1}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_M781}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_M732}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_090}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_CJB110}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_1169NT}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_2603}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_A909}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_H36B}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_JM9130013}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_COH1}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_M781}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_M732}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_090}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_CJB110}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_1169NT}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_2603}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_A909}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_H36B}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_JM9130013}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_COH1}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_M781}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_M732}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_090}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_CJB110}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_1169NT}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_2603}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_A909}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_H36B}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_JM9130013}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_COH1}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_M781}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_M732}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_090}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_CJB110}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_1169NT}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
Consensus	**_*****	*****	*****	*****	**_*****
msa442667.2{248_18RS21}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_2603}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_A909}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_H36B}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_JM9130013}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_COH1}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_M781}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_M732}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_090}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_CJB110}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_1169NT}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
Consensus	*****	*****	*****	*****	*****

Table 58: Comparative Sequences relating to SAG0182

msa442667.2{248_18RS21}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_2603}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_A909}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_H36B}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_JM9130013}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_COH1}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_M781}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_M732}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_090}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_CJB110}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_1169NT}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	TGTCCAGATC	ACAACGTGCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_2603}	TGTCCAGATC	ACAACGTGCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_A909}	TGTCCAGATC	ACAACGTGCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_H36B}	TGTCCAGATC	ACAACGTGCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_JM9130013}	TGTCCAGATC	ACAACGTGCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_COH1}	TGTCCAGATC	ACAACGTGCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_M781}	TGTCCAGATC	ACAACGTGCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_M732}	TGTCCAGATC	ACAACGTGCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_090}	TGTCCAGATC	ACAACGTGCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_CJB110}	TGTCCAGATC	ACAACGTGCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_1169NT}	TGTCCAGATC	ACAACGTGCA	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	AATAAATGAT	AAAACGTGg	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_2603}	AATAAATGAT	AAAACGTGg	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_A909}	AATAAATGAT	AAAACGTGg	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_H36B}	AATAAATGAT	AAAACGTGg	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_JM9130013}	AATAAATGAT	AAAACGTGg	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_COH1}	AATAAATGAT	AAAACGTGg	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_M781}	AATAAATGAT	AAAACGTGg	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_M732}	AATAAATGAT	AAAACGTGg	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_090}	AATAAATGAT	AAAACGTGg	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_CJB110}	AATAAATGAT	AAAACGTGg	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_1169NT}	AATAAATGAT	AAAACGTGg	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_2603}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_A909}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_H36B}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_JM9130013}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_COH1}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_M781}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_M732}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_090}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_CJB110}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_1169NT}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_2603}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_A909}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_H36B}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_JM9130013}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_COH1}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_M781}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_M732}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_090}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_CJB110}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_1169NT}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_2603}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_A909}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_H36B}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_JM9130013}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_COH1}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_M781}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_M732}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_090}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_CJB110}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_1169NT}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
Consensus	*****	*****	*****	*****	*****

Table 58: Comparative Sequences relating to SAG0182

msa442667.2{248_18RS21}		1151	1200	
msa442667.2{248_2603}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT
msa442667.2{248_A909}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT
msa442667.2{248_H36B}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT
msa442667.2{248_JM9130013}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT
msa442667.2{248_COH1}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT
msa442667.2{248_M781}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT
msa442667.2{248_M732}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT
msa442667.2{248_090}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT
msa442667.2{248_CJB110}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT
msa442667.2{248_1169NT}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT
Consensus		*****	*****	*****
msa442667.2{248_18RS21}		1201	1250	
msa442667.2{248_2603}		AAAGCACGTT	ATGCACGTG	GCAGTTAAGT
msa442667.2{248_A909}		AAAGCACGTT	ATGCACGTG	GCAGTTAAGT
msa442667.2{248_H36B}		AAAGCACGTT	ATGCACGTG	GCAGTTAAGT
msa442667.2{248_JM9130013}		AAAGCACGTT	ATGCACGTG	GCAGTTAAGT
msa442667.2{248_COH1}		AAAGCACGTT	ATGCACGTG	GCAGTTAAGT
msa442667.2{248_M781}		AAAGCACGTT	ATGCACGTG	GCAGTTAAGT
msa442667.2{248_M732}		AAAGCACGTT	ATGCACGTG	GCAGTTAAGT
msa442667.2{248_090}		AAAGCACGTT	ATGCACGTG	GCAGTTAAGT
msa442667.2{248_CJB110}		AAAGCACGTT	ATGCACGTG	GCAGTTAAGT
msa442667.2{248_1169NT}		AAAGCACGTT	ATGCACGTG	GCAGTTAAGT
Consensus		*****	*****	*****
msa442667.2{248_18RS21}		1251	1300	
msa442667.2{248_2603}		GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT
msa442667.2{248_A909}		GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT
msa442667.2{248_H36B}		GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT
msa442667.2{248_JM9130013}		GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT
msa442667.2{248_COH1}		GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT
msa442667.2{248_M781}		GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT
msa442667.2{248_M732}		GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT
msa442667.2{248_090}		GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT
msa442667.2{248_CJB110}		GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT
msa442667.2{248_1169NT}		GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT
Consensus		***-*****	*****	*****
msa442667.2{248_18RS21}		1301	1350	
msa442667.2{248_2603}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC
msa442667.2{248_A909}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC
msa442667.2{248_H36B}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC
msa442667.2{248_JM9130013}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC
msa442667.2{248_COH1}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC
msa442667.2{248_M781}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC
msa442667.2{248_M732}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC
msa442667.2{248_090}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC
msa442667.2{248_CJB110}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC
msa442667.2{248_1169NT}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC
Consensus		*****	*****	*****
msa442667.2{248_18RS21}		1351	1400	
msa442667.2{248_2603}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA
msa442667.2{248_A909}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA
msa442667.2{248_H36B}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA
msa442667.2{248_JM9130013}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA
msa442667.2{248_COH1}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA
msa442667.2{248_M781}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA
msa442667.2{248_M732}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA
msa442667.2{248_090}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA
msa442667.2{248_CJB110}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA
msa442667.2{248_1169NT}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA
Consensus		*****	*****	*****
msa442667.2{248_18RS21}		1401	1450	
msa442667.2{248_2603}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG
msa442667.2{248_A909}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG
msa442667.2{248_H36B}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG
msa442667.2{248_JM9130013}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG
msa442667.2{248_COH1}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG
msa442667.2{248_M781}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG
msa442667.2{248_M732}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG
msa442667.2{248_090}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG
msa442667.2{248_CJB110}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG
msa442667.2{248_1169NT}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG
Consensus		*****	*****	*****

		1451					1501
msa442667.2	{248_18RS21}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT	
msa442667.2	{248_2603}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT	
msa442667.2	{248_A909}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT	
msa442667.2	{248_H36B}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT	
msa442667.2	{248_JM9130013}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT	
msa442667.2	{248_COH1}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT	
msa442667.2	{248_M781}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT	
msa442667.2	{248_M732}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT	
msa442667.2	{248_090}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT	
msa442667.2	{248_CJB110}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT	
msa442667.2	{248_1169NT}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT	
Consensus		*****	*****	*****	*****	*****	
		1501					1551
msa442667.2	{248_18RS21}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA	
msa442667.2	{248_2603}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA	
msa442667.2	{248_A909}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA	
msa442667.2	{248_H36B}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA	
msa442667.2	{248_JM9130013}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA	
msa442667.2	{248_COH1}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA	
msa442667.2	{248_M781}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA	
msa442667.2	{248_M732}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA	
msa442667.2	{248_090}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA	
msa442667.2	{248_CJB110}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA	
msa442667.2	{248_1169NT}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA	
Consensus		*****	*****	*****	*****	*****	
		1551					1600
msa442667.2	{248_18RS21}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGtACA	GGTACTGCTC	
msa442667.2	{248_2603}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGtACA	GGTACTGCTC	
msa442667.2	{248_A909}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGtACA	GGTACTGCTC	
msa442667.2	{248_H36B}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGtACA	GGTACTGCTC	
msa442667.2	{248_JM9130013}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGtACA	GGTACTGCTC	
msa442667.2	{248_COH1}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGgACA	GGTACTGCTC	
msa442667.2	{248_M781}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGgACA	GGTACTGCTC	
msa442667.2	{248_M732}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGgACA	GGTACTGCTC	
msa442667.2	{248_090}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGtACA	GGTACTGCTC	
msa442667.2	{248_CJB110}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGtACA	GGTACTGCTC	
msa442667.2	{248_1169NT}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGtACA	GGTACTGCTC	
Consensus		*****	*****	*****	*****-***	*****	
		1601					1650
msa442667.2	{248_18RS21}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGTC	
msa442667.2	{248_2603}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGTC	
msa442667.2	{248_A909}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGTC	
msa442667.2	{248_H36B}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGTC	
msa442667.2	{248_JM9130013}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGTC	
msa442667.2	{248_COH1}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGTC	
msa442667.2	{248_M781}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGTC	
msa442667.2	{248_M732}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGTC	
msa4426							



Table 58: Comparative Sequences relating to SAG0182

Consensus \*\*\*\*\*

SEQ ID NO. 5811

STRAIN 2603 frame: 1

LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVVISNITGIEIKG  
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF  
 YIVSSVLVGI VSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI  
 PMMILNSLGSSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE  
 I I KRHTNFDAVGLTDRSNVLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS  
 CPDHNQCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT  
 EEQNKLASMAEIKALQAQINPHFFFNAINTSALIRIDSDKARYALMQLSTFFRTSLQGG  
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF  
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLQETVAESKGTGTALVNLNLR  
 LNLLYGSVSVCLHFSDDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5812

STRAIN 090 frame: 1

LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVVISNITGIEIKG  
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF  
 YIVSSVLVGI VSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI  
 PMMILNSLGSSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE  
 I I KRHTNFDAVGLTDRSNVLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS  
 CPDHNQCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT  
 EEQNKLASMAEIKALQAQINPHFFFNAINTSALIRIDSDKARYALMQLSTFFRTSLQGG  
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF  
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLQETVAESKGTGTALVNLNLR  
 LNLLYGSVSVCLHFSDDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5813

STRAIN A909 frame: 1

LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVVISNITGIEIKG  
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF  
 YIVSSVLVGI VSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI  
 PMMILNSLGSSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE  
 I I KRHTNFDAVGLTDRSNVLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS  
 CPDHNQCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT  
 EEQNKLASMAEIKALQAQINPHFFFNAINTSALIRIDSDKARYALMQLSTFFRTSLQGG  
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF  
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLQETVAESKGTGTALVNLNLR  
 LNLLYGSVSVCLHFSDDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5814

STRAIN H36B frame: 1

LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVVISNITGIEIKG  
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF  
 YIVSSVLVGI VSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI  
 PMMILNSLGSSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE  
 I I KRHTNFDAVGLTDRSNVLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS  
 CPDHNQCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT  
 EEQNKLASMAEIKALQAQINPHFFFNAINTSALIRIDSDKARYALMQLSTFFRTSLQGG  
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF  
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLQETVAESKGTGTALVNLNLR  
 LNLLYGSVSVCLHFSDDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5815

STRAIN 18RS21 frame: 1

LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVVISNITGIEIKG  
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF  
 YIVSSVLVGI VSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI  
 PMMILNSLGSSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE  
 I I KRHTNFDAVGLTDRSNVLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS  
 CPDHNQCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT  
 EEQNKLASMAEIKALQAQINPHFFFNAINTSALIRIDSDKARYALMQLSTFFRTSLQGG  
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF  
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLQETVAESKGTGTALVNLNLR  
 LNLLYGSVSVCLHFSDDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5816

STRAIN M732 frame: 1

LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVVISNITGIEIKG  
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF  
 YIVSSVLVGI VSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI  
 PMMILNSLGSSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE  
 I I KRHTNFDAVGLTDRSNVLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS  
 CPDHNQCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT  
 EEQNKLASMAEIKALQAQINPHFFFNAINTSALIRIDSDKARYALMQLSTFFRTSLQGG  
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF  
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLQETVAESKGTGTALVNLNLR  
 LNLLYGSVSVCLHFSDDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5817

Table 58: Comparative Sequences relating to SAG0182

STRAIN COH1 frame: 1

LMVLLFQRLGIIMILAFLLVNNYSYFRQLIEERSKRETVVLVIIFGLFVIIISNITGIEIKG  
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF  
 YIVSSVLVGVISGKIGDKLENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI  
 PMMILNSLGSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE  
 IIKRHTNFDVAGLTDNRNLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS  
 CPDHCNQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT  
 EEQNKLASMAEIKALQAQINPHFFFNAINITISALIRIDSDKARYALMQLSTFFRTSLQGG  
 QDREVTLEQEKSHVDAYMNVKELRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF  
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGOETVAESKGTGTALVNLNLR  
 LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5818

STRAIN M781 frame: 1

LMVLLFQRLGIIMILAFLLVNNYSYFRQLIEERSKRETVVLVIIFGLFVIIISNITGIEIKG  
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF  
 YIVSSVLVGVISGKIGDKLENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI  
 PMMILNSLGSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE  
 IIKRHTNFDVAGLTDNRNLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS  
 CPDHCNQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT  
 EEQNKLASMAEIKALQAQINPHFFFNAINITISALIRIDSDKARYALMQLSTFFRTSLQGG  
 QDREVTLEQEKSHVDAYMNVKELRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF  
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGOETVAESKGTGTALVNLNLR  
 LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5819

STRAIN CJB110 frame: 1

LMVLLFQRLGIIMILAFLLVNNYSYFRQLIEERSKRETVVLVIIFGLFVIIISNITGIEIKG  
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF  
 YIVSSVLVGVISGKIGDKLENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI  
 PMMILNSLGSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE  
 IIKRHTNFDVAGLTDNRNLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS  
 CPDHCNQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT  
 EEQNKLASMAEIKALQAQINPHFFFNAINITISALIRIDSDKARYALMQLSTFFRTSLQGG  
 QDREVTLEQEKSHVDAYMNVKELRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF  
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGOETVAESKGTGTALVNLNLR  
 LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5820

STRAIN 1169NT frame: 1

LMVLLFQRLGIIMILAFLLVNNYSYFRQLIEERSKRETVVLVIIFGLFVIIISNITGIEIKG  
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF  
 YIVSSVLVGVISGKIGDKLENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI  
 PMMILNSLGSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE  
 IIKRHTNFDVAGLTDNRNLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS  
 CPDHCNQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT  
 EEQNKLASMAEIKALQAQINPHFFFNAINITISALIRIDSDKARYALMQLSTFFRTSLQGG  
 QDREVTLEQEKSHVDAYMNVKELRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF  
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGOETVAESKGTGTALVNLNLR  
 LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5821

STRAIN JM9130013 frame: 1

LMVLLFQRLGIIMILAFLLVNNYSYFRQLIEERSKRETVVLVIIFGLFVIIISNITGIEIKG  
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF  
 YIVSSVLVGVISGKIGDKLENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI  
 PMMILNSLGSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE  
 IIKRHTNFDVAGLTDNRNLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS  
 CPDHCNQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT  
 EEQNKLASMAEIKALQAQINPHFFFNAINITISALIRIDSDKARYALMQLSTFFRTSLQGG  
 QDREVTLEQEKSHVDAYMNVKELRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF  
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGOETVAESKGTGTALVNLNLR  
 LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

PRETTY of: /biotmp/msa442834.2{\*} January 13, 2003 06:47 ..

	1		50
msa442834.2{248_090}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_1169NT}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_18921}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_2603}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_A909}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_CJB110}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_H36B}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_JM9130013}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_COH1}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_M781}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_M732}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
Consensus	*****	*****	*****
	51		100
msa442834.2{248_090}	SNITGIEIKG	DRSLVERPFL TTISHSDSLA	NTRTLVITTA SLVGGPLVGS
msa442834.2{248_1169NT}	SNITGIEIKG	DRSLVERPFL TTISHSDSLA	NTRTLVITTA SLVGGPLVGS

Table 58: Comparative Sequences relating to SAG0182

msa442834.2{248_18RS21}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTTLVITTA	SLVGGPLVGS
msa442834.2{248_2603}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTTLVITTA	SLVGGPLVGS
msa442834.2{248_A909}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTTLVITTA	SLVGGPLVGS
msa442834.2{248_CJB110}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTTLVITTA	SLVGGPLVGS
msa442834.2{248_H36B}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTTLVITTA	SLVGGPLVGS
msa442834.2{248_JM9130013}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTTLVITTA	SLVGGPLVGS
msa442834.2{248_COH1}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTTLVITTA	SLVGGPLVGS
msa442834.2{248_M781}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTTLVITTA	SLVGGPLVGS
msa442834.2{248_M732}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTTLVITTA	SLVGGPLVGS
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_1169NT}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_18RS21}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_2603}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_A909}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_CJB110}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_H36B}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_JM9130013}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_COH1}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_M781}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_M732}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_1169NT}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_18RS21}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_2603}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_A909}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_CJB110}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_H36B}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_JM9130013}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_COH1}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_M781}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_M732}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_1169NT}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_18RS21}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_2603}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_A909}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_CJB110}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_H36B}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_JM9130013}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_COH1}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_M781}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_M732}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_1169NT}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_18RS21}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_2603}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_A909}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_CJB110}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_H36B}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_JM9130013}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_COH1}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_M781}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_M732}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_1169NT}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_18RS21}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_2603}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_A909}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_CJB110}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_H36B}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_JM9130013}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_COH1}	CPDHNCQLNS	AIVVPLKIND	KTVcALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_M781}	CPDHNCQLNS	AIVVPLKIND	KTVcALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_M732}	CPDHNCQLNS	AIVVPLKIND	KTVcALKMYF	AGDKTMSEVE	ENLVLGLAQI
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNIAINT	ISALIRIDSD

Table 58: Comparative Sequences relating to SAG0182

msa442834.2{248_1169NT}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_18RS21}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_2603}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_A909}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_CJB110}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_H36B}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_JM9130013}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_COH1}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_M781}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_M732}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYY
msa442834.2{248_1169NT}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYY
msa442834.2{248_18RS21}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYY
msa442834.2{248_2603}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYY
msa442834.2{248_A909}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYY
msa442834.2{248_CJB110}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYY
msa442834.2{248_H36B}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYY
msa442834.2{248_JM9130013}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYY
msa442834.2{248_COH1}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYY
msa442834.2{248_M781}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYY
msa442834.2{248_M732}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYY
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_1169NT}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_18RS21}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_2603}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_A909}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_CJB110}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_H36B}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_JM9130013}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_COH1}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_M781}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_M732}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_1169NT}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_18RS21}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_2603}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_A909}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_CJB110}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_H36B}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_JM9130013}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_COH1}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_M781}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_M732}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_1169NT}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_18RS21}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_2603}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_A909}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_CJB110}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_H36B}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_JM9130013}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_COH1}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_M781}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_M732}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
Consensus	*****	*****	*****		

Table 59: Comparative Sequences relating to SAG2147

## SEQ ID NO. 5901

## STRAIN 2603

ATGAATAAAGAGAAATTTATCAAAATTTGAATGTAAAAAACATCATTTAGCTTTATGGA  
GCTATCACITTTAGTAGCCCTTTTTCATGTATTTTGGCTGTATGGTCATCTTTAAAGT  
TCACAAGTTACTACTGAATCTTTGTCAAAAGCAGATAAAGTTCGCGTAGCCAAAAAATCA  
AAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAAAACAGGCTCCAAACCT  
TCTCAGGCATCTAATGAAGCCCCAAATCAAGTTCTCAATCTACAGAAGCTAATTCTCAG  
CAACAAGTTTACTGCGAGTGAAGAGGCAGCTGTAGAACAAAGCAGTTGTAAACAGAAACACC  
CCTGCTACCAAGTCAGGCACAAACAGCTTATGCTGTTACTGAGACAACTTATAGACCTGCT  
CAACACCAGACGAGTGGCCAAATTTAGTAAATGGAATACTGACGGGGCTATTGGCTCA  
GCAGCTGCAGACAAAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTGGGAAcATATT  
ATTGCCCGTGAATCAAATGGTAACTCCTAATGTTGCTAATGCCTCAGGAGCTTCAGGACTT  
TTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGGATCAAGTTAATTAGCT  
ATTAAGCTTATCTGCTCAAGGTTTATCAGCTTGGGGTTACTAG

## SEQ ID NO. 5902

## STRAIN JM9130013

AAAAGTTCAAGTTACTACTGAATCTTTGTCAAA  
AGCAGATAAAGTTTCGCGTAGCCAAAAATCAAAATGAATAAGGCAACAT  
CTAAATCAAAAGTAGAAGGTGTAAAAACAGGCTCCAAACCAAGTTCTCAA  
TCTACAGAAGCTAATTCTCAGCAACAAAGTTACTGCGAGTGAAGAGGCGAGC  
TGTAGAACAAAGCAGTTGTAAACAGAAATACCCCTGCTACCAGTCAAGCAC  
AACAAGCTTATGCTGTTACTGAGACAACTTATAGACCTGCTCAACACCAG  
CCGAGTGGCCAAAGTATTGAGCAATGGAATACTGACGGGGTTATTGGCTC  
AGCAGCAGCAGCACAAATGGCTGCTGCAACGGGAGTTCCTCAGTCTACTT  
GGGAACATATTATTGCCCGTGAATCAAATGGTAACTCCTAACGTTGCTAAT  
GGCTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAAC  
AGCTACAGTTCAGGATCAAGTTAATCAGCTATTAAAGCTTATCGTGCTC  
AAGGTTTATCAGCTTGGGGTTAC

## SEQ ID NO. 5903

## STRAIN 1169NT reverse complement

AAAAGTTCAAGTTACTACTGAATCTTTGTCAAAAGCAGATAAAGTTTCGCGTAGCC  
AAAAAATCAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAAAACAGGCT  
CCAAACCTTTCTCAGGCATCTAATGAAGTCCCAAAATCAAGTTCTCAATCTACAGAAGCT  
AATTCTCAGCAACAAAGTTACTGCGAGTGAAGAGGCGGCTGTAGAACAAAGCAGTTGTAAAC  
GAAAATACCCCTGCTACCAGTCAGGCACAACTTATGCTGTTACTGAGACAACTTAC  
AAACCTGCTCAACACCAGACAAAGTGGCCAAAGTATTGAGCAATGGAATACTGACGGGGCG  
GTCGGATCTGCTGCTGACGACAAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTGG  
GAACATATTATTGCCCGTGAATCAAATGGTAACTCCTAATGTTGCTAATGCCTCAGGAGCT  
TCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGGATCAAGTT  
AATTACAGCTATTAAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGGTTAC

## SEQ ID NO. 5904

## STRAIN 18RS21 reverse complement

AAAAGTTCAAGTTACTACTGAATCTTTGTCAAAAGCAGATAAAGTTTC  
GCGTAGCCAAAAATCAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAA  
AACAGGCTCCAAACCTTTCTCAGGCATCTAATGAAGCCCCAAATCAAGTTCTCAATCTA  
CAGAAGCTAATTCTCAGCAACAAAGTTACTGCGAGTGAAGAGGCGAGCTGTAGAACAAAGCAG  
TTGTAAACAGAAACACCCCTGCTACCAGTCAGGCACAAACAGCTTATGCTGTTACTGAGA  
CAACTTATAGACCTGCTCAACACCAGACGAGTGGCCAAAGTATTGAGTAATGGAAATACTG  
CAGGGGCTATTGGCTCAGCAGCTGCAGCACAAATGGCTGCTGCAACAGGAGTCCCTCAGT  
CTACTTGGGAACATATTATTGCCCGTGAATCAAATGGTAACTCCTAATGTTGCTAATGCCT  
CAGGAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGG  
ATCAAGTTAATTACAGCTATTAAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGGTTAC

## SEQ ID NO. 5905

## STRAIN 090 reverse complement

TAGCCAAAAAATCAAAATGATTAAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAAAAC  
AGGCTCCAAACCTTTCTCAGGCATCTAATGAAGCCCCAAATCAAGTTCTCAATCTACAG  
AAGCTAATTCTCAGCAACAAAGTTACTGCGAGTGAAGAGGCGAGCTGTAGAACAAAGCAGTTG  
TAACAGAAAAACCCCTGCTACCAGTCAGGCACAAACAGCTTATGCTGTTACTGAGACAA  
CTTATAGACCTGCTCAACACCAGACGAGTGGCCAAAGTATTGAGTAATGGAAATACTGAG  
GGGCTATTGGCTCAGCAGCTGCAGCACAAATGGCTGCTGCAACAGGAGTCCCTCAGTCTA  
CTTGGGAACATATTATTGCCCGTGAATCAAATGGTAACTCCTAATGTTGCTAATGCCTCAG  
GAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGGA

## SEQ ID NO. 5906

## STRAIN A909 reverse complement

AAGGCGACATCTAAATCAAAAGTAGAAGATGTAAAAACAGGCTCCAAACCTTTCTCAGGCA  
TCTAATGAAGCCCCAAATCAAGTTCTCAATCTACAGAAGCTAATTCTCAGCAACAAAGTT  
ACTGCGAGTGAAGAGGCGAGCTGTAGAACAAAGCAGTTGTAAACAGAAACACCCCTGCTACC  
AGTCAGGCACAAACAGCTTATGCTGTTACTGAGACAACTTATAGACCTGCTCAACACCAG  
ACAAGTGGCCAAAGTATTGAGTAATGGAATACTGACGGGGCTATTGGCTCAGCAGCTGCA  
GCACAAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTGGGAACATATTATTGCCCGT  
GAATCAAATGGTAACTCCTAATGTTGCTAATGCCTCAGGAGCTTCAGGACTTTTCCAAACG  
ATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGAAATCAAGTTAATTACAGCTATTAAAGCT  
TATCGTGCTCAAGGTTTATCA

## SEQ ID NO. 5907

## STRAIN CJB110 reverse complement

AATCTTTGTCAAAAGCAGATAAAGTTTCGCGTAGCCAAAAATCAAAATGACTAAGGCGA

Table 59: Comparative Sequences relating to SAG2147

CATCTAAATCAAAAGTAGAAGATGTAAACAGGGCTCCAAAACCTTCTCAGGCATCTAATG  
 AAGCCCCAAAATCAAGTTCTCAATCTACAGAGCTAATTTCTCAGCAACAAGTTACTGCGA  
 GTGAAGAGGCAGCTGTAGAACAAAGCAGTTGTAAACAGAAAACACCCCTGCTACCAAGTCAGG  
 CACAACAAGCTTATGCTGTTACTGAGACAACCTTATAGACCTGCTCAACACCAGACGAGTG  
 GCCAAGTATTGAGTAATGGAAATCTGAGGGGCTATTGGCTCAGCAGCTGCAGCACAAA  
 TGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTGGGAACATATTATTGCCCGTGAATCAA  
 ATGGTAATCCTAATGTTGCTAATGCCCTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAG  
 GTTGGGGTTCAACAGCTACAGTTCAAGATCAAGTTAATTCAGCTATTAAAGCTTATCGTG  
 CTCAGGTTTATCAGCTTGGGGTTAC

## SEQ ID NO. 5908

STRAIN COH1 reverse complement

AAAAGTTCACAAGTTACTACTGAATCTTTGTCAAAAGCAGATAA  
 AGTTCGCGTAGCCAAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGA  
 TGTAAACAGGCTCCAAAACCTTCTCAGGCATCTAATGAAGCCCCAAAATCAAGTTCTCA  
 ATCTACAGAAGCTAATTTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGGCTGTAGAACA  
 AGCAGTTGTAAACAGAAAATACCCCTGCTACCAAGTCAGGCACAACAACTTATGCTGTTAC  
 TGAGACAACCTTACAACCTGCTCAACACCAGACAAGTGGCCAAAGTATTGAGCAATGGAAA  
 TACTGCGAGGGGCGGTCTGGATCTGCTGCTGAGCACAATGGCTGCTGCAACAGGAGTCCC  
 TCAGTCTACTTGGGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAA  
 TGCTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGT  
 TCAGGATCAAGTTAATTCAGCTATTAAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGG  
 TTAC

## SEQ ID NO. 5909

STRAIN H36B reverse complement

AAAAGTTCACAAGTTACTACTGAATCTTTGTCAAAAGC  
 AGATAAAGTTCGCGTAGCCAAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAAGT  
 AGAAGATGTAAACAGGCTCCAAAACCTTCTCAGGCATCTAATGAAGCCCCAAAATCAAG  
 TTCTCAATCTACAGAAGCTAATTTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGAGCTGT  
 AGAACAAGCAGTTGTAAACAGAAAACACCCCTGCTACCAAGTCAGGCACAACAAGCTTATGC  
 TGTACTGAGACAACCTTATAGACCTGCTCAACACCAGACAAGTGGCCAAGTATTGAGTAA  
 TGGAAATACTGCGAGGGGCTATTGGCTCAGCAGCTGCAGCACAATGGCTGCTGCAACAGG  
 AGTCCCTCAGTCTACTTGGGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGTT  
 TGCTAATGCCTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGC  
 TACAGTTCAGGATCAAGTTAATTCAGCTATTAAAGCTT

## SEQ ID NO. 5910

STRAIN M732 reverse complement

AAAAGTTCACAAGTTACTACTGAATCTTTGTCAAAAGCAGATAAAGTTCGCGTAGC  
 CAAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAACAGGC  
 TCCAAAACCTTCTCAGGCATCTAATGAAGCCCCAAAATCAAGTTCTCAATCTACAGAAGC  
 TAATTTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGGCTGTAGAACAAGCAGTTGTAAAC  
 AGAAAATACCCCTGCTACCAAGTCAGGCACAACAACCTTATGCTGTTACTGAGACAACCTTA  
 CAAACCTGCTCAACACCAGACAAGTGGCCAAGTATTGAGCAATGGAAATACTGCGAGGGGC  
 GGTGGATCTGCTGCTGTCAGCACAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTG  
 GGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAATGCCTCAGGAGC  
 TTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAAGATCAAGT  
 TAATTCAGCTATTAAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGGTTA

## SEQ ID NO. 5911

STRAIN M781 reverse complement

TCCTTGTCAAAAGCAGATAAAGTTCGCGTAGCCAAAAAATCAAAAATGACTAAGGCGACA  
 TCTAAATCAAAAGTAGAAGATGTAAACAGGCTCCAAAACCTTCTCAGGCATCTAATGAA  
 GCCCAAAATCAAGTTCTCAATCTACAGAAGCTAATTTCTCAGCAACAAGTTACTGCGAGT  
 GAAGAGGCGGCTGTAGAACAAGCAGTTGTAAACAGAAAATACCCCTGCTACCAAGTCAGGCA  
 CAACAACTTATGCTGTTACTGAGACAACCTTACAACCTGCTCAACACCAGACAAGTGGC  
 CAAGTATTGAGCAATGGAAATACTGCGAGGGGCGGTCTGCTGCTGAGCACAATG  
 GCTGCTGCAACAGGAGTCCCTCAGTCTACTTGGGAACATATTATTGCCCGTGAATCAAAT  
 GGTAAATCCTAATGTTGCTAATGCCTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAGG  
 TGGGGTTCAACAGCTACAGTTCAAGATCAAGTTAATTCAGCTATTAAAGCTTATCGTGCT  
 CAAGGTTTATCAGCTTGGGGTTAC

PRETTY of: /biotmp/msa519780.2{\*} March 10, 2003 06:25 ..

	1					50
msa519780.2{25_COH1}	-----	-----	-----	-----	-----	-----
msa519780.2{25_M781}	-----	-----	-----	-----	-----	-----
msa519780.2{25_M732}	-----	-----	-----	-----	-----	-----
msa519780.2{25_1169NT}	-----	-----	-----	-----	-----	-----
msa519780.2{25_18RS21}	-----	-----	-----	-----	-----	-----
msa519780.2{25_A909}	-----	-----	-----	-----	-----	-----
msa519780.2{25_090}	-----	-----	-----	-----	-----	-----
msa519780.2{25_CJB110}	-----	-----	-----	-----	-----	-----
msa519780.2{2603}	atgaataaaa	gaagaaaatt	atcaaaaattg	aatgtaaaaa	aacatcattt	
msa519780.2{25_H36B}	-----	-----	-----	-----	-----	-----
msa519780.2{25_JM9130013}	-----	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****	*****
	51					100
msa519780.2{25_COH1}	-----	-----	-----	-----	-----	-----
msa519780.2{25_M781}	-----	-----	-----	-----	-----	-----
msa519780.2{25_M732}	-----	-----	-----	-----	-----	-----

[illegible]

Table 59: Comparative Sequences relating to SAG2147

msa519780.2{25_M732}	AGAAAAACC	CCTGCTACCA	GTCAgGCACA	ACAAaCTTAT	GCTGTTACTG
msa519780.2{25_1169NT}	AGAAAAACC	CCTGCTACCA	GTCAgGCACA	ACAAaCTTAT	GCTGTTACTG
msa519780.2{25_18RS21}	AGAAAAACC	CCTGCTACCA	GTCAgGCACA	ACAAgCTTAT	GCTGTTACTG
msa519780.2{25_A909}	AGAAAAACC	CCTGCTACCA	GTCAgGCACA	ACAAgCTTAT	GCTGTTACTG
msa519780.2{25_090}	AGAAAAACC	CCTGCTACCA	GTCAgGCACA	ACAAgCTTAT	GCTGTTACTG
msa519780.2{25_CJB110}	AGAAAAACC	CCTGCTACCA	GTCAgGCACA	ACAAgCTTAT	GCTGTTACTG
msa519780.2{2603}	AGAAAAACC	CCTGCTACCA	GTCAgGCACA	ACAAgCTTAT	GCTGTTACTG
msa519780.2{25_H36B}	AGAAAAACC	CCTGCTACCA	GTCAgGCACA	ACAAgCTTAT	GCTGTTACTG
msa519780.2{25_JM9130013}	AGAAAAACC	CCTGCTACCA	GTCAgGCACA	ACAAgCTTAT	GCTGTTACTG
Consensus	*****-***	*****-***	*****-***	*****-***	*****-***
msa519780.2{25_COH1}	AGACAACTTA	cAaACCTGCT	CAACACCAGA	CaAGTGGCCA	AGTATTGAGc
msa519780.2{25_M781}	AGACAACTTA	cAaACCTGCT	CAACACCAGA	CaAGTGGCCA	AGTATTGAGc
msa519780.2{25_M732}	AGACAACTTA	cAaACCTGCT	CAACACCAGA	CaAGTGGCCA	AGTATTGAGc
msa519780.2{25_1169NT}	AGACAACTTA	cAaACCTGCT	CAACACCAGA	CaAGTGGCCA	AGTATTGAGc
msa519780.2{25_18RS21}	AGACAACTTA	tAgACCTGCT	CAACACCAGA	CgAGTGGCCA	AGTATTGAGt
msa519780.2{25_A909}	AGACAACTTA	tAgACCTGCT	CAACACCAGA	CgAGTGGCCA	AGTATTGAGt
msa519780.2{25_090}	AGACAACTTA	tAgACCTGCT	CAACACCAGA	CgAGTGGCCA	AGTATTGAGt
msa519780.2{25_CJB110}	AGACAACTTA	tAgACCTGCT	CAACACCAGA	CgAGTGGCCA	AGTATTGAGt
msa519780.2{2603}	AGACAACTTA	tAgACCTGCT	CAACACCAGA	CgAGTGGCCA	AGTATTGAGt
msa519780.2{25_H36B}	AGACAACTTA	tAgACCTGCT	CAACACCAGA	CgAGTGGCCA	AGTATTGAGt
msa519780.2{25_JM9130013}	AGACAACTTA	tAgACCTGCT	CAACACCAGc	CgAGTGGCCA	AGTATTGAGc
Consensus	*****-***	*****-***	*****-***	*****-***	*****-***
msa519780.2{25_COH1}	AATGGAAATA	CTGCAGGGGc	ggTcGGaTcT	GcTgCtGCAG	CACAAATGGC
msa519780.2{25_M781}	AATGGAAATA	CTGCAGGGGc	ggTcGGaTcT	GcTgCtGCAG	CACAAATGGC
msa519780.2{25_M732}	AATGGAAATA	CTGCAGGGGc	ggTcGGaTcT	GcTgCtGCAG	CACAAATGGC
msa519780.2{25_1169NT}	AATGGAAATA	CTGCAGGGGc	ggTcGGaTcT	GcTgCtGCAG	CACAAATGGC
msa519780.2{25_18RS21}	AATGGAAATA	CTGCAGGGGc	taTtGGcTcA	GcAgCtGCAG	CACAAATGGC
msa519780.2{25_A909}	AATGGAAATA	CTGCAGGGGc	taTtGGcTcA	GcAgCtGCAG	CACAAATGGC
msa519780.2{25_090}	AATGGAAATA	CTGCAGGGGc	taTtGGcTcA	GcAgCtGCAG	CACAAATGGC
msa519780.2{25_CJB110}	AATGGAAATA	CTGCAGGGGc	taTtGGcTcA	GcAgCtGCAG	CACAAATGGC
msa519780.2{2603}	AATGGAAATA	CTGCAGGGGc	taTtGGcTcA	GcAgCtGCAG	CACAAATGGC
msa519780.2{25_H36B}	AATGGAAATA	CTGCAGGGGc	taTtGGcTcA	GcAgCtGCAG	CACAAATGGC
msa519780.2{25_JM9130013}	AATGGAAATA	CTGCAGGGGt	taTtGGcTcA	GcAgCaGCAG	CACAAATGGC
Consensus	*****-***	*****-***	*****-***	*****-***	*****-***
msa519780.2{25_COH1}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_M781}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_M732}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_1169NT}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_18RS21}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_A909}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_090}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_CJB110}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{2603}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_H36B}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_JM9130013}	TGCTGCAACg	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
Consensus	*****-***	*****-***	*****-***	*****-***	*****-***
msa519780.2{25_COH1}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_M781}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_M732}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_1169NT}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_18RS21}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_A909}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_090}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_CJB110}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{2603}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_H36B}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_JM9130013}	AATCAAATGG	TAATCCTAAC	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
Consensus	*****-***	*****-***	*****-***	*****-***	*****-***
msa519780.2{25_COH1}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_M781}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_M732}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_1169NT}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_18RS21}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_A909}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_090}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgA-----
msa519780.2{25_CJB110}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{2603}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_H36B}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_JM9130013}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
Consensus	*****-***	*****-***	*****-***	*****-***	*****-***
msa519780.2{25_COH1}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt



Table 59: Comparative Sequences relating to SAG2147

msa519780.2{25_M781}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt
msa519780.2{25_M732}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt
msa519780.2{25_1169NT}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt
msa519780.2{25_18RS21}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt
msa519780.2{25_A909}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt
msa519780.2{25_090}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt
msa519780.2{25_CJB110}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt
msa519780.2{2603}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt
msa519780.2{25_H36B}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt
msa519780.2{25_JM9130013}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt
Consensus	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt

	701
msa519780.2{25_COH1}	ac---
msa519780.2{25_M781}	ac---
msa519780.2{25_M732}	a----
msa519780.2{25_1169NT}	ac---
msa519780.2{25_18RS21}	ac---
msa519780.2{25_A909}	-----
msa519780.2{25_090}	-----
msa519780.2{25_CJB110}	ac---
msa519780.2{2603}	actag
msa519780.2{25_H36B}	-----
msa519780.2{25_JM9130013}	ac---
Consensus	---***

## SEQ ID NO. 5912

STRAIN 2603 frame: 1

MNKRRLSKLNVKKHLLAYGAITLVALFSCILAVMVIKSSQVTTESLSKADKVRVAKKS  
KMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTAEEAAVEQAVVTENT  
PATSSQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI GSAAAAQMAAATGVPQSTWEHI  
IARESNGNPNVANASGASGLFQTMPGWGSTATVQDQVNSAIKAYRAQGLSAWGY

## SEQ ID NO. 5913

STRAIN 1169NT frame: 1

KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEVPKSSSQSTEAN  
SQQQVTASEEAAVEQAVVTENTPATSSQAQQTYAVTETTYKPAQHQTSGQVLSNGNTAGAV  
GSAAAAQMAAATGVPQSTWEHI IARESNGNPNVANASGASGLFQTMPGWGSTATVQDQVN  
SAIKAYRAQGLSAWGY

## SEQ ID NO. 5914

STRAIN 18RS21 frame: 1

KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN  
SQQQVTASEEAAVEQAVVTENTPATSSQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI  
GSAAAAQMAAATGVPQSTWEHI IARESNGNPNVANASGASGLFQTMPGWGSTATVQDQVN  
SAIKAYRAQGLSAWGY

## SEQ ID NO. 5915

STRAIN 2603 frame: 1

KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN  
SQQQVTASEEAAVEQAVVTENTPATSSQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI  
GSAAAAQMAAATGVPQSTWEHI IARESNGNPNVANASGASGLFQTMPGWGSTATVQDQVN  
SAIKAYRAQGLSAWGY

## SEQ ID NO. 5916

STRAIN 090 frame: 3

AKKSKMIKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTAEEAAVEQAVV  
TENTPATSSQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI GSAAAAQMAAATGVPQST  
WEHI IARESNGNPNVANASGASGLFQTMPGWGSTATVQ

## SEQ ID NO. 5917

STRAIN A909 frame: 1

KATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTAEEAAVEQAVVTENTPAT  
SQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI GSAAAAQMAAATGVPQSTWEHI IAR  
ESNGNPNVANASGASGLFQTMPGWGSTATVQDQVNSAIKAYRAQGLS

## SEQ ID NO. 5918

STRAIN CJB110 frame: 3

SLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTAS  
EEAAVEQAVVTENTPATSSQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI GSAAAAQ  
MAAATGVPQSTWEHI IARESNGNPNVANASGASGLFQTMPGWGSTATVQDQVNSAIKAYRA  
QGLSAWGY

## SEQ ID NO. 5919

STRAIN COH1 frame: 1

KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN  
SQQQVTASEEAAVEQAVVTENTPATSSQAQQTYAVTETTYKPAQHQTSGQVLSNGNTAGAV  
GSAAAAQMAAATGVPQSTWEHI IARESNGNPNVANASGASGLFQTMPGWGSTATVQDQVN  
SAIKAYRAQGLSAWGY

## SEQ ID NO. 5920

STRAIN H36B frame: 1

Table 59: Comparative Sequences relating to SAG2147

KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN  
 SQQVVTASEEAAVEQAVVTENTPATSOAQQYAVTETTYRPAQHQTSGQVLSNGNTAGAV  
 GSAAAAQMAAATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN  
 SAIKA

SEQ ID NO. 5921

STRAIN M732 frame: 1

KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN  
 SQQVVTASEEAAVEQAVVTENTPATSOAQQYAVTETTYRPAQHQTSGQVLSNGNTAGAV  
 GSAAAAQMAAATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN  
 SAIKAYRAQGLSAWG

SEQ ID NO. 5922

STRAIN M781 frame: 4

SLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTAS  
 EEAAVEQAVVTENTPATSOAQQYAVTETTYRPAQHQTSGQVLSNGNTAGAVGSAAAAQMA  
 AATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVNSAIKAYRA  
 QGLSAWG

SEQ ID NO. 5923

STRAIN JM9130013 frame: 1

KSSQVTTESLSKADKVRVAKKSKMNKATSKSKVEGVKQAPKPSQSTEANSQQQVTASEE  
 AAVEQAVVTENTPATSOAQQYAVTETTYRPAQHQTSGQVLSNGNTAGVIGSAAAAQMAA  
 ATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVNSAIKAYRAQ  
 LSAWG

#### MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa519418.2{\*} March 10, 2003 06:15 ..

	1					50
msa519418.2{25_090}	-----	-----	-----	-----	-----	-----
msa519418.2{25_H36B}	-----	-----	-----	-----	-----KS	SQVTTESLSK
msa519418.2{25_COH1}	-----	-----	-----	-----	-----KS	SQVTTESLSK
msa519418.2{25_M781}	-----	-----	-----	-----	-----	-----SLSK
msa519418.2{25_1169NT}	-----	-----	-----	-----	-----KS	SQVTTESLSK
msa519418.2{25_M732}	-----	-----	-----	-----	-----KS	SQVTTESLSK
msa519418.2{25_18RS21}	-----	-----	-----	-----	-----KS	SQVTTESLSK
msa519418.2{25_CJB110}	-----	-----	-----	-----	-----	-----SLSK
msa519418.2{25_2603}	-----	-----	-----	-----	-----KS	SQVTTESLSK
msa519418.2{2603}	mnkrrklsl	nvkhhlayg	aitlvalfsc	ilavmvifks	-----	SQVTTESLSK
msa519418.2{25_A909}	-----	-----	-----	-----	-----	-----
msa519418.2{25_JM9130013}	-----	-----	-----	-----	-----KS	SQVTTESLSK
Consensus	*****	*****	*****	*****	*****	*****
	51					100
msa519418.2{25_090}	-----akks	kmiKATSKSK	VBdVKQAPKP	sqasneapks	SSQSTEANSQ	
msa519418.2{25_H36B}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ	
msa519418.2{25_COH1}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ	
msa519418.2{25_M781}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ	
msa519418.2{25_1169NT}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ	
msa519418.2{25_M732}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ	
msa519418.2{25_18RS21}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ	
msa519418.2{25_CJB110}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ	
msa519418.2{25_2603}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ	
msa519418.2{25_A909}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ	
msa519418.2{25_JM9130013}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ	
Consensus	*****	*****	*****	*****	*****	*****
	101					150
msa519418.2{25_090}	QQVTASEEAA	VEQAVVTENT	PATSOAQQaY	AVTETTYrPA	QHQtSGQVLS	
msa519418.2{25_H36B}	QQVTASEEAA	VEQAVVTENT	PATSOAQQaY	AVTETTYrPA	QHQtSGQVLS	
msa519418.2{25_COH1}	QQVTASEEAA	VEQAVVTENT	PATSOAQQtY	AVTETTYkPA	QHQtSGQVLS	
msa519418.2{25_M781}	QQVTASEEAA	VEQAVVTENT	PATSOAQQtY	AVTETTYkPA	QHQtSGQVLS	
msa519418.2{25_1169NT}	QQVTASEEAA	VEQAVVTENT	PATSOAQQtY	AVTETTYkPA	QHQtSGQVLS	
msa519418.2{25_M732}	QQVTASEEAA	VEQAVVTENT	PATSOAQQtY	AVTETTYkPA	QHQtSGQVLS	
msa519418.2{25_18RS21}	QQVTASEEAA	VEQAVVTENT	PATSOAQQaY	AVTETTYrPA	QHQtSGQVLS	
msa519418.2{25_CJB110}	QQVTASEEAA	VEQAVVTENT	PATSOAQQaY	AVTETTYrPA	QHQtSGQVLS	
msa519418.2{25_2603}	QQVTASEEAA	VEQAVVTENT	PATSOAQQaY	AVTETTYrPA	QHQtSGQVLS	
msa519418.2{25_A909}	QQVTASEEAA	VEQAVVTENT	PATSOAQQaY	AVTETTYrPA	QHQtSGQVLS	
msa519418.2{25_JM9130013}	QQVTASEEAA	VEQAVVTENT	PATSOAQQaY	AVTETTYrPA	QHQtSGQVLS	
Consensus	*****	*****	*****	*****	*****	*****
	151					200
msa519418.2{25_090}	NGNTAGaiGS	AAAAQMAAAT	GVPQSTWEHI	IARESNNGNPN	VANASGASGL	
msa519418.2{25_H36B}	NGNTAGaiGS	AAAAQMAAAT	GVPQSTWEHI	IARESNNGNPN	VANASGASGL	
msa519418.2{25_COH1}	NGNTAGavGS	AAAAQMAAAT	GVPQSTWEHI	IARESNNGNPN	VANASGASGL	
msa519418.2{25_M781}	NGNTAGavGS	AAAAQMAAAT	GVPQSTWEHI	IARESNNGNPN	VANASGASGL	
msa519418.2{25_1169NT}	NGNTAGavGS	AAAAQMAAAT	GVPQSTWEHI	IARESNNGNPN	VANASGASGL	
msa519418.2{25_M732}	NGNTAGavGS	AAAAQMAAAT	GVPQSTWEHI	IARESNNGNPN	VANASGASGL	
msa519418.2{25_18RS21}	NGNTAGaiGS	AAAAQMAAAT	GVPQSTWEHI	IARESNNGNPN	VANASGASGL	
msa519418.2{25_CJB110}	NGNTAGaiGS	AAAAQMAAAT	GVPQSTWEHI	IARESNNGNPN	VANASGASGL	

**Table 59: Comparative Sequences relating to SAG2147**

msa519418.2{25_2603}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNGNPN	VANASGASGL
msa519418.2{2603}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNGNPN	VANASGASGL
msa519418.2{25_A909}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNGNPN	VANASGASGL
msa519418.2{25_JM9130013}	NGNTAGviGS	AAAAQMAAAT	GVPQSTWEHI	IARESNGNPN	VANASGASGL
Consensus	*****--**	*****--**	*****--**	*****--**	*****--**
		201		234	
msa519418.2{25_090}	FQTMPGWGST	ATVQ-----	-----	-----	-----
msa519418.2{25_H36B}	FQTMPGWGST	ATVQDQVNSA	IKA-----	-----	-----
msa519418.2{25_COH1}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_M781}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_1169NT}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_M732}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWG-	
msa519418.2{25_18RS21}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_CJB110}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_2603}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{2603}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_A909}	FQTMPGWGST	ATVQnQVNSA	IKAYRAQGLS	-----	
msa519418.2{25_JM9130013}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
Consensus	*****--**	*****--**	*****--**	*****--**	*****--**

Table 60: Comparative Sequences relating to SAG1945

## SEQ ID NO. 6001

## STRAIN 2603

ATGAAAGAAAAACAGTCGAAAAGGCTTATTTATATACTACTGGTTGTTTCCATTATTTT  
ATAAGTGTTTTACATACAGTATAGCCAGCCTTCTAAACTACTTCCACCAAAAGAATTA  
GTTATTCTAAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTTGAGGAA  
AAATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTAATAGATAGATTA  
AGTAAGGAGGGTAAGCAGTTGAAGGCGGATATTTCTTTGGAGGAAATTATACGCAATTT  
GAAAGTCATAAGGCATTGTTTGAGTCTTACGTATCAAAGAATGTTCACTACTGTTATCCA  
GACTATATCCATCCAGTGATACGGCGACACCTTATACTATAAATGGGAGTGCTTGATT  
GTAATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTATTATACAGCCT  
TCCTTAAAAGGTAAAATTGCTTTGCGAGATCCGAATACCTTCTAGTGCTTTCTCACA  
CTCACTAATATACTCTTGGCCAAGGGTGGTTACCCAATCCAAAAGCGTGGAACTATGTT  
AAAAAGCTACAACATAATATTAATGCTATCAAATCTTCTAGCTCTCAGAAGTTTATCAA  
TCAGTTGCAGAAAGGAAAAATGATGTGGGGCTGACTTACGAAGACCCCTAGTGCTAATTG  
CAAAAAGTGGTGCAATGTTTCTATTGTATATCCGACAGAAGGGACAGTTTGTGCCA  
TCTTCGGTTGCAATATAAAGAATGCTCCTTCTATGAAAGAAGCAAGTTATTATTAAT  
TTTATGCTTTCTTAGATGTTCAAAATGCCTTTGGGCGAGTCAACGAGTAACCGACCTATT  
CGTAAAGATGCCCAACGAGTAATGGCATGAAGCTTTAAAGGATATTGCTACTCTTAAA  
GAAGATTATCGCTATGCTACTAAGCATAAGGGCCAAATCCTTAAACCTATAATCGTATT  
CGTAGAAATGCTGAT

## SEQ ID NO. 6002

## STRAIN 090

CAGCCTTCTAAACTACTTCCACCAAAAGAATTAGTTATTCTAAGT  
CCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTTTGGAGAAAA  
ATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTAATAG  
ATAGATTAAAGTAAGGAGGGTAAGCAGTTGAAGCGGATATTTCTTTGGA  
GGAAATTATACGCAATTTGAAAGTCATAGGCATTGTTTGAGTCTTACGT  
ATCAAGAATGTTCACTACTGTTATTTCCAGACTATATCCATCCAAGTGATA  
CGCGACACCTTATACTATAAATGGGAGTGCTTGATTGTAATAACGAA  
TTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTATTACAGCCTTC  
CTTAAAAGGTAAAATTGCTTTGCGAGATCCGAATACCTTCTAGTGCTT  
TCTCACAACCTCACTAATATACTCTTGGCCAAGGGTGGTTACCCAATCCA  
AAGCGTGGAACTATGTTAAAAAGCTACAACATAATATTAATGCTATCAA  
ATCTTCTAGCTCTTCAAGATTTATCAATCAGTTGCAGAAAGGAAAAATGA  
TTTGGGGCTGACTTACGAAGACCTAGTGCTCAATTTGCAAAAAGTGGT  
GCCAATGTTTCTATTGTATATCCGACAGAAGGGACAGTTTGTGCCATC  
TTGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAAGCAAGTTAT  
TTATTAATTTTATGCTTTCTTATAGTGTCAAATGCCTTTGGGCGAGTCA  
ACGAGTAACCGACCTATTGCTAAAGATGCCCAACGAGTAATGGCATGAA  
AGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGCTACTA  
AGCATAAGGGCCAAATCCTTAAACCTATAATCGTATTTCGTAGAAATGCT  
GAT

## SEQ ID NO. 6003

## STRAIN A909

CAGCCTTCTAAACTACTTCCACCAAAAGAATTAG  
TTATTCTAAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCT  
TTTGAGGAAAAATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGG  
TCAACTAATAGATAGATTAAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATA  
TTTCTTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTT  
GAGTCTTACGTATCAAAGAATATTCACTGTTATTCCAGATTATATCCA  
TCCGAGTGATACGGCGACACCTTATACTATAAATGGGAGTGCTTGATTG  
TAAATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTA  
TTACAGCCTTCTTAAAAGGTAAAATTGCTTTGCGAGATCCGAATACCTC  
CTCTAGTGCTTTCTCACAACCTCACTAATATACTCTTGGCCAAGGGTGGTT  
ACCCAATCCAAAGCGTGGAACTATGTTAAAAGCTACAACATAATATT  
AATGCTATCAAATCTTCTAGCTCTTCAAGAGTTTATCAATCAGTTGCAGA  
AGGAAAAATGATGTGGGGTTGACTTACGAAGACCCCTAGTGCTAATTGTC  
AAAAAGTGGTGCCAATGTTTCTATTGTATATCCGACAGAAGGGACAGTT  
TTTGTCCTATCTTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGA  
AGCAAGTTATTATTAAATTTTATGCTTTCTTTAGATGTTCAAAATGCTT  
TTGGGCGAGTCAACGAGTAACCGACCTATTGTAAGATGCCCAACGAGT  
AATGGCATGAAGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCG  
CTATGCTACTAAGCATAAGGGCCAAATCCTTAAACCTATAATCGTATTTC  
GTAGAAATGCTGAT

## SEQ ID NO. 6004

## STRAIN H36B

TAAACTACTTCCACCAAAAGAATTAGTTATTCTAAGTCCAAATAGTCAAG  
CCATTTTAAACAGGAACGATTCCAGCTTTTGGAGAAAAATACGGTATAAAA  
GTTAAGCTTATTCAAGGTGGGACAGGTCAACTAATAGATAGATTAAAGTAA  
GGAGGGTAAGCAGTTGAAGGCGGATATTTCTTTGGAGGAAATTATACGC  
AATTTGAAAGTCATAAGGCATTGTTTGAGTCTTACGTATCAAAGAATATT  
CATACTGTTATTCCAGATTATATCCATCCGAGTGATACGGCGACACCTTA  
TACTATAAATGGGAGTGCTTGATTGTAATAACGAATTAGTTAAGGGAC  
TTACCATCAAGAGTTATGAAGATTTATTACAGCCTTCTTAAAAGGTAAA  
ATTGCTTTGCGAGATCCGAATACCTTCTAGTGCTTTCTCACAACCTCAC  
TAATATACTCTTGGCCAAGGGTGGTTACCCAATCCAAAAGCGTGGAACT  
ATGTTAAAAGCTACAACATAATATTAATGCTATCAAATCTTCTAGCTCT  
TCAGAAGTTTATCAATCAGTTGCAGAAAGGAAAAATGATGTGGGGTTGAC  
TTACGAAGACCCCTAGTGCTAATTTGCAAAAAGTGGTGCCAATGTTTCTA  
TTGTATATCCGACAGAAGGGACAGTTTGTGCCATCTTCGGTTGCAATT

Table 60: Comparative Sequences relating to SAG1945

ATAAAGAATGCTCCTTCTATGAAAGAAGCAAAGTTATTATTAAATTTTAT  
GCTTTCTTTAGATGTTCAAATGTCCTTTGGGCAGTCAACGAGTAACCGAC  
CTATTGCTAAAGATGCCCAAACGAGTAATGGCATGAAAGCTTTAAAGGAT  
ATTGCTACTCTTAAAGAAGATTATCGCTATGTCATAAGCATAAGGGCCA  
AATCCTTAAACCTATAATCGTATTCTGTAGAAATGCTGAT

SEQ ID NO. 6005

STRAIN 18RS21

CAGCCTTCTAAACTACTTCCACCAAAGAATTAGTTATTCTAAGTCCAAA  
TAGTCAAGCCATTTTAACAGGAACGATTCCAGCTTTTGAGGAAAAATACG  
GTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTAATAGATAGA  
TTAAGTAAGGAGGGTAAGCAGTTGAAGGCCGATATTTCTTTGGAGGAAA  
TTATACGCAATTTGAAAGTCATAAGGCATTGTTTGAGTCTTACGTATCAA  
AGAATGTTTATCTACTGTTATTCCAGACTATATCCATCCAAGTGATACGGC  
ACACCTTATCTATAAATGGGAGTGTCTTGATTGTAATAACGAATTAGC  
TAAGGGACTTACCATCAAGAGTTATGAAGATTATACAGCCTTCCCTTAA  
AAGGTAAATTTGCTTTGCGAGATCCGAATACTTCTCTAGTGCTTTCTCA  
CAACTCATAATATACTCTTGCCCAAGGGTGGTTACACCAATCCAAAAGC  
GTGGAACCTATGTTAAAAGCTACACATAATATTAAATGCTATCAAATCTT  
CTAGCTCTTCAGAAATTATCAATCAGTTGCAAGGAAAAATGATTGTG  
GGGCTGACTTACGAAGACCTTAGTGTCAATTTGCAAAAAGTGGTGCCAA  
TGTTTCTATTGTATATCCGACAGAAGGGACAGTTTGTGCCATCTTCGG  
TTGCAATTATAAAGAATGCTCCTTCTATGAAAGAAGCAAAGTTATTATT  
AATTTATGCTTTCTTTAGATGTTCAAATGCTTTGGGCAGTCAACGAG  
TAACCGACCTATTGCTAAAGATGCCCAAACGAGTAATGGCATGAAAGCTT  
TAAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGTCATAAGCAT  
AAGGCCAAATCCTTAAACCTATAATCGTATTCTGTAGAAATGCTGAT

SEQ ID NO. 6006

STRAIN M732

CAGCCTTCTAAACTACTTCCACCAAAGAATTAGT  
TATTCTAAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTT  
TTGAGGAAAAATACGGTATAAAGTTAAGCTTATTCAAGGTGGGACAGGG  
CAACTAATAGATAGATTAAAGTAAGGAGGGTAAGCAGTTGAAGCGGATAT  
TTTCTTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTG  
AGTCTTACGTATCAAAGAATGTTCACTACTGTTATTCCAGACTATATCCAT  
CCGAGTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGT  
AATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTAT  
TACAGCCTTCCCTTAAAGGTAAAATTGCTTTGCGAGATCCGAATACTTCC  
TCTAGTGCTTTCTCACAACCTCACTAATATACTCTTGGCCAAGGGTGGTTA  
CACCATCCAAAAGCGTGAAGTATGTTAAAAGCTACAAACATAATATTA  
ATGCTATCAAATCTTCTAGCTCTTCAAGAGTTATCAATCAGTTGCGAGAA  
GGAAAATGATTGTGGGGTTGACTTACGAAGACCTTAGTGTCAATTTGCA  
AAAAAGTGGTGCCAAATGTTCTATTGTATACCGACAGAAGGGACAGTTT  
TTGTCCCATCTTGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAA  
GCAAAGTTATTTATTAATTTTATGCTTTCTTTAGATGTTCAAATGCTT  
TGGGCAGTCAACGAGTAACCGACCTATTGCTAAAGATGCCCAAACAGTA  
ATGGCATGAAAGCTTTAAAGGATATCGCTACTCTTAAAGAAGATTATCGC  
TATGTCATAAGCATAAGAGCCAAATCCTTAAACCTATAATCGCATTCG  
TAGAAATGCTGAT

SEQ ID NO. 6007

STRAIN COH1

CAGCCTTCTAAACTACTTCCACCAAAGAATTAGT  
ATTCTAAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTT  
TGAGGAAAAATACGGTATAAAGTTAAGCTTATTCAAGGTGGGACAGGGC  
AACTAATAGATAGATTAAAGTAAGGAGGGTAAGCAGTTGAAGCGGATATT  
TTCTTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTGA  
GTCCTTACGTATCAAAGAATGTTCACTACTGTTATTCCAGACTATATCCATC  
CGAGTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGTA  
AATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTATT  
ACAGCCTTCCCTTAAAGGTAAAATTGCTTTGCGAGATCCGAATACTTCCCT  
CTAGTGCTTTCTCACAACCTCACTAATATACTCTTGGCCAAGGGTGGTTAC  
ACCAATCCAAAAGCGTGAAGTATGTTAAAAGCTACAAACATAATATTAA  
TGCTATCAAATCTTCTAGCTCTTCAAGAGTTATCAATCAGTTGCGAGAAG  
GAAAATGATTGTGGGGTTGACTTACGAAGACCTTAGTGTCAATTTGCAA  
AAAAGTGGTGCCAAATGTTCTATTGTATACCGACAGAAGGGACAGTTT  
TGTCCCATCTTGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAAG  
CAAAGTTATTATTAATTTTATGCTTTCTTTAGATGTTCAAATGCTTT  
GGGCAGTCAACGAGTAACCGACCTATTGCTAAAGATGCCCAAACAGTAA  
TGGCATGAAAGCTTTAAAGGATATCGCTACTCTTAAAGAAGATTATCGCT  
ATGTCATAAGCATAAGAGCCAAATCCTTAAACCTATAATCGCATTCGT  
AGAAATGCTGAT

SEQ ID NO. 6008

STRAIN M781

CAGCCTTCTAAACTACTTCCACCAAAGAATTAGTTATT  
CTAAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTTGA  
GAAAAATACGGTATAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAAC  
TAATAGATAGATTAAAGTAAGGAGGGTAAGCAGTTGAAGCGGATATTTC  
TTTGAGGAAAAATATACGCAATTTGAAAGTCATAAGGCATTGTTGAGTC  
TTACGTATCAAAGAATGTTCACTACTGTTATTCCAGACTATATCCATCCGA  
GTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGTAAAT

Table 60: Comparative Sequences relating to SAG1945

AACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTATTACA  
 GCCTTCCTTAAAGGTAAGTAAATTCCTTTGCAGATCCGAATCTTCTCTA  
 GTGCTTTCTCACAACCTCACTAATATACTCTTGGCCAAGGGTGGTTACACC  
 AATCCAAAGCGTGGAACTATGTTAAAGGCTACAACATAATATTATATGC  
 TATCAAATCTTCTAGCTCTTCAAGAGTTTATCAATCAGTTGCAGAAAGGAA  
 AAATGATGTGGGGTTGACTTACGAAGACCCCTAGTGTCAATTTGCAAAAA  
 AGTGGTGCCAATGTTTCTATTGTATACCCGACAGAAGGGACAGTTTGT  
 CCCATCTTCGGTTGCAATTATAAAGAAATGCTCCTTCTATGAAAGAAGCAA  
 AGTTATTTATTAAATTTATGCTTTCTTTAGATGTTCAAAATGCCTTTGGG  
 CAGTCAACGAGTAACCGACCTATTTCGTAAGATGCCCAACAAAGTAATGG  
 CATGAAAGCTTTAAAGGATATCGCTACTCTTAAAGAAGATTATCGCTATG  
 TCACTAAGCATAAGAGCCAAATCCTTAAACCTATAATCGCATTTCGTAGA  
 AATGCTGAT

## SEQ ID NO. 6009

STRAIN CJB110

CAGCCTTTTAAACTACTTCCACCAAAAGAATTAGTTATTCT  
 AAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTTTGAGG  
 AAAAAATACCGGTATAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTA  
 ATAGATAGATTAAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATATTTCTT  
 TGGAGGAAATTTATACGCAATTTGAAAGTCATAAGGCATTGTTTGAGTCTT  
 ACGTATCAAAGAATGTTTCACTACTGTTATTCCAGACTATATCCATCCAAGT  
 GATACGGCGACACCTTATCTATATAAATGGGAGTGTCTTGATTGTAATAA  
 CGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTATTACAGC  
 CTTCTTAAAGGTAAGTAAATTCCTTTGCAGATCCGAATACTTCTCTAGT  
 GCTTTCTCACAACCTCACTAATATACTCTTGGCCAAGGGTGGTTACACCAA  
 TCCAAAAGCGTGGAACTATGTTAAAGGCTACAACATAATATTAAATGCTA  
 TCAATCTTCTAGCTCTTCAAGGTTTATCAATCAGTTGCAGAAAGGAAAA  
 ATGATTTGTGGGGCTGACTTACGAAGACCCCTAGTGTCAATTTGCAAAAAAG  
 TGGTGCCAATGTTTCTATTGTATATCCGACAGAAGGGACAGTTTGTGCTC  
 CATCTTCGGTTGCAATTATAAAGAAATGCTCCTTCTATGAAAGAAGCAAAG  
 TTAATTTATTAAATTTATGCTTTCTTTAGATGTTCAAAATGCCTTTGGGCA  
 GTCACAGGTAACCGACCTATTTCGTAAGATGCCCAACAGTAATGGCA  
 TGAAAGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGTC  
 ACTAAGCATAAGGGCCAAATCCTTAAACCTATAATCGTATTTCGTAGAAA  
 TGCTGAT

## SEQ ID NO. 6010

STRAIN 1169NT

ATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTTTGAGGAAAAATAC  
 GGTATAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTAATAGATAG  
 ATTAAGTAAGGAGGGTAAGCATTGAAAGGCGGATATTTCTTGGAGGAA  
 ATTATACGCAATTTGAAAGTCATAAGGCATTGTTTGAGTCTTACGTATCA  
 AAGAATGTTTCACTGTTATTCCAGACTATATCCATCCAAGTGATACGGC  
 GACACCTTATCTATAAATGGGAGTGTCTTGATTGTAATAACGAATTAG  
 CTAAGGGACTTACCATCAAGAGTTATGAAGATTATTACAGCCTTCTTAA  
 AAGGTAATTTGCCCTTGCAGATCCGAATACTTCTCTAGTGCTTTCTC  
 ACAACTCACAATATACTCTTGGCAAAGGGTGGTTACACCAATCCAAAAG  
 CGTGGAACTATGTTAAAGGCTACAACATAATATTAAATGCTATCAAATCT  
 TCTAGCTCTTCAAGGTTTATCAATCAGTTGCAGAAAGGAAAAATGATTGT  
 GGGGTTGACTTACGAAGACCCCTAGTGTCAATTTGCAAAAAAGTGGTGCCA  
 ATGTTTCTATTGTATATCCGACAGAAGGGACAGTTTGTGCTCCATCTTCG  
 GTTGCAATTATAAAGAAATGCTCCTTCTATGAAAGAAGCAAAGTTATTAT  
 TAAATTTATGCTTTCTTTAGATGTTCAAAATGCCTTTGGGCAGTCAACGA  
 GTAACCGACCTATTTCGTAAGATGCCCAACAGTAATGGCATGAAAGCT  
 TTAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGTCATAAGCA  
 TAAGGGCCAAATCCTTAAACCTATAATCGTATTTCGTAGAAATGCTGAT

## SEQ ID NO. 6011

STRAIN JM91130013

CAGCCTTCTAAACTACTTCCACCAAAAGAATTAGT  
 TATTCTAAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTT  
 TTGAGGAAAAATACGGTATAAAGTTAAGCTTATTCAAGGTGGGACAGGG  
 CAACTAATAGATAGATTAAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATGT  
 TTTCTTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTG  
 AGTCTTACGTATCAAAGAATGTTTCACTGTTATTCCAGACTATATCCAT  
 CCGAGTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGT  
 AAATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTAT  
 TACAGCCTTCTTAAAGGTAAGTAAATTCCTTTGCAGATCCGAATACTTCC  
 TCTAGTGCTTTCTCACAACCTCACCATAATATACTCTTGGCAAAGGGTGGTTA  
 CACCAATCCAAAAGCGTGGAACTATGTTAAAGGCTACAACATAATATTA  
 ATGCTATCAAATCTTCTAGCTCTTCAAGGTTTATCAATCAGTTGCAGAA  
 GGCAAAATGATTGTGGGGCTGACTTACGAAGACCCCTAGTGTCAATTTGCA  
 AAAAAAGTGGTGCCAATGTTTCTATTGTGTATCCGACAGAAGGGACAGTTT  
 TGTCCCATCTTCGGTTGCAATTATAAAGAAATGCTCCTTCTATGAAAGAA  
 GCAAGTATTTATTAAATTTATGCTTTCTTTAGATGTTCAAAATGCCTT  
 TGGCGAGTCAACGAGTAACCGACCTATTTCGTAAGATGCCCAACAGGTA  
 ATGGCATGAAAGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCGC  
 TATGTCATAAGCATAAGGGCCAAATCCTTAAACCTATAATCGTATTTCG  
 TAGAAATGCTGAT

PRETTY of: /biotmp/msa523010.2{\*} April 28, 2003 08:55 ..

Table 60: Comparative Sequences relating to SAG1945

	1				50
msa523010.2{263_COH1}	-----	-----	-----	-----	-----
msa523010.2{263_M732}	-----	-----	-----	-----	-----
msa523010.2{263_M781}	-----	-----	-----	-----	-----
msa523010.2{263_A909}	-----	-----	-----	-----	-----
msa523010.2{263_H36B}	-----	-----	-----	-----	-----
msa523010.2{263_090}	-----	-----	-----	-----	-----
msa523010.2{263_18RS21}	-----	-----	-----	-----	-----
msa523010.2{263_2603}	atgaaagaaa	aacagtcgaa	aaggcttatt	tataactac	tggttggttc
msa523010.2{263_CJB110}	-----	-----	-----	-----	-----
msa523010.2{263_1169NT}	-----	-----	-----	-----	-----
msa523010.2{263_JM91130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa523010.2{263_COH1}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_M732}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_M781}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_A909}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_H36B}	-----	-----	-----	-----taaac	-----
msa523010.2{263_090}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_18RS21}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_2603}	cattattttt	ataagtgtt	ttacatacag	tattagccag	ccttctaaac
msa523010.2{263_CJB110}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_1169NT}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_JM91130013}	-----	-----	-----	-----cag	ccttctaaac
Consensus	*****	*****	*****	*****	-----
	101				150
msa523010.2{263_COH1}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_M732}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_M781}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_A909}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_H36B}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_090}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_18RS21}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_2603}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_CJB110}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_1169NT}	-----	-----	-----	-----ATAG	TCAAGCCATT
msa523010.2{263_JM91130013}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
Consensus	-----	-----	-----	-----****	*****
	151				200
msa523010.2{263_COH1}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_M732}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_M781}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_A909}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_H36B}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_090}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_18RS21}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_2603}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_CJB110}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_1169NT}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_JM91130013}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
Consensus	*****	*****	*****	*****	*****
	201				250
msa523010.2{263_COH1}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_M732}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_M781}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_A909}	GCTTATTCAA	GGTGGGACAG	GtCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_H36B}	GCTTATTCAA	GGTGGGACAG	GtCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_090}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_18RS21}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_2603}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_CJB110}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_1169NT}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_JM91130013}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
Consensus	*****	*****	*****	*****	*****
	251				300
msa523010.2{263_COH1}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_M732}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_M781}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_A909}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_H36B}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_090}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_18RS21}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_2603}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_CJB110}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_1169NT}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_JM91130013}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
Consensus	*****	*****	*****	*****	*****

Table 60: Comparative Sequences relating to SAG1945

		301			350
msa523010.2{263_COH1}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_M732}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_M781}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_A909}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATaTTCATAC
msa523010.2{263_H36B}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATaTTCATAC
msa523010.2{263_090}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_18RS21}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_2603}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_CJB110}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_1169NT}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_JM91130013}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
Consensus	*****	*****	*****	*****	*_*_*_*_*_*_*_*
		351			400
msa523010.2{263_COH1}	TGTTATTCCA	GACtATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACtA
msa523010.2{263_M732}	TGTTATTCCA	GACtATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACtA
msa523010.2{263_M781}	TGTTATTCCA	GACtATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACtA
msa523010.2{263_A909}	TGTTATTCCA	GACtATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACtA
msa523010.2{263_H36B}	TGTTATTCCA	GACtATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACtA
msa523010.2{263_090}	TGTTATTCCA	GACtATATCC	ATCCaAGTGA	TACGGCGACA	CCTTATACtA
msa523010.2{263_18RS21}	TGTTATTCCA	GACtATATCC	ATCCaAGTGA	TACGGCGACA	CCTTATACtA
msa523010.2{263_2603}	TGTTATTCCA	GACtATATCC	ATCCaAGTGA	TACGGCGACA	CCTTATACtA
msa523010.2{263_CJB110}	TGTTATTCCA	GACtATATCC	ATCCaAGTGA	TACGGCGACA	CCTTATACtA
msa523010.2{263_1169NT}	TGTTATTCCA	GACtATATCC	ATCCaAGTGA	TACGGCGACA	CCTTATACtA
msa523010.2{263_JM91130013}	TGTTATTCCA	GACtATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACtA
Consensus	*****	**_*_*_*_*_*_*	*****	*****	*****
		401			450
msa523010.2{263_COH1}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_M732}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_M781}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_A909}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_H36B}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_090}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_18RS21}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_2603}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_CJB110}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_1169NT}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_JM91130013}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
Consensus	*****	*****	*****	*****_***	*****
		451			500
msa523010.2{263_COH1}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTAATAATTGC
msa523010.2{263_M732}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTAATAATTGC
msa523010.2{263_M781}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTAATAATTGC
msa523010.2{263_A909}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTAATAATTGC
msa523010.2{263_H36B}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTAATAATTGC
msa523010.2{263_090}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTAATAATTGC
msa523010.2{263_18RS21}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTAATAATTGC
msa523010.2{263_2603}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTAATAATTGC
msa523010.2{263_CJB110}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTAATAATTGC
msa523010.2{263_1169NT}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTAATAATTGC
msa523010.2{263_JM91130013}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTAATAATTGC
Consensus	*****	*****	*****	*****	*****
		501			550
msa523010.2{263_COH1}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_M732}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_M781}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_A909}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_H36B}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_090}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_18RS21}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_2603}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_CJB110}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_1169NT}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_JM91130013}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
Consensus	*****	*****	*****	*****	*****_****
		551			600
msa523010.2{263_COH1}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_M732}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_M781}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_A909}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_H36B}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_090}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_18RS21}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_2603}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_CJB110}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_1169NT}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_JM91130013}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT



Table 60: Comparative Sequences relating to SAG1945

Consensus	*****	*****	*****	*****	*****
	601				650
msa523010.2{263_COH1}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_M732}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_M781}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_A909}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_H36B}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_090}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_18RS21}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_2603}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_CJB110}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_1169NT}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_JM91130013}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
Consensus	*****	*****	*****	*****	*****
	651				700
msa523010.2{263_COH1}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_M732}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_M781}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_A909}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_H36B}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_090}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_18RS21}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_2603}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_CJB110}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_1169NT}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_JM91130013}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
Consensus	*****	*****	*****	*****	*****
	701				750
msa523010.2{263_COH1}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_M732}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_M781}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_A909}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_H36B}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_090}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_18RS21}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_2603}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_CJB110}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_1169NT}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_JM91130013}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTg
Consensus	*****	*****	*****	*****	*****
	751				800
msa523010.2{263_COH1}	TaCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_M732}	TaCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_M781}	TaCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_A909}	TaCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_H36B}	TaCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_090}	TaCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_18RS21}	TaCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_2603}	TaCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_CJB110}	TaCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_1169NT}	TaCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_JM91130013}	TaCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
Consensus	**	*****	*****	*****	*****
	801				850
msa523010.2{263_COH1}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_M732}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_M781}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_A909}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_H36B}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_090}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_18RS21}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_2603}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_CJB110}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_1169NT}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_JM91130013}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
Consensus	*****	*****	*****	*****	*****
	851				900
msa523010.2{263_COH1}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_M732}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_M781}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_A909}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_H36B}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_090}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_18RS21}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_2603}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_CJB110}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_1169NT}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT

Table 60: Comparative Sequences relating to SAG1945

msa523010.2{263_JM91130013}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
Consensus	*****	*****	*****	*****	*****
	901				950
msa523010.2{263_COH1}	CGTAAAGATG	CCCAAACaAG	TAATGGCATG	AAAGCTTTAA	AGGATATcGC
msa523010.2{263_M732}	CGTAAAGATG	CCCAAACaAG	TAATGGCATG	AAAGCTTTAA	AGGATATcGC
msa523010.2{263_M781}	CGTAAAGATG	CCCAAACaAG	TAATGGCATG	AAAGCTTTAA	AGGATATcGC
msa523010.2{263_A909}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_H36B}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_090}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_18RS21}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_2603}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_CJB110}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_1169NT}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_JM91130013}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
Consensus	*****	*****	*****	*****	*****
	951				1000
msa523010.2{263_COH1}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	agCCAAATCC
msa523010.2{263_M732}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	agCCAAATCC
msa523010.2{263_M781}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	agCCAAATCC
msa523010.2{263_A909}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
msa523010.2{263_H36B}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
msa523010.2{263_090}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
msa523010.2{263_18RS21}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
msa523010.2{263_2603}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
msa523010.2{263_CJB110}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
msa523010.2{263_1169NT}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
msa523010.2{263_JM91130013}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
Consensus	*****	*****	*****	*****	*****
	1001				1035
msa523010.2{263_COH1}	TTAAAACCTA	TAATCGcATT	CGTAGAAATG	CTGAT	
msa523010.2{263_M732}	TTAAAACCTA	TAATCGcATT	CGTAGAAATG	CTGAT	
msa523010.2{263_M781}	TTAAAACCTA	TAATCGcATT	CGTAGAAATG	CTGAT	
msa523010.2{263_A909}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_H36B}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_090}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_18RS21}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_2603}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_CJB110}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_1169NT}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_JM91130013}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
Consensus	*****	*****	*****	*****	

## SEQ ID NO. 6012

STRAIN 2603 frame: 1

MKEKQSKRLIYILLVSIIFISVFTYSISQPSKLLPPKELVILSPNSQAILTGTIPAFEE  
 KYGIKVKLIQGGTGQLIDRLSKEGKQLKADIFFGGNYTQFESHKALFESYVSKNVHTVIP  
 DYIHPSDTATPYTINGSVLIVNNELAKGLTIKSYEDLLQPSLKGKIAFADPNTSSSAFSQ  
 LTNILLAKGGYTNPKAWNYVKKLQHNINAIKSSSSSEVYQSVAEKGMIVGLTYEDPSVNL  
 QKSGANVSIVYPTEGTVPFVSSVAIIKNAPSMKEAKLFINFMLS LDVQNAFGQSTSNRPI  
 RKDAQTSNGMKALKDIA TLKEDYRYVT KHKGQILKTYNRI RRNAD

## SEQ ID NO. 6013

STRAIN 090 frame: 1

QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA  
 DIFFGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL  
 TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA  
 IKSSSSSEVYQSVAEKGMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVPFVSSVAIIKNA  
 PSMKEAKLFINFMLS LDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIA TLKEDYRYVT KH  
 KGQILKTYNRI RRNAD

## SEQ ID NO. 6014

STRAIN A909 frame: 1

QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA  
 DIFFGNYTQFESHKALFESYVSKNIHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL  
 TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA  
 IKSSSSSEVYQSVAEKGMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVPFVSSVAIIKNA  
 PSMKEAKLFINFMLS LDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIA TLKEDYRYVT KH  
 KGQILKTYNRI RRNAD

## SEQ ID NO. 6015

STRAIN H36B frame: 2

KLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKADIF  
 FGGNYTQFESHKALFESYVSKNIHTVIPDYIHPSDTATPYTINGSVLIVNNELVKGLTIK  
 SYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA  
 SSSSEVYQSVAEKGMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVPFVSSVAIIKNAPSM  
 KEAKLFINFMLS LDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIA TLKEDYRYVT KHKGQ  
 ILKTYNRI RRNAD

## SEQ ID NO. 6016

**Table 60: Comparative Sequences relating to SAG1945**

STRAIN 18RS21 frame: 1  
QPSKLLPPLKEVLVLSNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA  
DIFFGGNYTQFESHKALFADSPYNSKNVHTVTPDYIHPSDTATPYTNGSVLIVNNELAKGL  
TIKSYEDLVQPSLKGKIAFESDVPNTSSSAFSQLNTILAKGGTYTNPKAWNVVKLLQHNI  
IKSSSSSELYQSVAEGRMIVGLTYBEDPSNVLQKSGANVSIVYPTGTVFVFPSSVAIIKNA  
PSMKEAKLFINFMLSLDVQNAFGQSTSNRP IRKDAQTSNGMKALKDILTKEDYRYVTKH  
KGKLLTKYNRIRNRAD

SEQ ID NO. 6017

STRAIN M732 frame: 1

QPSKLLPPKELVILSPNSQAILTGTPAFEEKYGIKVLIKQGGTGQIDLRLSKEGKOLKA  
LIDFFGGNYTQFESHKALFESYVSKNVHTVLPDIYHPSDTPATPTYINGSVLIVNNEAKGL  
TIKSYEDLLQPSKLGKIAFADNPNTSSSAFQVLTINLLAKGGTYNPKNAWNYVKKLQHNINA  
IKSSSSSEYVQSVAEGKMI VGLTYEDPSVNLQKSGANVSIVYPTBGTVPFVSPVAIIKNA  
PSMKEAKLFINMLSLSDVQNAFGQSTSNRP IRKDAQTSNGMKALKDIALTKEDYRYVTKH  
KSIQLTKTYNRI RRDND

SEQ ID NO. 6018

STRAIN COH1 frame: 1

QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQILDRLSKKGKQLKA  
DIFFGNGYQFQSHKALFESVYSKNVHTVIPDYIHPSDTPATYTINGSVLIVNVELAKGL  
TIKSYEDLLQPSKLGKTAFAADPNTSSSAFQLNTILLAKGGYTPNPAWNVVKLQHNIA  
IKSSSSSEVVQSAVEGKMIVGLTYEDPSVNLQKSGANVSI VYPTEGVTFVFPSSVAI I KNA  
PSMKEAKLFINFMLSLDVQNAFGQSTSNRP IRKDAQTSNGMKALKDIALTKEDRYVYTKH  
KSQIKLTYNRI RNAD

SEQ ID NO. 6019

STRAIN M781 frame: 1

QPSKLLPPKELVILSPNSQAILTGITPAFEEKYGIKVLLIQGGTQGLIDRLSKHGKQLKA  
DITFFGNGYTOFQSHKALFESYVSKNVHTVIPDYIHPSDTPATPYINGSVILVNNELAKGL  
TKSYEDBLQPSKLGKIAFADYDTPNTSSAFSQTIVLLILAKGGYTNPKAWNYVKKLQHNINA  
IKSSSSSEVVQSVABGKMI VGLTYEDPSVNLQKSGANVSI VYPTEGTVFPSSVAI I KNA  
PSMKEAKLFI NFMLSLDVQNAFGQSTSNRP IRKDAQTSNGMKALKDIALTKEDRYRYVTKH  
KSKQLITKYNIRLDA

SEQ ID NO. 6020

STRAIN CJB110 frame: 1

QPFKLLPPELVLSPNSQAILTGTIPAFEBEKYGIKVKLIQGGTGQLIDRLSKBEGKOLKA  
DIFFGNYDQPSFESHKALFESYVSKNVHTVIPDYIHPSDTPATPTYTNGSVLIVNNEAKGL  
TISKSYEDLLQPSLKGKIAFADPNPTSSAFSQTLNIIKLAKGTYTNPKAWNIVKVLQHNINA  
IKSSSSSEVYQSVAGKMI VGLTYEDPSVNLQKSGANVSI VYPTBGTVPVPSSVAIIKNA  
PSMKEAKLFINMFLSLDVQNAFGQSTSNRP IRKDAQTSNGMKALDIALTKLEDYRYVTKH  
KGQILKTYNRI RRDND

SEQ ID NO. 6021

STRAIN 1169NT frame: 3

SQAILTGTPAFEKEYGKIVKLIQGGTGQLIDRLSKEGKHLKADIFFGGNYTQFESHKAL  
 FESYVSKNVHTVIPDYIHPSDATPYTINGSVLIVNNELAKGLTKSYEDLLQPSLKGGKI  
 AFADPNTSSSAFSLKNILLAKGGYTPKAWNVYKKLQHNAINAKSSSSSEVYQSVABGK  
 MIVGLTYEDPSVLNQLKSGANVISYVPTGTEVFVPSVAIIKNAPSMEAKFLINFLMSLD  
 VQNAFGOSTSNRPKIRKDAQTSNGMKALKDIALTKEDYRYVTKHKGQILKTYNRIARNAD

SEQ ID NO. 6022

STRAIN JM91130013 frame: 1

QPSKLLPPKELVILSPNSQAILTGTIPAFEEEKYGIKVKLIQGGTGQLIDRLSKEGKQKA  
DVFFGGNYTQFESHALKFESYKSNVHFIIPDYIHPSDTPATPYTNGSVLIVNNEALGL  
TIKSYEDLLQPSLKGKIAFADNPNTSSAFSOLNTLILAKGGYTNPKAWVVKLQHNIA  
IKSSSSSEVYQSAEGKMI VGLTYEDPSVNLQKSGANVSIYYPBTBGTVFVPSSVAIIKNA  
PSMKEAKFLINFMLSLDVQNAFGQSTSNRPIRKDAQTSNGMKALDIA TLKLEDYRYVTKH  
KGOILTKYNRIRSD

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PRETTY of: /biotmp/msa523117.2{*} April 28, 2003 08:56 ..
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1
50
msa523117.2{263_COH1} -----q pskl1ppkel vilspnSQAI
msa523117.2{263_M732} -----q pskl1ppkel vilspnSQAI
msa523117.2{263_M781} -----q pskl1ppkel vilspnSQAI
msa523117.2{263_1169NT} -----SQAI
msa523117.2{263_CJB110} -----q pfkl1ppkel vilspnSQAI
msa523117.2{263_090} -----q pskl1ppkel vilspnSQAI
msa523117.2{263_18RS21} -----q pskl1ppkel vilspnSQAI
msa523117.2{263_2603} mkekqskrli yillvvsii f iavftysisq pskl1ppkel vilspnSQAI
msa523117.2{263_A909} -----q pskl1ppkel vilspnSQAI
msa523117.2{263_JM91130013} -----q pskl1ppkel vilspnSQAI
msa523117.2{263_H36B} -----q pskl1ppkel vilspnSQAI
msa523117.2{263_H36B} -----k1ppkel vilspnSQAI
Consensus *****

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	51	100
msa523117.2{263_COH1}	LTGTIPAFEE KYGIKVKLIQ GGTGQLIDRL SKEGKqLKAD iFFGGNYTQF	
msa523117.2{263_M732}	LTGTIPAFEE KYGIKVKLIQ GGTGQLIDRL SKEGKqLKAD iFFGGNYTQF	
msa523117.2{263_M781}	LTGTIPAFEE KYGIKVKLIQ GGTGQLIDRL SKEGKqLKAD iFFGGNYTQF	
msa523117.2{263_1169NT}	LTGTIPAFEE KYGIKVKLIQ GGTGQLIDRL SKEGKhLKAD iFFGGNYTQF	

Table 60: Comparative Sequences relating to SAG1945

msa523117.2{263_CJB110}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
msa523117.2{263_090}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
msa523117.2{263_18RS21}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
msa523117.2{263_2603}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
msa523117.2{263_A909}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
msa523117.2{263_JM91130013}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	vFFGGNYTQF
msa523117.2{263_H36B}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
Consensus	*****	*****	*****	*****	*****
msa523117.2{263_COH1}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_M732}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_M781}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_1169NT}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_CJB110}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_090}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_18RS21}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_2603}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_A909}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_JM91130013}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_H36B}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELvKGLT
Consensus	*****	*****	*****	*****	*****
msa523117.2{263_COH1}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_M732}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_M781}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_1169NT}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_CJB110}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_090}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_18RS21}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_2603}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_A909}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_JM91130013}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_H36B}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
Consensus	*****	*****	*****	*****	*****
msa523117.2{263_COH1}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_M732}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_M781}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_1169NT}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_CJB110}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_090}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_18RS21}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_2603}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_A909}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_JM91130013}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_H36B}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
Consensus	*****	*****	*****	*****	*****
msa523117.2{263_COH1}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_M732}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_M781}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_1169NT}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_CJB110}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_090}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_18RS21}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_2603}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_A909}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_JM91130013}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_H36B}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
Consensus	*****	*****	*****	*****	*****
msa523117.2{263_COH1}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_M732}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_M781}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_1169NT}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_CJB110}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_090}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_18RS21}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_2603}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_A909}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_JM91130013}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_H36B}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
Consensus	*****	*****	*****	*****	*****

Table 61: Comparative Sequences relating to SAG1030

## SEQ ID NO. 6101

## STRAIN 2603

ATGGTAAAAGTTAGTGTAAAGTTCTGTAGGAACCTCAAGCATCAACAGTAGCTATTTCTATG  
 TTTAGTCGTGTATCGGCTTTAAATGATGCAATAACAAAACCTATCATCTTTTGCAGAGGCT  
 GCAACTCTTCAAGGGACTGCTTATTCAAATGCAAAAAGCTATGCTACTGGAACGTTAACT  
 CCGATGCTTCAAGGAATGATTCCTTTCTCTGAAACATTGAGTGAGAAATGTACAGAATTA  
 CAAACCTTATATGTCTCAATTTGTGGTGTAGGATTTAGACTCTGTCTGTTTAGAATCA  
 AAATTAGCAAGTGTAGGGCATCATTAAGATTGTGAAGCACITTTAGAGCATCTTAAC  
 GATGATCCAGAACCTTCCAAATCTGCCATAAGTTCTACAAAAAGTAATATTAAAAAATTA  
 AAAAAACGTATAAAATCTAATCAAAAGAAATTAGACAACCTTAATGAATTTAACGCCCAT  
 TCAGCAACAGTATTTGCGGACATTTCTAATGCACAGTCAACTGTTAACCAAGCACTAGCG  
 GCTGTTTCAACAGGATTTTCTGGATATAATAGTAAACCCGAGCTTTTGGAAAACCAACA  
 TCCGGACAGATGGAATGGACAAAGACAGTTAAGAAGAATTGGAAGAGCGAGAAGACGCC  
 AAAGCTGAAGAACTGAAAAGTAAAAAGGCTGAAGAAAAGTAAGAAGCTTCAAAAATTGAA  
 AATACTACTAAAAAAGTAATGTTTCAGTTGATAAAAAGAAATTAATAAAGCGGCTAAT  
 GAAGCGTATAAATTAGGAGAAATTAAAAAGATACCTATGAATCAATTATCAGTGGTTTA  
 AGTAATGCATCGGCTGCCTTACTTAAAGAGGTAGCTAAATCAAAATTGACTGACACAGCT  
 CGGCTATTGATG

## SEQ ID NO. 6102

## STRAIN 090

TTAAATGATGCAATAACAAAACCTATCATCTTTTGCAGAGGCT  
 GCAACTCTTCAAGGGACTGCTTATTCAAATGCAAAAAGCTATGCTACTGG  
 AACGTTAACTCCGATGCTTCAAGGAATGATTCTTTCTCTGAAACATTGA  
 GTGAGAAATGTACAGAATTACAAACCTTATATGTCTCAATTTGTGGTGT  
 GAGGATTTAGACTCTGTCTGTTTAGAATCAAAATTAGCAAGTGTAGGGC  
 ATCATTAAAGATTGTGTAAGCACTTTTAGAGCATCTTAACGATGATCCAG  
 AACCTTCCAAATCTGCCATAAGTTCTACAAAAAGTAATATTAAAAAATTA  
 AAAAAACGTATAAAATCTAATCAAAAGAAATTAGACAACCTTAATGAAT  
 TAAGCCCATTCAGCAACAGTATTTGCGGACATTTCTAATGCACAGTCAA  
 CTGTTAACCAAGCACTAGCGGCTGTTTCAACAGGATTTTCTGGATATAAT  
 AGTAAAAACGGAGCTTTTGGAAAACCAACATCCGACAGATGGAATGGAC  
 AAAGACAGTTAAGAAGAATTGGAAGAGCGAGAAGACGCCAAAGCTGAAG  
 AACTGAAAAGTAAAAAGGCTGAAGAAAAGTAAGAAGCTTCAAAAATTGAA  
 AATACTACTAAAAAAGTAATGTTTCAGTTGATAAAAAGAAATTAATAAA  
 AGCGGCTAATGAAGCGTATAAATTAGGAGAAATTAAAAAGATACCTATG  
 AATCAATTATCAGTGGTTAAGTAATGCATCGGCTGCCTTACTTAAAGAG  
 GTAGCTAAATCAAAATTGACTGACACAGCTCGGCTATTGATG

## SEQ ID NO. 6103

## STRAIN 18RS21

TTAAATGATGCAATAACAAAACCTATCATCTTTTGCAGAGGCT  
 TGCAACTCTTCAAGGGACTGCTTATTCAAATGCAAAAAGCTATGCTACTG  
 GAACGTTAACTCCGATGCTTCAAGGAATGATTCTTTCTCTGAAACATTG  
 AGTGAGAAATGTACAGAATTACAAACCTTATATGTCTCAATTTGTGGTGA  
 TGAGGATTTAGACTCTGTCTGTTTAGAATCAAAATTAGCAAGTGTAGGG  
 CATCATTAAAGATTGTGTAAGCACTTTTAGAGCATCTTAACGATGATCCA  
 GAACCTTCCAAATCTGCCATAAGTTCTACAAAAAGTAATATTAAAAAATTA  
 AAAAAACGTATAAAATCTAATCAAAAGAAATTAGACAACCTTAATGAAT  
 TTAACGCCCATTCAGCAACAGTATTTGCGGACATTTCTAATGCACAGTCA  
 ACTGTTAACCAAGCACTAGCGGCTGTTTCAACAGGATTTTCTGGATATAA  
 TAGTAAAACCGAGCTTTTGGAAAACCAACATCCGACAGATGGAATGGGA  
 CAAAGACAGTTAAGAAGAATTGGAAGAGCGAGAAGACGCCAAAGCTGAAG  
 GAACGAAAAGTAAAAAGGCTGAAGAAAAGTAAGAAGCTTCAAAAATTGA  
 AATACTACTAAAAAAGTAATGTTTCAGTTGATAAAAAGAAATTAATAAA  
 AAGCGGCTAATGAAGCGTATAAATTAGGAGAAATTAAAAAGATACCTAT  
 GAATCAATTATCAGTGGTTAAGTAATGCATCGGCTGCCTTACTTAAAGA  
 GGTAGCTAAATCAAAATTGACTGACACAGCTCGGCTATTGATG

PRETTY of: /biotmp/msa185066.2{\*} May 13, 2003 07:01 ..

	1				50
msa185066.2{270_090}	-----	-----	-----	-----	-----
msa185066.2{270_18RS21}	-----	-----	-----	-----	-----
msa185066.2{270_2603}	atggtaaaag	ttagtgtgaag	ttctgttagga	actcaagcat	caacagtagc
Consensus	*****	*****	*****	*****	*****
	51				100
msa185066.2{270_090}	-----	-----	-----TT	AAATGATGCA	ATAACAAAAC
msa185066.2{270_18RS21}	-----	-----	-----TT	AAATGATGCA	ATAACAAAAC
msa185066.2{270_2603}	tattttctatg	tttagtcgtg	tatcggcttt	AAATGATGCA	ATAACAAAAC
Consensus	*****	*****	*****	*****	*****
	101				150
msa185066.2{270_090}	TATCATCTTT	TGCAGAGGCT	GCAACTCTTC	AAGGGACTGC	TTATTCAAAT
msa185066.2{270_18RS21}	TATCATCTTT	TGCAGAGGCT	GCAACTCTTC	AAGGGACTGC	TTATTCAAAT
msa185066.2{270_2603}	TATCATCTTT	TGCAGAGGCT	GCAACTCTTC	AAGGGACTGC	TTATTCAAAT
Consensus	*****	*****	*****	*****	*****
	151				200
msa185066.2{270_090}	GCAAAAAGCT	ATGCTACTGG	AACGTTAACT	CCGATGCTTC	AAGGAATGAT
msa185066.2{270_18RS21}	GCAAAAAGCT	ATGCTACTGG	AACGTTAACT	CCGATGCTTC	AAGGAATGAT
msa185066.2{270_2603}	GCAAAAAGCT	ATGCTACTGG	AACGTTAACT	CCGATGCTTC	AAGGAATGAT

Table 61: Comparative Sequences relating to SAG1030

Consensus	*****	*****	*****	*****	*****
	201				250
msa185066.2{270_090}	TCTTTTCTCT	GAAACATTGA	GTGAGAAATG	TACAGAATTA	CAAACCTTAT
msa185066.2{270_18RS21}	TCTTTTCTCT	GAAACATTGA	GTGAGAAATG	TACAGAATTA	CAAACCTTAT
msa185066.2{270_2603}	TCTTTTCTCT	GAAACATTGA	GTGAGAAATG	TACAGAATTA	CAAACCTTAT
Consensus	*****	*****	*****	*****	*****
	251				300
msa185066.2{270_090}	ATGTCCTCAAT	TTGTGGTGAT	GAGGATTTAG	ACTCTGTCGT	TTTAGAATCA
msa185066.2{270_18RS21}	ATGTCCTCAAT	TTGTGGTGAT	GAGGATTTAG	ACTCTGTCGT	TTTAGAATCA
msa185066.2{270_2603}	ATGTCCTCAAT	TTGTGGTGAT	GAGGATTTAG	ACTCTGTCGT	TTTAGAATCA
Consensus	*****	*****	*****	*****	*****
	301				350
msa185066.2{270_090}	AAATTAGCAA	GTGATAGGGC	ATCATTAAAG	ATTGCTGAAG	CACCTTTAGA
msa185066.2{270_18RS21}	AAATTAGCAA	GTGATAGGGC	ATCATTAAAG	ATTGCTGAAG	CACCTTTAGA
msa185066.2{270_2603}	AAATTAGCAA	GTGATAGGGC	ATCATTAAAG	ATTGCTGAAG	CACCTTTAGA
Consensus	*****	*****	*****	*****	*****
	351				400
msa185066.2{270_090}	GCATCTTAAC	GATGATCCAG	AACCTTCCAA	ATCTGCCATA	AGTTCTACAA
msa185066.2{270_18RS21}	GCATCTTAAC	GATGATCCAG	AACCTTCCAA	ATCTGCCATA	AGTTCTACAA
msa185066.2{270_2603}	GCATCTTAAC	GATGATCCAG	AACCTTCCAA	ATCTGCCATA	AGTTCTACAA
Consensus	*****	*****	*****	*****	*****
	401				450
msa185066.2{270_090}	AAAGTAATAT	TAAAAAATTA	AAAAAACGTA	TAAATCTAA	TCAAAAGAAA
msa185066.2{270_18RS21}	AAAGTAATAT	TAAAAAATTA	AAAAAACGTA	TAAATCTAA	TCAAAAGAAA
msa185066.2{270_2603}	AAAGTAATAT	TAAAAAATTA	AAAAAACGTA	TAAATCTAA	TCAAAAGAAA
Consensus	*****	*****	*****	*****	*****
	451				500
msa185066.2{270_090}	TTAGACAACC	TTAATGAATT	TAACGCCCAT	TCAGCAACAG	TATTTGCGGA
msa185066.2{270_18RS21}	TTAGACAACC	TTAATGAATT	TAACGCCCAT	TCAGCAACAG	TATTTGCGGA
msa185066.2{270_2603}	TTAGACAACC	TTAATGAATT	TAACGCCCAT	TCAGCAACAG	TATTTGCGGA
Consensus	*****	*****	*****	*****	*****
	501				550
msa185066.2{270_090}	CATTTCTAAT	GCACAGTCAA	CTGTTAACCA	AGCACTAGCG	GCTGTTTCAA
msa185066.2{270_18RS21}	CATTTCTAAT	GCACAGTCAA	CTGTTAACCA	AGCACTAGCG	GCTGTTTCAA
msa185066.2{270_2603}	CATTTCTAAT	GCACAGTCAA	CTGTTAACCA	AGCACTAGCG	GCTGTTTCAA
Consensus	*****	*****	*****	*****	*****
	551				600
msa185066.2{270_090}	CAGGATTTTC	TGGATATAAT	AGTAAACCG	GAGCTTTTGG	AAAACCAACA
msa185066.2{270_18RS21}	CAGGATTTTC	TGGATATAAT	AGTAAACCG	GAGCTTTTGG	AAAACCAACA
msa185066.2{270_2603}	CAGGATTTTC	TGGATATAAT	AGTAAACCG	GAGCTTTTGG	AAAACCAACA
Consensus	*****	*****	*****	*****	*****
	601				650
msa185066.2{270_090}	TCCGGACAGA	TGGAATGGAC	AAAGACAGTT	AAGAAGAATT	GGAAAGAGCG
msa185066.2{270_18RS21}	TCCGGACAGA	TGGAATGGAC	AAAGACAGTT	AAGAAGAATT	GGAAAGAGCG
msa185066.2{270_2603}	TCCGGACAGA	TGGAATGGAC	AAAGACAGTT	AAGAAGAATT	GGAAAGAGCG
Consensus	*****	*****	*****	*****	*****
	651				700
msa185066.2{270_090}	AGAAGACGCC	AAAGCTGAAG	AACTGAAAAG	TAAAAAGGCT	GAAGAAAGTA
msa185066.2{270_18RS21}	AGAAGACGCC	AAAGCTGAAG	AACTGAAAAG	TAAAAAGGCT	GAAGAAAGTA
msa185066.2{270_2603}	AGAAGACGCC	AAAGCTGAAG	AACTGAAAAG	TAAAAAGGCT	GAAGAAAGTA
Consensus	*****	*****	*****	*****	*****
	701				750
msa185066.2{270_090}	AGAAAGCTTC	AAAAATTGAA	AATACTACTA	AAAAAAGTAA	TGTTTCAGTT
msa185066.2{270_18RS21}	AGAAAGCTTC	AAAAATTGAA	AATACTACTA	AAAAAAGTAA	TGTTTCAGTT
msa185066.2{270_2603}	AGAAAGCTTC	AAAAATTGAA	AATACTACTA	AAAAAAGTAA	TGTTTCAGTT
Consensus	*****	*****	*****	*****	*****
	751				800
msa185066.2{270_090}	GATAAAAAGA	AATTAATAAA	AGCGGCTAAT	GAAGCGTATA	AATTAGGAGA
msa185066.2{270_18RS21}	GATAAAAAGA	AATTAATAAA	AGCGGCTAAT	GAAGCGTATA	AATTAGGAGA
msa185066.2{270_2603}	GATAAAAAGA	AATTAATAAA	AGCGGCTAAT	GAAGCGTATA	AATTAGGAGA
Consensus	*****	*****	*****	*****	*****
	801				850
msa185066.2{270_090}	AATTAAAAAA	GATACCTATG	AATCAATTAT	CAGTGGTTTA	AGTAATGCAT
msa185066.2{270_18RS21}	AATTAAAAAA	GATACCTATG	AATCAATTAT	CAGTGGTTTA	AGTAATGCAT
msa185066.2{270_2603}	AATTAAAAAA	GATACCTATG	AATCAATTAT	CAGTGGTTTA	AGTAATGCAT
Consensus	*****	*****	*****	*****	*****
	851				900
msa185066.2{270_090}	CGGCTGCCTT	ACTTAAAGAG	GTAGCTAAAT	CAAAATTGAC	TGACACAGCT
msa185066.2{270_18RS21}	CGGCTGCCTT	ACTTAAAGAG	GTAGCTAAAT	CAAAATTGAC	TGACACAGCT

Table 61: Comparative Sequences relating to SAG1030

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msa185066.2{270_2603} CGGCTGCCTT ACTTAAAGAG GTAGCTAAAT CAAAATTGAC TGACACAGCT
Consensus *****
          901          912
msa185066.2{270_090} CGGCTATTGA TG
msa185066.2{270_18RS21} CGGCTATTGA TG
msa185066.2{270_2603} CGGCTATTGA TG
Consensus ***** **

SEQ ID NO. 6104
STRAIN 2603 frame: 1
MVKVSVSSVGTQASTVAISMFSRVSA LNDAITKLSSFABEAATLQGTAYSNKSYATGTLT
PMLQGMILFSETLSEKCTELQTLTVSICGDEDLDVSVLESKLASDRASLKIAEALLEHLN
DDPEPSKSAISSTKSNIKKLKKRIKSNQKKLDNLNEFNAHSATVFADISNAQSTVNQALA
AVSTGFSGYNSKTGAFGKPTSGQMEWTKTVKKNWKEREDAKAEELKSKKAEESKKASKIE
NTTKKSNVSVDDKKLIKAANEAYKLGEIKKDTYESIISGLSNASAALLKEVAKSKLTDTA
RLLM

SEQ ID NO. 6105
STRAIN 090 frame: 1
LNDAITKLSSFABEAATLQGTAYSNKSYATGTLTPMLQGMILFSETLSEKCTELQTLTVS
ICGDEDLDVSVLESKLASDRASLKIAEALLEHLNDDPEPSKSAISSTKSNIKKLKKRIKS
NQKKLDNLNEFNAHSATVFADISNAQSTVNQALAAVSTGFSGYNSKTGAFGKPTSGQMEW
TKTVKKNWKEREDAKAEELKSKKAEESKKASKIENTTKKSNVSVDDKKLIKAANEAYKLGE
IKKDTYESIISGLSNASAALLKEVAKSKLTDARLLM

SEQ ID NO. 6106
STRAIN 18RS21 frame: 1
LNDAITKLSSFABEAATLQGTAYSNKSYATGTLTPMLQGMILFSETLSEKCTELQTLTVS
ICGDEDLDVSVLESKLASDRASLKIAEALLEHLNDDPEPSKSAISSTKSNIKKLKKRIKS
NQKKLDNLNEFNAHSATVFADISNAQSTVNQALAAVSTGFSGYNSKTGAFGKPTSGQMEW
TKTVKKNWKEREDAKAEELKSKKAEESKKASKIENTTKKSNVSVDDKKLIKAANEAYKLGE
IKKDTYESIISGLSNASAALLKEVAKSKLTDARLLM
PRETTY of: /biotmp/msa185181.2{*} May 13, 2003 07:03 ..

          1          50
msa185181.2{270_090} ~~~~~~LND AITKLSSFABEAATLQGTAYSN
msa185181.2{270_18RS21} ~~~~~~LND AITKLSSFABEAATLQGTAYSN
msa185181.2{270_2603} mvkvs svsg tqastvaism fersva LNDAITKLSSFABEAATLQGTAYSN
Consensus *****

          51          100
msa185181.2{270_090} AKSYATGTLT PMLQGMILFS ETLSEKCTEL QTLVVSICGD EDLDSVVLES
msa185181.2{270_18RS21} AKSYATGTLT PMLQGMILFS ETLSEKCTEL QTLVVSICGD EDLDSVVLES
msa185181.2{270_2603} AKSYATGTLT PMLQGMILFS ETLSEKCTEL QTLVVSICGD EDLDSVVLES
Consensus *****

          101          150
msa185181.2{270_090} KLASDRASLK IAEALLEHLN DDPEPSKSAI SSTKSNIKKL KKRIKSNQKK
msa185181.2{270_18RS21} KLASDRASLK IAEALLEHLN DDPEPSKSAI SSTKSNIKKL KKRIKSNQKK
msa185181.2{270_2603} KLASDRASLK IAEALLEHLN DDPEPSKSAI SSTKSNIKKL KKRIKSNQKK
Consensus *****

          151          200
msa185181.2{270_090} LDNLNEFNAH SATVFADISN AQSTVNQALA AVSTGFSGYN SKTGAFGKPT
msa185181.2{270_18RS21} LDNLNEFNAH SATVFADISN AQSTVNQALA AVSTGFSGYN SKTGAFGKPT
msa185181.2{270_2603} LDNLNEFNAH SATVFADISN AQSTVNQALA AVSTGFSGYN SKTGAFGKPT
Consensus *****

          201          250
msa185181.2{270_090} SGQMEWTKTV KKNWKEREDA KAEELKSKKA EESKKASKIE NTTKKNVSV
msa185181.2{270_18RS21} SGQMEWTKTV KKNWKEREDA KAEELKSKKA EESKKASKIE NTTKKNVSV
msa185181.2{270_2603} SGQMEWTKTV KKNWKEREDA KAEELKSKKA EESKKASKIE NTTKKNVSV
Consensus *****

          251          300
msa185181.2{270_090} DKKKLIKAAN EAYKLGEIKK DYESIISGL SNASAALLKE VAKSKLTDTA
msa185181.2{270_18RS21} DKKKLIKAAN EAYKLGEIKK DYESIISGL SNASAALLKE VAKSKLTDTA
msa185181.2{270_2603} DKKKLIKAAN EAYKLGEIKK DYESIISGL SNASAALLKE VAKSKLTDTA
Consensus *****

          301
msa185181.2{270_090} RLLM
msa185181.2{270_18RS21} RLLM
msa185181.2{270_2603} RLLM
Consensus ****

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Table 62: Comparative Sequences relating to SAG0690

SEQ ID NO. 6201

STRAIN 2603

ATGATTTTAAAAATTTGTCGTGCAGCATATAGTTTACAATGGGGAGGTGTTTACCAATTA  
 GCTTTGCTGGATTATCCTCGAATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATA  
 GCTTACGAGAAACAATATAAAAGAAAACTGAGATACAATGTGACGATAAACATCTCCTC  
 GCAAAATTTGTTCAATTTTAAAAATACAATAGTTTACTTTTCCCTATATTTCCCAATAT  
 AGAGAAGCGGCAGCTACTTTTAAATGAGGATGGTATTAGTTTAACTTCTGATTTTAAAGC  
 CATACATGTACGATTGAACTGCAAACTAATTTTAAAGAAGGTAAAACTTATCAGCA  
 GTTAAAGCCTTTAATAAGCCTGCTGAAGTACTGGTAAAGATAAGAGGAATGCTGCTGGA  
 GACCTTAAAGATTACTTTGACTATGTGATGTTGAACCTGGTCAAATACCAATCTCGTTAT  
 CGTTTAGTAATGGAAAGATTGTTAGGCAAGCACCATCTGAACAGGAGTTAACAGTAGGT  
 TTTAAGCCAGGGGTCAGTTTTCATTTTACTTATCAAGATATCATCAATCATCCTGATTCT  
 ATTTTGTATGGTTATCATCCTGCTGCTAAAAATAAAAATCAGCTTCTTTAGCAGAACATTTA  
 GTTGATGTGTTATCCCAAAACATTATCAAGAAGATTATCAAGCCTTGTGCCCAATGAC  
 TTGAAACACAGGGTTTATTATTTAGATTACTGTAACGAAACACTTTATGAGTGGAATCAA  
 AAAGTTTATGATTTTCTTTGTCAATTGGAAAAATAA

SEQ ID NO. 6202

STRAIN 090

TGGATTATCCTCTAATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTC  
 ATAGCTTACGAGAAACAATATAAAAGAAAAATTGAGATACAATGTGACGA  
 TAAACATCTCCTCACAAAATTTGTTCAATTTTAAAAATACAATAGTTTAA  
 CTTTTCCCTATATTTCCCAATATAGAGAAGCGGCAGCTACTTTTAAATGAG  
 GATGGTATTAGTTTAACTTCTGATTTTAAAGCCATACATGTACGATTGA  
 AACTGCAAACTAATTTTAAAGAAGGTAAAACTTATCAGCAGTTAAAG  
 CCTTTAATAAGCCTGCTGAAGTACTGGTAAATGATAAGAGGAATGCTGCT  
 GGAGACCTTAAAGATTACTTTGACTATGTGATGTTGAACCTGGTCAAATAC  
 CAATCTCGTTTATCGTTTAGTAATGGAAAGATTGTTAGGCAAGCACCAT  
 CTGAACAGGAGTTAACAGTAGCTTTTAAAGCCAGGGGTCAGCTTTCATTTT  
 AATTATCAAGATATCATCAATCATCCTGATTCTATTTTGTATGGTTATCA  
 TCCTGCTAAAATTAATAATCAACTTTCTTTAGCAGAACATTTAGTTGAT  
 GTGTTATCCCAAAACATTATCAAGAAGATTATCAAGCCTTGTGCCCTAAT  
 GACTTGAAACACAGAGTTTATTATTTAGATTACTGTAACGAAACACTTTA  
 TGAGTGGAATCAAAAAGTTTATGATTTCTTTGTCAATTGGAAAAATAA

SEQ ID NO. 6203

STRAIN A909

TTGCTGGATTATCCTCGAATTAAGGCGTTTGAATTGGAAAGGATA  
 GGAGCTTTCTAGCTTACGAGAAACAATATAAAAGAAAAATTGAGATACA  
 ATGTGACGATAAACATCTCCTCACAAAATTTGTTCAATTTTAAAAATACA  
 ATAGTTTACTTTTCCCTATATTTCCCAATATAGAGAAGCGGCAGCTACT  
 TTTAATGAGGATGGTATAGTTTAACTTCTGATTTTAAAGCCATACATG  
 TACGATTGAACTGCAAACTAATTTTAAAGAAGGTAAAACTTATCAG  
 CAGTTAAAGCCTTTAATAAGCCTGCTGAAGTACTGGTAAATGATAAGAGG  
 AATGCTGCTGGAGACCTTAAAGATTACTTTGACTATGTGATGTTGAACCTG  
 GTCAAATACCAATCTCGTTTATCGTTTAGTAATGGAAAGATTGTTAGGCA  
 AAGCACCATCTGAACAGGAGTTAACAGTAGCTTTTAAAGCCAGGGGTCAGC  
 TTTCAATTTAATTATCAAGATATCATCAATCATCCTGATTCTATTTTGA  
 TGGTTATCATCTGCTAAAATTAATAATCAACTTTCTTTAGCAGAACATT  
 TAGTTGCAATGTGTTATCCCAAAACATTATCAAGAAGATTATCAAGCCTT  
 GTGCCCTAATGACTTGAAACACAGAGTTTATTATTTAGATTACTGTAACGA  
 AACACTTTATGAGTGGAATCAAAAAGTTTATGATTTCTTTGTCAATTGG  
 AAAATAA

SEQ ID NO. 6204

STRAIN H36B

TTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGAAA  
 CAATATAAAAGAAAAATTGAGATACAATGTGACGATAAACATCTCCTCAC  
 AAAAATTTGTTCAATTTTAAAAATACAATAGTTTACTTTTCCCTATATTC  
 CCAATATAGAGAAGCGGCAGCTACTTTTAAATGAGGATGGTATTAGTTTA  
 ACTTCTGATTTTAAAGCCATACATGTACGATTGAAACTGCAAACTAAT  
 TTTTAAAGAAGGTAAAACTTATCAGCAGTTAAAGCCTTTAATAAGCCTG  
 CTGAAGTACTGGTAAATGATAAGAGGAATGCTGCTGGAGACCTTAAAGAT  
 TACTTTGACTATGTGATGTTGAACCTGGTCAAATACCAATCTCGTTTATCG  
 TTTAGTAATGGAAAGATTGTTAGGCAAGCACCATCTGAACAGGAGTTAA  
 CAGTAGCTTTTAAAGCCAGGGGTCAGCTTTCATTTTAAATTATCAAGATATC  
 ATCAATCATCCTGATTCTATTTTGTATGGTTATCATCCTGCTAAAATTA  
 AATCAACTTTCTTTAGCAGAACATTAGTTGATGTGTTATCCCAAAAC  
 ATTATCAAGAAGATTATCAAGCCTTGTGCCCTAATGACTTGAAACACAGA  
 GTTTATTATTTAGATTACTGTAACGAAACACTTTATGAGTGGAATCAAAA  
 AGTTTATGATTTTCTTTGTCAATTGGAAAAATAA

SEQ ID NO. 6205

STRAIN 18RS21

TTGCTGGATTATCCTCGAATTAAGGCGTT  
 TGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGAAACAATATAAA  
 GAAAACTGAGATACAATGTGACGATAAACATCTCCTCGCAAAATTTGTT  
 CATTTTAAAAATACAATAGTTTACTTTTCCCTATATTTCCCAATATAG  
 AGAAGCGGCAGCTACTTTTAAATGAGGATGGTATTAGTTTAACTTCTGATT  
 TTTTAAAGCCATACATGTACGATTGAACTGCAAACTAATTTTAAAGAA  
 GGTAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCCTGCTGAAGTACT  
 GGTAAAGATAAGAGGAATGCTGCTGGAGACCTTAAAGATTACTTTGACT  
 ATGTGATGTTGAACCTGGTCAAATACCAATCTCGTTTATGTAATG



Table 62: Comparative Sequences relating to SAG0690

GAAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAACAGTAGGTTT  
 TAAGCCAGGGGTGAGTTTTCATTTTACTTATCAAGATATCATCAATCATC  
 CTGATTCTATTTTGTATGGTTATCATCCTGCTAAAATTAAAAATCAGCTT  
 TCTTTAGCAGAACATTAGTTGCATGTGTATCCCAAAACATTATCAAGA  
 AGATTATCAAAGCCTTGTGCCAATGACTTGAACACAGGGTTTATTATT  
 TAGATTACTGTAACGAAACACTTTATGAGTGGAATCAAAAAGTTTATGAT  
 TTTCTTTGTCATTTGGAAAATAAA

## SEQ ID NO. 6206

## STRAIN M732

TTGCTGGATTATCCTCGAATTAAGGCGTT  
 TGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGAAACAATATAAAA  
 GAAAACTGAGATACAATGTGACGATAAACATCTCCTCGCAAAAATTTGTT  
 CATTTTAAATAACAATAGTTTACITTTCCCTATATCCCAAAATATAG  
 AGAAGCGGCAGCTACTTTAATGAGGATGGTATTAGTTAACTTCTGATT  
 TTTTAAAGCCATACATGTACGATTGAAACTGCAAACTAATTTTAAAGAA  
 GGTAAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCCTGCTGAAGTACT  
 GGTAAAAGATAAGAGGAATGCTGCTGGAGACCCTAAAGATTACTTTGACT  
 ATGTGATGTTGAAGTGGTCAAAATACCAATTCTGGTTATCGTTTAGTAATG  
 GAAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAACAGTAGGTTT  
 TAAGCCAGGGGTGAGTTTTCATTTTACTTATCAAGATATCATCAATCATC  
 CTGATTCTATTTTGTATGGTTATCATCCTGCTAAAATTAAAAATCAGCTT  
 TCTTTAGCAGAACATTAGTTGCATGTGTATCCCAAAACATTATCAAGA  
 AGATTATCAAAGCCTTGTGCCAATGACTTGAACACAGGGTTTATTATT  
 TAGATTACTGTAACGAAACACTTTATGAGTGGAATCAAAAAGTTTATGAT  
 TTTCTTTGTCATTTGGAAAATAAA

## SEQ ID NO. 6207

## STRAIN COH1

## TTGCTGGAT

TATCCTCGAATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATAGC  
 TTACGAGAAACAATATAAAAGAAAACTGAGATACAATGTGACGATAAAC  
 ATCTCCTCGCAAAAATTTGTTTCAITTTTAAATAACAATAGTTTACTTTT  
 CCTATATTTCCCAATATAGAGAAGCGGCAGCTACTTTAATGAGGATGG  
 TATTAGTTTAACTTCTGATTTTTAAAGCCATACATGTACGATTGAAACTG  
 CAAACTAATTTTAAAGAAAGGTAAAATCTTATCAGCAGTTAAAGCCTTT  
 AATAAGCCTGCTGAAGTACTGGTAAAAGATAAGAGGAATGCTGCTGGAGA  
 CCTTAAAGATTACTTTGACTATGTGATGTTGAAGTGGTCAAAATACCAAT  
 CTGGTTATCGTTTAGTAATGGAAGATTGTTAGGCAAAGCACCATCTGAA  
 CAGGAGTTAACAGTAGGTTTAAAGCCAGGGGTGAGTTTTCATTTTACTTA  
 TCAAGATATCATCAATCATCTCTGATTCTATTTTGTATGGTTATCATCTG  
 CTAAAATTAATAATCAGCTTCTTTAGCAGAACATTAGTTGCATGTGTT  
 ATCCCAAAACATTATCAAGAAGATTATCAAAGCCTTGTGCCCAATGACTT  
 GAAACACAGGGTTTATTATTAGATTACTGTAAACGAAACACTTTATGAGT  
 GGAATCAAAAAGTTTATGATTTTCTTTGGCAITTTGGAAAATAAA

## SEQ ID NO. 6208

## STRAIN M781

## TTGCTGGA

TTATCCTCGAATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATAG  
 CTTACGAGAAACAATATAAAAGAAAACTGAGATACAATGTGACGATAAA  
 CATCTCCTCGCAAAAATTTGTTTCAITTTTAAATAACAATAGTTTACTTT  
 TCCTATATTTCCCAATATAGAGAAGCGGCAGCTACTTTAATGAGGATG  
 GTATTAGTTTAACTTCTGATTTTTAAAGCCATACATGTACGATTGAACT  
 GCAAACTAATTTTAAAGAAAGGTAAAATCTTATCAGCAGTTAAAGCCTT  
 TAATAAGCCTGCTGAAGTACTGGTAAAAGATAAGAGGAATGCTGCTGGAG  
 ACCCTAAAGATTACTTTGACTATGTGATGTTGAAGTGGTCAAAATACCAAT  
 TCTGGTTATCGTTTAGTAATGGAAGATTGTTAGGCAAAGCACCATCTGA  
 ACAGGAGTTAAACAGTAGGTTTAAAGCCAGGGGTGAGTTTTCATTTTACTT  
 ATCAAGATATCATCAATCATCTCTGATTCTATTTTGTATGGTTATCATCT  
 GCTAAAATTAATAATCAGCTTCTTTAGCAGAACATTAGTTGCATGTGT  
 TATCCCAAAACATTATCAAGAAGATTATCAAAGCCTTGTGCCCAATGACT  
 TGAACACAGGGTTTATTATTAGATTACTGTAAACGAAACACTTTATGAGT  
 TGAATCAAAAAGTTTATGATTTTCTTTGTCATTTGGAAAATAAA

## SEQ ID NO. 6209

## STRAIN CJB110

## TTGCTGGATTATCCTCGAATTAAGGC

GTTTGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGAAACAATATA  
 AAAGAAAAATTTAGATACAATGTGACGATAAACATCTCCTCACAATAAT  
 GTTCATTTTAAATAACAATAGTTTACTTTTCCCTATATTTCCCAATA  
 TAGAGAAGCGGCAGCTACTTTAATGAGGATGGTATTAGTTTAACTTCTG  
 ATTTTAAAGCCATACATGTACGATTGAACTGCAAACTAATTTTAA  
 GAAGTAAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCCTGCTGAAGT  
 ACTGGTAAATGATAAGAGGAATGCTGCTGGAGACCCTAAAGATTACTTTG  
 ACTATGTGATGTTGAAGTGGTCAAAATACCAATTCTGGTTATCGTTTAGTA  
 ATGGAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAACAGTAGC  
 TTTTAAAGCCAGGGGTGAGCTTTTCAITTTAATTATCAAGATATCATCAATC  
 ATCCTGATTCTATTTTGTATGGTTATCATCTGCTAAAATTAATAATCA  
 CTTTCTTTAGCAGAACATTAGTTGCATGTGTATCCCAAAACATTATCA  
 AGAAGATTATCAAAGCCTTGTGCTTAATGACTTGAACACAGAGTTTATT  
 ATTTAGATTACTGTAACGAAACACTTTATGAGTGAATCAAAAAGTTTAT  
 GATTTCTTTGTCATTTGGAAAATAAA

Table 62: Comparative Sequences relating to SAG0690

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SEQ ID NO. 6210
STRAIN 1169NT
AATTAAGCGCTTTGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGA
AACAAATATAAAAGAAAGAACTGAGATACAATGTGACGATAAACATCTCCTC
GCAAAAATTGTTTCAATTTTAAATACAAATAGTTTACTTTTCCCTATAT
TCCCAAATATAGAGAAGCGGCGAGCTACITTTAATGAGGATGCTATTAGTT
TAACCTTCTGATTTTAAAGCCATACATGTACGATTGAAAGTCAAAAGCTA
ATTTTAAAGAAGGTAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCC
TGCTGAAGTACTGGTAAATGATAAGAGGAATGCTGCTGGAGACCCATAAG
ATTACTTTGACTATGTGATGTTGAAGTGGTCAAATACCAATTCTGTTAT
CGTTTAGTAATGGAAAGATTGTTAGGCAAGCACCATCTGAACAGGAGTT
AACAGTAGGTTTAAAGCCAGGGGTCAGCTTTCATTTACTTATCAAGATA
TCATCAATCATCCTGATTCTATTTTGTATGGTTATCATCCTGCTAAAT
AAAAATCAGCTTCTTTAGCAGAACATTAGTTGCGTGTGTATCCCAA
ACATTATCAAGAAGATTATCAAAATCTTGTGCCCAATGACTTGAAACACA
GAGTTTATTTAGATTACTGTAACGAAACACTTTATGAGTGGAAATCAA
AAAGTTTATGATTTCTTTGTCATTTGGAATAA

SEQ ID NO. 6211
STRAIN JM9130013
ATAGGAGCTTTCATAGCTTACGAGAAACAATATAAAAGAAAAATTGAGAT
ACAATGTGACGATAAACATCTCCTCACAATAATTGTTCAATTTTTAAAT
ACAATAGTTTTACTTTTCCCTATATTTCCCAAATATAGAGAAGCGGCGAGCT
ACTTTTAAATGAGGATGGTATTAGTTTAACTTCTGATTTTAAAGCCATAC
ATGTACGATTGAAAGTCAAAAGCTAAATTTTAAAGAAGGTAAATCTTAT
CAGCAGTTAAAGCCTTTAAAGCCTGCTGAAGTACTGGTAAATGATAAG
AGGAATGCTGCTGGAGACCCATAAGATTACTTTGACTATGTGATGTTGAA
CTGGTCAAATACCAATTCTGGTTATCGTTTAGTAATGGAAAGATTGTTAG
GCAAAGCACCATCTGAACAGGAGTTAAACAGTAGCTTTAAAGCCAGGGGTC
AGCTTTCATTTTAAATATCAAGATATCATCAATCATCCTGATTCTATTTT
TGATGGTTATCATCCTGCTAAATTAATAATCAACTTCTTTAGCAGAAC
ATTTAGTTGCAATGTGTTATCCCAAACATTATCAAGAAGATTATCAAGAC
CTTGTGCTAATGACTTGAACACAGAGTTTATTTATTTAGATTACTGTAA
CGAAACACTTTATGAGTGAATCAAAAAGTTTATGATTTTCTTTGTCATT
TGGAATAA

PRETTY of: /biotmp/msa185284.2(*) May 13, 2003 07:08 ..

      1                                     50
msa185284.2{271_090} ~~~~~~
msa185284.2{271_H36B} ~~~~~~
msa185284.2{271_JM9130013} ~~~~~~
msa185284.2{271_A909} ~~~~~~
msa185284.2{271_CJB110} ~~~~~~
msa185284.2{271_18RS21} ~~~~~~
msa185284.2{271_2603} atgattttaa aaatttgtcg tgcagcatat agtttacaat ggggaggtgt
msa185284.2{271_M732} ~~~~~~
msa185284.2{271_M781} ~~~~~~
msa185284.2{271_COH1} ~~~~~~
msa185284.2{271_1169NT} ~~~~~~
Consensus *****

      51                                     100
msa185284.2{271_090} ~~~~~~ -tgg attatcctct aattaaggcg tttgaattgg
msa185284.2{271_H36B} ~~~~~~ -ttaaggcg tttgaattgg
msa185284.2{271_JM9130013} ~~~~~~
msa185284.2{271_A909} ~~~~~~ -TTGctgg attatcctcg aattaaggcg tttgaattgg
msa185284.2{271_CJB110} ~~~~~~ -TTGctgg attatcctcg aattaaggcg tttgaattgg
msa185284.2{271_18RS21} ~~~~~~ -TTGctgg attatcctcg aattaaggcg tttgaattgg
msa185284.2{271_2603} ttaccaatta gctTTGctgg attatcctcg aattaaggcg tttgaattgg
msa185284.2{271_M732} ~~~~~~ -TTGctgg attatcctcg aattaaggcg tttgaattgg
msa185284.2{271_M781} ~~~~~~ -TTGctgg attatcctcg aattaaggcg tttgaattgg
msa185284.2{271_COH1} ~~~~~~ -TTGctgg attatcctcg aattaaggcg tttgaattgg
msa185284.2{271_1169NT} ~~~~~~ aattaaggcg tttgaattgg
Consensus *****

      101                                    150
msa185284.2{271_090} aaaggATAGG AGCTTTCATA GCTTACGAGA AACAAATATAA AAGAAAAAaT
msa185284.2{271_H36B} aaaggATAGG AGCTTTCATA GCTTACGAGA AACAAATATAA AAGAAAAAaT
msa185284.2{271_JM9130013} -----ATAGG AGCTTTCATA GCTTACGAGA AACAAATATAA AAGAAAAAaT
msa185284.2{271_A909} aaaggATAGG AGCTTTCATA GCTTACGAGA AACAAATATAA AAGAAAAAaT
msa185284.2{271_CJB110} aaaggATAGG AGCTTTCATA GCTTACGAGA AACAAATATAA AAGAAAAAaT
msa185284.2{271_18RS21} aaaggATAGG AGCTTTCATA GCTTACGAGA AACAAATATAA AAGAAAAAaT
msa185284.2{271_2603} aaaggATAGG AGCTTTCATA GCTTACGAGA AACAAATATAA AAGAAAAAaT
msa185284.2{271_M732} aaaggATAGG AGCTTTCATA GCTTACGAGA AACAAATATAA AAGAAAAAaT
msa185284.2{271_M781} aaaggATAGG AGCTTTCATA GCTTACGAGA AACAAATATAA AAGAAAAAaT
msa185284.2{271_COH1} aaaggATAGG AGCTTTCATA GCTTACGAGA AACAAATATAA AAGAAAAAaT
msa185284.2{271_1169NT} aaaggATAGG AGCTTTCATA GCTTACGAGA AACAAATATAA AAGAAAAAaT
Consensus -----*****

      151                                    200
msa185284.2{271_090} GAGATACAAT GTGACGATAA ACATCTCCTC aCAAAAATTG TTCATTTTTT

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Table 62: Comparative Sequences relating to SAG0690

msa185284.2{271_H36B}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	aCAAAAATTG	TTCATTTTTT
msa185284.2{271_JM9130013}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	aCAAAAATTG	TTCATTTTTT
msa185284.2{271_A909}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	aCAAAAATTG	TTCATTTTTT
msa185284.2{271_CJB110}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	aCAAAAATTG	TTCATTTTTT
msa185284.2{271_18RS21}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
msa185284.2{271_2603}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
msa185284.2{271_M732}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
msa185284.2{271_M781}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
msa185284.2{271_COH1}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
msa185284.2{271_1169NT}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
Consensus	*****	*****	*****	-*****	*****
201					250
msa185284.2{271_090}	AAAATACAAT	AGTTTTACTT	TCCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_H36B}	AAAATACAAT	AGTTTTACTT	TCCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_JM9130013}	AAAATACAAT	AGTTTTACTT	TCCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_A909}	AAAATACAAT	AGTTTTACTT	TCCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_CJB110}	AAAATACAAT	AGTTTTACTT	TCCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_18RS21}	AAAATACAAT	AGTTTTACTT	TCCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_2603}	AAAATACAAT	AGTTTTACTT	TCCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_M732}	AAAATACAAT	AGTTTTACTT	TCCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_M781}	AAAATACAAT	AGTTTTACTT	TCCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_COH1}	AAAATACAAT	AGTTTTACTT	TCCCTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_1169NT}	AAAATACAAT	AGTTTTACTT	TCCCTATAT	TCCCAAATAT	AGAGAAGCGG
Consensus	*****	*****	*****	*****	*****
251					300
msa185284.2{271_090}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_H36B}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_JM9130013}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_A909}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_CJB110}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_18RS21}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_2603}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_M732}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_M781}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_COH1}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_1169NT}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
Consensus	*****	*****	*****	*****	*****
301					350
msa185284.2{271_090}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_H36B}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_JM9130013}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_A909}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_CJB110}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_18RS21}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_2603}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_M732}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_M781}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_COH1}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_1169NT}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
Consensus	*****	*****	*****	*****	*****
351					400
msa185284.2{271_090}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_H36B}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_JM9130013}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_A909}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_CJB110}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_18RS21}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_2603}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_M732}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_M781}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_COH1}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_1169NT}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
Consensus	*****	*****	*****	*****	*****
401					450
msa185284.2{271_090}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_H36B}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_JM9130013}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_A909}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_CJB110}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_18RS21}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_2603}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_M732}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_M781}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_COH1}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_1169NT}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
Consensus	*****	*****	*****	*****	*****

Table 62: Comparative Sequences relating to SAG0690

msa185284.2{271_090}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_H36B}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_JM9130013}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_A909}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_CJB110}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_18RS21}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_2603}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_M732}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_M781}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_COH1}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_1169NT}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	GTTAGGCCAAA	GCACCATCTG	AACAGGAGTT	AACAGTAGcT	TTTAAGCCAG
msa185284.2{271_H36B}	GTTAGGCCAAA	GCACCATCTG	AACAGGAGTT	AACAGTAGcT	TTTAAGCCAG
msa185284.2{271_JM9130013}	GTTAGGCCAAA	GCACCATCTG	AACAGGAGTT	AACAGTAGcT	TTTAAGCCAG
msa185284.2{271_A909}	GTTAGGCCAAA	GCACCATCTG	AACAGGAGTT	AACAGTAGcT	TTTAAGCCAG
msa185284.2{271_CJB110}	GTTAGGCCAAA	GCACCATCTG	AACAGGAGTT	AACAGTAGcT	TTTAAGCCAG
msa185284.2{271_18RS21}	GTTAGGCCAAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
msa185284.2{271_2603}	GTTAGGCCAAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
msa185284.2{271_M732}	GTTAGGCCAAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
msa185284.2{271_M781}	GTTAGGCCAAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
msa185284.2{271_COH1}	GTTAGGCCAAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
msa185284.2{271_1169NT}	GTTAGGCCAAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_H36B}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_JM9130013}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_A909}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_CJB110}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_18RS21}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_2603}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_M732}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_M781}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_COH1}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_1169NT}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAaC	TTTCTTTAGC
msa185284.2{271_H36B}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAaC	TTTCTTTAGC
msa185284.2{271_JM9130013}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAaC	TTTCTTTAGC
msa185284.2{271_A909}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAaC	TTTCTTTAGC
msa185284.2{271_CJB110}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAaC	TTTCTTTAGC
msa185284.2{271_18RS21}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
msa185284.2{271_2603}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
msa185284.2{271_M732}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
msa185284.2{271_M781}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
msa185284.2{271_COH1}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
msa185284.2{271_1169NT}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_H36B}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_JM9130013}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_A909}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_CJB110}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_18RS21}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_2603}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_M732}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_M781}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_COH1}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_1169NT}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	AAAgcCTTGT	GCCTAATGAC	TTGAAACACA	GaGTTTATTA	TTTAGATTAC
msa185284.2{271_H36B}	AAAgcCTTGT	GCCTAATGAC	TTGAAACACA	GaGTTTATTA	TTTAGATTAC
msa185284.2{271_JM9130013}	AAAgcCTTGT	GCCTAATGAC	TTGAAACACA	GaGTTTATTA	TTTAGATTAC
msa185284.2{271_A909}	AAAgcCTTGT	GCCTAATGAC	TTGAAACACA	GaGTTTATTA	TTTAGATTAC
msa185284.2{271_CJB110}	AAAgcCTTGT	GCCTAATGAC	TTGAAACACA	GaGTTTATTA	TTTAGATTAC
msa185284.2{271_18RS21}	AAAgcCTTGT	GCCcAATGAC	TTGAAACACA	GgGTTTATTA	TTTAGATTAC
msa185284.2{271_2603}	AAAgcCTTGT	GCCcAATGAC	TTGAAACACA	GgGTTTATTA	TTTAGATTAC
msa185284.2{271_M732}	AAAgcCTTGT	GCCcAATGAC	TTGAAACACA	GgGTTTATTA	TTTAGATTAC
msa185284.2{271_M781}	AAAgcCTTGT	GCCcAATGAC	TTGAAACACA	GgGTTTATTA	TTTAGATTAC
msa185284.2{271_COH1}	AAAgcCTTGT	GCCcAATGAC	TTGAAACACA	GgGTTTATTA	TTTAGATTAC
msa185284.2{271_1169NT}	AAAgcCTTGT	GCCcAATGAC	TTGAAACACA	GgGTTTATTA	TTTAGATTAC
Consensus	*****	*****	*****	*****	*****

Table 62: Comparative Sequences relating to SAG0690

		751		800
msa185284.2{271_090}		TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG		
msa185284.2{271_H36B}		TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG		
msa185284.2{271_JM9130013}		TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG		
msa185284.2{271_A909}		TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG		
msa185284.2{271_CJB110}		TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG		
msa185284.2{271_18RS21}		TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG		
msa185284.2{271_2603}		TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG		
msa185284.2{271_M732}		TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG		
msa185284.2{271_M781}		TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG		
msa185284.2{271_COH1}		TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG		
msa185284.2{271_1169NT}		TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG		
Consensus		*****	*****	*****
		801	816	
msa185284.2{271_090}		tCATTTGGAA AATAAA		
msa185284.2{271_H36B}		tCATTTGGAA AATAAA		
msa185284.2{271_JM9130013}		tCATTTGGAA AATAAA		
msa185284.2{271_A909}		tCATTTGGAA AATAAA		
msa185284.2{271_CJB110}		tCATTTGGAA AATAAA		
msa185284.2{271_18RS21}		tCATTTGGAA AATAAA		
msa185284.2{271_2603}		tCATTTGGAA AATAAA		
msa185284.2{271_M732}		nCATTTGGAA AATAAA		
msa185284.2{271_M781}		tCATTTGGAA AATAAA		
msa185284.2{271_COH1}		gCATTTGGAA AATAAA		
msa185284.2{271_1169NT}		tCATTTGGAA AATAAA		
Consensus		*****	*****	

## SEQ ID NO. 6212

## STRAIN 2603 frame: 1

MILKICRAAYSLQWGVYQLALLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHL  
AKIVHFLKYNSTFPYIPKYREAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSA  
VKAENKPAEVLVKDKRNAAGDPKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVG  
FKPGVSPHFYQDI INHPDSIFDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPND  
LKHRYVYLDYCNETLYEWNQKVYDFLCHLENK

## SEQ ID NO. 6213

## STRAIN A909 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKIEIQCDDKHLTKIVHFLKYNSTFPYIPKYR  
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGD  
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSPHFYQDI INHPDSI  
FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRYVYLDYCNETLYEWNQK  
VYDFLCHLENK

## SEQ ID NO. 6214

## STRAIN H36B frame: 3

KAFELERIGAFIAYEKQYKRKIEIQCDDKHLTKIVHFLKYNSTFPYIPKYREAAATFN  
EDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGDPKDYFDY  
VMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSPHFYQDI INHPDSIFDGYHPA  
KIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRYVYLDYCNETLYEWNQKVYDFLCH  
LENK

## SEQ ID NO. 6215

## STRAIN 18RS21 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLAKIVHFLKYNSTFPYIPKYR  
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVKDKRNAAGD  
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSPHFYQDI INHPDSI  
FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRYVYLDYCNETLYEWNQK  
VYDFLCHLENK

## SEQ ID NO. 6216

## STRAIN M732 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLAKIVHFLKYNSTFPYIPKYR  
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVKDKRNAAGD  
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSPHFYQDI INHPDSI  
FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRYVYLDYCNETLYEWNQK  
VYDFLCHLENK

## SEQ ID NO. 6217

## STRAIN COH1 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLAKIVHFLKYNSTFPYIPKYR  
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVKDKRNAAGD  
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSPHFYQDI INHPDSI  
FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRYVYLDYCNETLYEWNQK  
VYDFLCHLENK

## SEQ ID NO. 6218

## STRAIN M781 frame: 1

Table 62: Comparative Sequences relating to SAG0690

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQDDKHLLAKIVHFLKYNSTFFPYIPKYR  
 EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGD  
 PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSFHFYQDIINHPDSI  
 FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYLDYCNETLYEWNQK  
 VYDFLCHLENK

SEQ ID NO. 6219

STRAIN CJB110 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKIEIQDDKHLLTKIVHFLKYNSTFFPYIPKYR  
 EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGD  
 PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSFHFNYQDIINHPDSI  
 FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYLDYCNETLYEWNQK  
 VYDFLCHLENK

SEQ ID NO. 6220

STRAIN 1169NT frame: 2

IKAFELERIGAFIAYEKQYKRKTEIQDDKHLLAKIVHFLKYNSTFFPYIPKYREAAATF  
 NEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGD  
 PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSFHFYQDIINHPDSI  
 FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYLDYCNETLYEWNQKVYDFLC  
 HLENK

SEQ ID NO. 6221

STRAIN JM9130013 frame: 1

IGAFIAYEKQYKRKIEIQDDKHLLTKIVHFLKYNSTFFPYIPKYREAAATFNEDGISLT  
 SDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGD  
 PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSFHFNYQDIINHPDSI  
 FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYLDYCNETLYEWNQKVYDFLC  
 HLENK

SEQ ID NO. 6222

STRAIN 090 frame: 3

DYPLIKAFELERIGAFIAYEKQYKRKIEIQDDKHLLTKIVHFLKYNSTFFPYIPKYREA  
 AATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGD  
 PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSFHFNYQDIINHPDSI  
 FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYLDYCNETLYEWNQKVY  
 DFLCHLENK

PRETTY of: /biotmp/msa185358.2{\*} May 13, 2003 07:11 ..

	1		50
msa185358.2{271_090}	-----	---dyplika	felerIGAFI
msa185358.2{271_JM9130013}	-----	-----	IGAFI
msa185358.2{271_H36B}	-----	-----	ka
msa185358.2{271_A909}	-----	~LLdyprika	felerIGAFI
msa185358.2{271_CJB110}	-----	~LLdyprika	felerIGAFI
msa185358.2{271_1169NT}	-----	-----	ika
msa185358.2{271_18RS21}	-----	~LLdyprika	felerIGAFI
msa185358.2{271_2603}	milkcraay	slqwggyql	aLLdyprika
msa185358.2{271_M732}	-----	~LLdyprika	felerIGAFI
msa185358.2{271_M781}	-----	~LLdyprika	felerIGAFI
msa185358.2{271_COH1}	-----	~LLdyprika	felerIGAFI
Consensus	*****	*****	*****
	51		100
msa185358.2{271_090}	EIQDDKHLL	tkIVHFLKYN	SFTFPYIPKY
msa185358.2{271_JM9130013}	EIQDDKHLL	tkIVHFLKYN	SFTFPYIPKY
msa185358.2{271_H36B}	EIQDDKHLL	tkIVHFLKYN	SFTFPYIPKY
msa185358.2{271_A909}	EIQDDKHLL	tkIVHFLKYN	SFTFPYIPKY
msa185358.2{271_CJB110}	EIQDDKHLL	tkIVHFLKYN	SFTFPYIPKY
msa185358.2{271_1169NT}	EIQDDKHLL	akIVHFLKYN	SFTFPYIPKY
msa185358.2{271_18RS21}	EIQDDKHLL	akIVHFLKYN	SFTFPYIPKY
msa185358.2{271_2603}	EIQDDKHLL	akIVHFLKYN	SFTFPYIPKY
msa185358.2{271_M732}	EIQDDKHLL	akIVHFLKYN	SFTFPYIPKY
msa185358.2{271_M781}	EIQDDKHLL	akIVHFLKYN	SFTFPYIPKY
msa185358.2{271_COH1}	EIQDDKHLL	akIVHFLKYN	SFTFPYIPKY
Consensus	*****	*****	*****
	101		150
msa185358.2{271_090}	HTCTIETAKL	IFKEGKILSA	VKAFNKPAEV
msa185358.2{271_JM9130013}	HTCTIETAKL	IFKEGKILSA	VKAFNKPAEV
msa185358.2{271_H36B}	HTCTIETAKL	IFKEGKILSA	VKAFNKPAEV
msa185358.2{271_A909}	HTCTIETAKL	IFKEGKILSA	VKAFNKPAEV
msa185358.2{271_CJB110}	HTCTIETAKL	IFKEGKILSA	VKAFNKPAEV
msa185358.2{271_1169NT}	HTCTIETAKL	IFKEGKILSA	VKAFNKPAEV
msa185358.2{271_18RS21}	HTCTIETAKL	IFKEGKILSA	VKAFNKPAEV
msa185358.2{271_2603}	HTCTIETAKL	IFKEGKILSA	VKAFNKPAEV
msa185358.2{271_M732}	HTCTIETAKL	IFKEGKILSA	VKAFNKPAEV
msa185358.2{271_M781}	HTCTIETAKL	IFKEGKILSA	VKAFNKPAEV
msa185358.2{271_COH1}	HTCTIETAKL	IFKEGKILSA	VKAFNKPAEV

Table 62: Comparative Sequences relating to SAG0690

Consensus	*****	*****	*****	**-*****	*****
	151				200
msa185358.2{271_090}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVa	FKPGVSFHFh	YQDIINHPDS
msa185358.2{271_JM9130013}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVa	FKPGVSFHFh	YQDIINHPDS
msa185358.2{271_H36B}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVa	FKPGVSFHFh	YQDIINHPDS
msa185358.2{271_A909}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVa	FKPGVSFHFh	YQDIINHPDS
msa185358.2{271_CJB110}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVa	FKPGVSFHFh	YQDIINHPDS
msa185358.2{271_1169NT}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHFt	YQDIINHPDS
msa185358.2{271_18RS21}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHFt	YQDIINHPDS
msa185358.2{271_2603}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHFt	YQDIINHPDS
msa185358.2{271_M732}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHFt	YQDIINHPDS
msa185358.2{271_M781}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHFt	YQDIINHPDS
msa185358.2{271_COH1}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHFt	YQDIINHPDS
Consensus	*****	*****	*****-	*****-	*****
	201				250
msa185358.2{271_090}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_JM9130013}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_H36B}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_A909}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_CJB110}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_1169NT}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQnLVPND	LKHRVYYLDY
msa185358.2{271_18RS21}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_2603}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_M732}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_M781}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_COH1}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
Consensus	*****	*****	*****	*****	*****
	251				272
msa185358.2{271_090}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_JM9130013}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_H36B}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_A909}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_CJB110}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_1169NT}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_18RS21}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_2603}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_M732}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_M781}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_COH1}	CNETLYEWNQ	KVYDFLCHLE	NK		
Consensus	*****	*****-***	**		

Table 63: Comparative Sequences relating to SAG1912

## SEQ ID NO. 6301

## STRAIN 2603

ATGAAAAGTCGAAAAAAGATAAATTGGTATTGAGGTTAACAACAACACTATTGGTTTTT  
GGTTTGGGGTGGGGTTTGGTTTTATAATTATAAAAAATGATAATGTCCGAACCGACAGTCACT  
AGTGCAATCGGATCAAACGACGACTTTTATTCAAACGATTCTCCAACAGCTATTGAAATT  
TCTAAGACCTATGATTTGTATGCGTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCC  
AGTGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAA  
TATAAAGGTAAATCTGTCCAATGCCTACTTTAGAAGATGATGGGAAAGGCAATATGACT  
CAAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTGCTTCACTATATGATTATGCT  
GAGTTAGTATCTAGTCAAAGTATGCATCTGTTTGGAAATCAAATACCTCTTCTTATAAG  
GATGCTACTGACGCTCTAACAGGCTCTTATGCGACAGATACTGCTTATGCTAGTAAATTA  
AACCAAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

## SEQ ID NO. 6302

## STRAIN 090

GGGGTTTGGTTTTTATAATTATAA  
AAATGATAATGTCCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA  
CTTTTATTCAAACGATTCTCCAACAGCTATTGAAATTCTAAGACCTAT  
GATTTGTATGCGTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAG  
TGGACAATCAGATTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCA  
AAGGAGAATATAAAGGTAAATCTGTCCAATGCCTACTTTAGAAGATGAT  
GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA  
TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGT  
ATGCATCTGTTTGGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCA  
GCTCTAACAGGCTCTTATGCGACAGATACTGCTTATGCTAGTAAATTA  
CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

## SEQ ID NO. 6303

## STRAIN A909

GGGGTTTGGTTTTTATAATTATAA  
AAATGATAATGTCCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA  
CTTTTATTCAAACGATTCTCCAACAGCTATTGAAATTCTAAGACCTAT  
GATTTGTATGCGTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAG  
TGGACAATCAGATTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCA  
AAGGAGAATATAAAGGTAAATCTGTCCAATGCCTACTTTAGAAGATGAT  
GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA  
TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGT  
ATGCATCTGCTTGGAAATCAAATACTTCTTCTTATAAGGATGCTACTGCA  
GCTCTAACAGGCTCTTATGCGACAGATACTGCTTATGCTAGTAAATTA  
CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

## SEQ ID NO. 6304

## STRAIN H36B

GGGGTTTGGTTTTTATAATTATAAAAAATGATA  
ATGTCCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATT  
CAAACGATTCTCCAACAGCTATTGAAATTCTAAGACCTATGATTGTGA  
TGGCTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAGTGGACAAT  
CAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAA  
TATAAAGGTAAATCTGTCCAATGCCTACTTTAGAAGATGATGGGAAAGG  
CAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTG  
CTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGTATGCTACT  
GCTTGGAAATCAAATACTTCTTCTTATAAGGATGCTACTGACGCTCTAAC  
AGGCTCTTATGCGACAGATACTGCTTATGCTAGTAAATTAACCAAAATTA  
TTGAAACCTACAGTCTAGATGCTTATGATAAA

## SEQ ID NO. 6305

## STRAIN 18RS21

GGGGTTTGGTTTTTATAATTATAAAAAATGATAATG  
TCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATTCAA  
ACGATTCTCCAACAGCTATTGAAATTCTAAGACCTATGATTGTATGC  
GTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAGTGGACAATCAG  
ATTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAAATAT  
AAAGGTAAATCTGTCCAATGCCTACTTTAGAAGATGATGGGAAAGGCAA  
TATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTGCTT  
CACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGTATGCTACTGTT  
TGGAAATCAAATACCTCTTCTTATAAGGATGCTACTGACGCTCTAACAGG  
TCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAACCAAAATTAATG  
AAACCTACAGTCTAGATGCTTATGATAAA

## SEQ ID NO. 6306

## STRAIN M732

GGGGTTTGGTTTTTATAATTATAA  
AAATGATAATGTCCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA  
CTTTTATTCAAACGATTCTCCAACAGCTATTGAAATTCTAAGACCTAT  
GATTTGTATGCGTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAG  
TGGACAATCAGATTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCA  
AAGGAGAATATAAAGGTAAATCTGTCCAATGCCTACTTTAGAAGATGAT  
GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA  
TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGT  
ATGCATCTGTTTGGAAATCAAATACTTCTTCTTATAAGGATGCTACTGCA  
GCTCTAACAGGCTCTTATGCGACAGATACTGCTTATGCTAGTAAATTA  
CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA



Table 63: Comparative Sequences relating to SAG1912

## SEQ ID NO. 6307

## STRAIN COH1

GGGGTTTGGTTTATAATTATAA  
 AAATGATAATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA  
 CTTTTATTCAAACGATTCTCCAACAGCTATTGAAATTTCTAAGACCTAT  
 GATTGTATGCGTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAG  
 TGGACAAATCAGATTTGTCTAAGGCTCCTAATTAACCTCTTTGGCATCA  
 AAGGAGAATATAAAGGTAAATCTGTCCAATGCCTACTTTAGAAGATGAT  
 GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA  
 TTATCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGT  
 ATGCATCTGTTTGGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCA  
 GCTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTA  
 CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

## SEQ ID NO. 6308

## STRAIN M781

GGGGTTTGGTTTATAATTATAAAAAATGA  
 TAATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTA  
 TTCAAACGATTCTCCAACAGCTATTGAAATTTCTAAGACCTATGATTGG  
 TATGCGTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAGTGGACA  
 ATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAG  
 AATATAAAGGTAAATCTGTCCAATGCCTACTTTAGAAGATGATGGGAAA  
 GGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTC  
 TGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGTATGCTAT  
 CTGTTTGGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCAGCTCTA  
 ACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAACCAAAT  
 TATTGAAACCTACAGTCTAGATGCTTATGATAAA

## SEQ ID NO. 6309

## STRAIN CJB110

GGGGTTTGGTTTATAATTATAAAAAATGATAATGT  
 CGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATTCAA  
 CGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTATGATTGTATGCG  
 TCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAGTGGACAATCAGA  
 TTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAATATA  
 AAGGTAATCTGTCCAATGCCTACTTTAGAAGATGATGGGAAAGGCAAT  
 ATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTGCTTC  
 ACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGTATGCTATCTGTTT  
 GGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCAGCTCTAACAGGT  
 CTTTATGCGACAGATACTGCTTATGCTAGTAAATTAACCAAATATTGA  
 AACCTACAGTCTAGATGCTTATGATAAA

## SEQ ID NO. 6310

## STRAIN 1169NT

GGGGTTTGGTTTATAATTATAAAAAATGATAATGT  
 CGAACGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATTCAA  
 CGATTTCCCCAACAGCTATTGAAATTTCTAAGACCTATGATTGTATGCG  
 TCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAGTGGACAATCAGA  
 TTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAATATA  
 AAGGTAATCTGTCCAATGCCTACTTTAGAAGATGATGGGAAAGGCAAT  
 ATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTGCTTC  
 ACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGTATGCTATCTGTTT  
 GGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCAGCTCTAACAGGT  
 CTTTATGCGACAGATACTGCTTATGCTAGTAAATTAACCAAATATTGA  
 AACCTACAGTCTAGATGCTTATGATAAA

## SEQ ID NO. 6311

## STRAIN JM9130013

TTTGGTTTATAATTATAAAAAATGATAATGTCGAACCGACAGTCACTAGT  
 GCATCGGATCAAACGACGACTTTTATTCAAACGATTTCCCCAACAGCTAT  
 TGAAATTTCTAAGACCTATGATTGTATGCGTCAGTCTTATTAGCACAAAG  
 CTATTTTGGAAATCATCCAGTGGACAATCAGATTTGTCTAAGGCTCCTAAT  
 TATAACCTCTTTGGCATCAAAGGAGAATATAAAGGTAATCTGTTCAAAT  
 GCCTACTTTAGAAGATGATGGGAAAGGTAATATGACCCAAATCCAAGCTC  
 CTTTTCGCGCCTATCCAAATTATTCTGCTTCACTATATGATTATGCTGAG  
 TTAGTATCTAGTCAAAGTATGCTATCTGTTTGGAAATCAAATACCTCTTC  
 TTATAAGGATGCTACTGCAGCTCTAACAGGTCTTTATGCGACAGATACTG  
 CTTATGCTAGTAAATTAACCAAATATTGAAACTACAGTCTAGATGCT  
 TATGATAAA

PRETTY of: /biotmp/msa243324.2{\*} February 11, 2003 05:11 ..

	1				50
msa243324.2{275_A909}	-----	-----	-----	-----	-----
msa243324.2{275_H36B}	-----	-----	-----	-----	-----
msa243324.2{275_090}	-----	-----	-----	-----	-----
msa243324.2{275_18RS21}	-----	-----	-----	-----	-----
msa243324.2{275_2603}	atgaaaaagtc	gaaaaaaaaga	taaatgggta	ttgaggttaa	caacaacact
msa243324.2{275_CJB110}	-----	-----	-----	-----	-----
msa243324.2{275_COH1}	-----	-----	-----	-----	-----
msa243324.2{275_M732}	-----	-----	-----	-----	-----

Table 63: Comparative Sequences relating to SAG1912

msa243324.2{275_M781}	-----	-----	-----	-----	-----
msa243324.2{275_1169NT}	-----	-----	-----	-----	-----
msa243324.2{275_JM9130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
51					
msa243324.2{275_A909}	-----	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_H36B}	-----	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_090}	-----	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_18RS21}	-----	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_2603}	attggttttt	gggtttgggtg	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_CJB110}	-----	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_COH1}	-----	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_M732}	-----	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_M781}	-----	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_1169NT}	-----	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_JM9130013}	-----	-----	TTTGGTT	TTATAATTAT	AAAAATGATA
Consensus	*****	*****	-----	*****	*****
101					
msa243324.2{275_A909}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_H36B}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_090}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_18RS21}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_2603}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_CJB110}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_COH1}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_M732}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_M781}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_1169NT}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_JM9130013}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
Consensus	*****	*****	*****	*****	*****
151					
msa243324.2{275_A909}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_H36B}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_090}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_18RS21}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_2603}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_CJB110}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_COH1}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_M732}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_M781}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_1169NT}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_JM9130013}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
Consensus	*****	*****	*****	*****	*****
201					
msa243324.2{275_A909}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAAT
msa243324.2{275_H36B}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAAT
msa243324.2{275_090}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAAT
msa243324.2{275_18RS21}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAAT
msa243324.2{275_2603}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAAT
msa243324.2{275_CJB110}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAAT
msa243324.2{275_COH1}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAAT
msa243324.2{275_M732}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAAT
msa243324.2{275_M781}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAAT
msa243324.2{275_1169NT}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAAT
msa243324.2{275_JM9130013}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAAT
Consensus	*****	*****	*****	*****	*****
251					
msa243324.2{275_A909}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_H36B}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_090}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_18RS21}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_2603}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_CJB110}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_COH1}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_M732}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_M781}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_1169NT}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_JM9130013}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
Consensus	*****	*****	*****	*****	*****
301					
msa243324.2{275_A909}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_H36B}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_090}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_18RS21}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_2603}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_CJB110}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_COH1}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG

Table 63: Comparative Sequences relating to SAG1912

msa243324.2{275_M732}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_M781}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_1169NT}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_JM9130013}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
Consensus	*****	*****_**	*****	*****	*****
351					
msa243324.2{275_A909}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_H36B}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_090}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_18RS21}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_2603}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_CJB110}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_COH1}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_M732}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_M781}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_1169NT}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_JM9130013}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
Consensus	*****	*****	*****	*****	*****
401					
msa243324.2{275_A909}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_H36B}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_090}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_18RS21}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_2603}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_CJB110}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_COH1}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_M732}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_M781}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_1169NT}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_JM9130013}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
Consensus	*****	*****	*****	*****	*****
451					
msa243324.2{275_A909}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_H36B}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_090}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_18RS21}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_2603}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_CJB110}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_COH1}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_M732}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_M781}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_1169NT}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_JM9130013}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
Consensus	**_*****	*****_**	*****	*****	*****
501					
msa243324.2{275_A909}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_H36B}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_090}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_18RS21}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_2603}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_CJB110}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_COH1}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_M732}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_M781}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_1169NT}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_JM9130013}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
Consensus	*****	*****	*****	*****	*****
551					
msa243324.2{275_A909}	TTGAAAcCTA	CAGTCTAGAT	GCCTATGATA	AA	
msa243324.2{275_H36B}	TTGAAAcCTA	CAGTCTAGAT	GCCTATGATA	AA	
msa243324.2{275_090}	TTGAAAcCTA	CAGTCTAGAT	GCCTATGATA	AA	
msa243324.2{275_18RS21}	TTGAAAcCTA	CAGTCTAGAT	GCCTATGATA	AA	
msa243324.2{275_2603}	TTGAAAcCTA	CAGTCTAGAT	GCCTATGATA	AA	
msa243324.2{275_CJB110}	TTGAAAcCTA	CAGTCTAGAT	GCCTATGATA	AA	
msa243324.2{275_COH1}	TTGAAAcCTA	CAGTCTAGAT	GCCTATGATA	AA	
msa243324.2{275_M732}	TTGAAAcCTA	CAGTCTAGAT	GCCTATGATA	AA	
msa243324.2{275_M781}	TTGAAAcCTA	CAGTCTAGAT	GCCTATGATA	AA	
msa243324.2{275_1169NT}	TTGAAAcCTA	CAGTCTAGAT	GCCTATGATA	AA	
msa243324.2{275_JM9130013}	TTGAAAcCTA	CAGTCTAGAT	GCCTATGATA	AA	
Consensus	*****_***	*****	*****	**	
582					

SEQ ID NO. 6312

STRAIN 2603 frame: 1

MKSRKDKLVRLRLTTTLVFLGGVWFYNYKNDNVEPTVTSASDQTTTFIQTFISPTAIEI  
 SKTYDLIASVLLAQAILSSSGQSDLSKAPNYNLFQIKGEYKGSVQMPTLEDDGKGNMT  
 QIQAPFRAYPNYSASLYDYAELVSSQKYASVWKSNTSSYKDATAALTLGLYATDTAYASKL  
 NQIETYSLDAYDK

Table 63: Comparative Sequences relating to SAG1912

SEQ ID NO. 6313  
STRAIN 090 frame: 1  
GVWFFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ  
SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV  
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6314  
STRAIN A909 frame: 1  
GVWFFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ  
SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV  
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6315  
STRAIN H36B frame: 1  
GVWFFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ  
SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV  
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6316  
STRAIN 18RS21 frame: 1  
GVWFFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ  
SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV  
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6317  
STRAIN M732 frame: 1  
GVWFFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ  
SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV  
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6318  
STRAIN M781 frame: 1  
GVWFFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ  
SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV  
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6319  
STRAIN CJB110 frame: 1  
GVWFFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ  
SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV  
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6320  
STRAIN 1169NT frame: 1  
GVWFFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ  
SDLSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV  
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6321  
STRAIN JM9130013 frame: 3  
WFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQSD  
LSKAPNYNLFGIKGEYKGKSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELVSS  
QKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIENYSLDAYDK

PRETTY of: /biotmp/msa243476.2{\*} February 11, 2003 05:17 ..

	1				50
msa243476.2{275_090}	-----	-----	---gvWFFYNY	KNDNVEpTVT	SASDQTTTFI
msa243476.2{275_18RS21}	-----	-----	---gvWFFYNY	KNDNVEpTVT	SASDQTTTFI
msa243476.2{275_2603}	mksrkdkklv	lrltttllvf	glggvWFFYNY	KNDNVEpTVT	SASDQTTTFI
msa243476.2{275_CJB110}	-----	-----	---gvWFFYNY	KNDNVEpTVT	SASDQTTTFI
msa243476.2{275_M732}	-----	-----	---gvWFFYNY	KNDNVEpTVT	SASDQTTTFI
msa243476.2{275_M781}	-----	-----	---gvWFFYNY	KNDNVEpTVT	SASDQTTTFI
msa243476.2{275_A909}	-----	-----	---gvWFFYNY	KNDNVEpTVT	SASDQTTTFI
msa243476.2{275_H36B}	-----	-----	---gvWFFYNY	KNDNVEpTVT	SASDQTTTFI
msa243476.2{275_JM9130013}	-----	-----	-----WFYNY	KNDNVEpTVT	SASDQTTTFI
msa243476.2{275_1169NT}	-----	-----	---gvWFFYNY	KNDNVEpTVT	SASDQTTTFI
Consensus	*****	*****	***--*****	*****	*****
	51				100
msa243476.2{275_090}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE
msa243476.2{275_18RS21}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE
msa243476.2{275_2603}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE
msa243476.2{275_CJB110}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE
msa243476.2{275_M732}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE
msa243476.2{275_M781}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE
msa243476.2{275_A909}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE
msa243476.2{275_H36B}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE
msa243476.2{275_JM9130013}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE
msa243476.2{275_1169NT}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE
Consensus	*****	*****	*****	*****	*****

Table 63: Comparative Sequences relating to SAG1912

	101				150
msa243476.2{275_090}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_18RS21}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_2603}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_CJB110}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_M732}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_M781}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_A909}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_H36B}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_JM9130013}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_1169NT}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
Consensus	*****	*****	*****	*****	*****
	151				194
msa243476.2{275_090}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_18RS21}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_2603}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_CJB110}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_M732}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_M781}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_A909}	awKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_H36B}	awKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_JM9130013}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_1169NT}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
Consensus	-*****	*****	*****	*****	****

Table 64: Comparative Sequences relating to SAG 0827

## SEQ ID NO. 6401

## STRAIN 2603

ATGAACAAGTCTAAGAAAATCGAAAATTATCAATTATTATTACTACAAGCGCAAGCTCTA  
TTCTCAGATGAAACAAATGCTCTTGCCAACTTATCAAATGCTTCAGCTATGCTAAATGCT  
ATGCTTCCAAATCTGTATTTACAGGCTTTTATTTATTTGATGGAGAAGAGTTAAATCTT  
GGCCCTTTCCAGGGTGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGT  
GAATCTGCACAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGCATGCTAACTAT  
ATCTCCTGTGATTTCAAAGCTATGAGTGAAATCGTAGTACCTATGTTTAAAAATGGCAA  
CTTCTAGGAGTTCTAGATTAGATTCTTCTTTAGTAGCAGATTATGATGAGATTGATCAA  
GAATACTTAGAAAAATTTGTAGGTATTCTAGTAGAACATACGATTGGAATTTGGATATG  
TTTGGAGTTGAAAAG

## SEQ ID NO. 6402

## STRAIN 090

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTTA  
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTATTTAC  
AGGCTTTTATTTATTTGATGGAAAGGAGTTAATTCTTGGCCCTTTCCAGG  
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGAA  
TCTGCACAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATGC  
TAACTATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTACCTA  
TGTTTAAAAATGGCAAACCTTCTAGGAGTTCTAGATTAGATTCTTCTTTA  
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG  
TATTCTAGTAGAACATACGATTGGAATTTGGATA

## SEQ ID NO. 6403

## STRAIN A909

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAA  
CTTATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTAT  
TTACAGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTTGGCCCTTTTC  
CAGGGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGG  
TGAATCTGCACAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGC  
ATGCTAATATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTA  
CTATGTTTAAAAATGGCAAACCTTCTAGGAGTTCTAGATTAGATTCTTCT  
TTTAGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTG  
TAGGTATTCTAGTAGAACATACGATTGGAATTTGGATATGTTTGGAGTT  
GAAAAG

## SEQ ID NO. 6404

## STRAIN H36B

CTCTATTCTCAGATGAAACAAATGCTCTTGCC  
CAACTTATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGT  
TATTTACAGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTTGGCCCT  
TTCCAGGGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGT  
TGGTGAATCTGCACAACTGCTAAGACGCTGATCGTTGATGATGTTACAA  
AGCATGCTAATATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTA  
GTACCTATGTTTAAAAATGGCAAACCTTCTAGGAGTTCTAGATTAGATTCT  
TTCTTTAGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAAT  
TTGTAGGTATTCTAGTAGAACATACGATTGGAATTTGGATATGTTTGGAG  
TTGAAAAG

## SEQ ID NO. 6405

## STRAIN 18RS21

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT  
ATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTATTTA  
CAGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTTGGCCCTTTCCAG  
GGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA  
ATCTGCACAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGCATG  
CTAACTATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTACCT  
ATGTTTAAAAATGGCAAACCTTCTAGGAGTTCTAGATTAGATTCTTCTTT  
AGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAG  
GTATTCTAGTAGAACATACGATTGGAATTTGGATATGTTTGGAGTTGAA  
AAG

## SEQ ID NO. 6406

## STRAIN M732

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT  
ATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTATTTA  
CAGGCTTTTATTTATTTGATGGAGAGGAGTTAATTCTTGGCCCTTTTCAG  
GGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA  
ATCTGCACAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATG  
CTAACTATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTACCC  
ATGTTTAAAAATGGCAAACCTTCTAGGAGTTCTAGATTAGATTCTTCTTT  
AGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAG  
GTATTCTAGTAGAACATACGATTGGAATTTGGATATGTTTGGAGTTGAA  
AAG

## SEQ ID NO. 6407

## STRAIN COH1

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT  
TTATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTATTT  
TACAGGCTTTTATTTATTTGATGGAGAGGAGTTAATTCTTGGCCCTTTTC  
AGGGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGT

Table 64: Comparative Sequences relating to SAG 0827

GAATCTGCACAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCA  
TGCTAACTATATCTCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTAC  
CCATGTTTAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTCCTCT  
TTAGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGT  
AGGTATTCTAGTAGAACATACGATTGGAATTTGGATATGTTGGAGTTG  
AAAAG

SEQ ID NO. 6408

STRAIN M781

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT  
ATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCGTATTTA  
CAGGCTTTTATTTATTTGATGGAGAGGAGTTAATTCCTGGCCCTTTCCAG  
GGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA  
ATCTGCACAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATG  
CTAACTATATCTCTGTGATTCAAAGCTATGAGTGAAATCGTAGTACCC  
ATGTTTAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTCCTCTT  
AGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAG  
GTATTCTAGTAGAACATACGATTGGAATTTGGATATGTTTGGAGTTGAA  
AAG

SEQ ID NO. 6409

STRAIN CJB110

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT  
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCGTATTTAC  
AGGCTTTTATTTATTTGATGGAGAGGAGTTAATTCCTGGCCCTTTCCAGG  
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA  
TCTGCACAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATGC  
TAACCTATATCTCTGTGATTCAAAGCTATGAGTGAAATCGTAGTACCTA  
TGTTTAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTCCTCTT  
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG  
TATTCTAGTAGAACATACGATTGGAATTTGGATATGTTTGGAGTTGAA  
AG

SEQ ID NO. 6410

STRAIN 1169NT

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT  
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCGTATTTAC  
AGGCTTTTATTTATTTGATGGAGAGGAGTTAATTCCTGGCCCTTTCCAGG  
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA  
TCTGCACAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATGC  
TAACCTATATCTCTGTGATTCAAAGCTATGAGTGAAATCGTAGTACCCA  
TGTTTAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTCCTCTT  
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG  
TATTCTAGTAGAACATACGATTGGAATTTGGATATGTTTGGAGTTGAA  
AG

SEQ ID NO. 6411

STRAIN JM9130013

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT  
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCGTATTTAC  
AGGCTTTTATTTATTTGATGGAGAGGAGTTAATTCCTGGCCCTTTCCAGG  
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA  
TCTGCACAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGCATGC  
TAACCTATATCTCTGTGATTCAAAGCTATGAGTGAAATCGTAGTACCTA  
TGTTTAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTCCTCTT  
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG  
TATTCTAGTAGAACATACGATTGGAATTTGGATATGTTTGGAGTTGAA  
AG

PRETTY of: /biotmp/msa236796.2{\*} February 11, 2003 02:42 ..

	1				50
msa236796.2{282_COH1}	-----	-----	-----	-----	-----
msa236796.2{282_M732}	-----	-----	-----	-----	-----
msa236796.2{282_M781}	-----	-----	-----	-----	-----
msa236796.2{282_090}	-----	-----	-----	-----	-----
msa236796.2{282_CJB110}	-----	-----	-----	-----	-----
msa236796.2{282_18RS21}	-----	-----	-----	-----	-----
msa236796.2{282_2603}	atgaacaagt	ctaagaaaat	cgaaaattat	caattattat	tactacaagc
msa236796.2{282_A909}	-----	-----	-----	-----	-----
msa236796.2{282_H36B}	-----	-----	-----	-----	-----
msa236796.2{282_JM9130013}	-----	-----	-----	-----	-----
msa236796.2{282_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****

  

	51				100
msa236796.2{282_COH1}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG
msa236796.2{282_M732}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG
msa236796.2{282_M781}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG
msa236796.2{282_090}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG
msa236796.2{282_CJB110}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG
msa236796.2{282_18RS21}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG
msa236796.2{282_2603}	gcaagCTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG

Table 64: Comparative Sequences relating to SAG 0827

msa236796.2{282_A909}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG		
msa236796.2{282_H36B}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG		
msa236796.2{282_JM9130013}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG		
msa236796.2{282_1169NT}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG		
Consensus	*****	*****	*****	*****	*****		
msa236796.2{282_COH1}	101	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	150	TACAGGCTTT
msa236796.2{282_M732}		CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT		TACAGGCTTT
msa236796.2{282_M781}		CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT		TACAGGCTTT
msa236796.2{282_090}		CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT		TACAGGCTTT
msa236796.2{282_CJB110}		CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT		TACAGGCTTT
msa236796.2{282_18RS21}		CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT		TACAGGCTTT
msa236796.2{282_2603}		CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT		TACAGGCTTT
msa236796.2{282_A909}		CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT		TACAGGCTTT
msa236796.2{282_H36B}		CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT		TACAGGCTTT
msa236796.2{282_JM9130013}		CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT		TACAGGCTTT
msa236796.2{282_1169NT}		CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT		TACAGGCTTT
Consensus		*****	*****	*****	*****		*****
msa236796.2{282_COH1}	151	TATTTATTTG	ATGGAgAgGA	GTTAATTCTT	GGCCCTTTc	200	AGGGTGGTGT
msa236796.2{282_M732}		TATTTATTTG	ATGGAgAgGA	GTTAATTCTT	GGCCCTTTc		AGGGTGGTGT
msa236796.2{282_M781}		TATTTATTTG	ATGGAgAgGA	GTTAATTCTT	GGCCCTTTc		AGGGTGGTGT
msa236796.2{282_090}		TATTTATTTG	ATGGAgAgGA	GTTAATTCTT	GGCCCTTTc		AGGGTGGTGT
msa236796.2{282_CJB110}		TATTTATTTG	ATGGAgAgGA	GTTAATTCTT	GGCCCTTTc		AGGGTGGTGT
msa236796.2{282_18RS21}		TATTTATTTG	ATGGAgAgGA	GTTAATTCTT	GGCCCTTTc		AGGGTGGTGT
msa236796.2{282_2603}		TATTTATTTG	ATGGAgAgGA	GTTAATTCTT	GGCCCTTTc		AGGGTGGTGT
msa236796.2{282_A909}		TATTTATTTG	ATGGAgAgGA	GTTAATTCTT	GGCCCTTTc		AGGGTGGTGT
msa236796.2{282_H36B}		TATTTATTTG	ATGGAgAgGA	GTTAATTCTT	GGCCCTTTc		AGGGTGGTGT
msa236796.2{282_JM9130013}		TATTTATTTG	ATGGAgAgGA	GTTAATTCTT	GGCCCTTTc		AGGGTGGTGT
msa236796.2{282_1169NT}		TATTTATTTG	ATGGAgAgGA	GTTAATTCTT	GGCCCTTTc		AGGGTGGTGT
Consensus		*****	*****_***	*****	*****_*		*****
msa236796.2{282_COH1}	201	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	250	GAATCTGCAC
msa236796.2{282_M732}		ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT		GAATCTGCAC
msa236796.2{282_M781}		ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT		GAATCTGCAC
msa236796.2{282_090}		ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT		GAATCTGCAC
msa236796.2{282_CJB110}		ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT		GAATCTGCAC
msa236796.2{282_18RS21}		ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT		GAATCTGCAC
msa236796.2{282_2603}		ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT		GAATCTGCAC
msa236796.2{282_A909}		ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT		GAATCTGCAC
msa236796.2{282_H36B}		ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT		GAATCTGCAC
msa236796.2{282_JM9130013}		ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT		GAATCTGCAC
msa236796.2{282_1169NT}		ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT		GAATCTGCAC
Consensus		*****	*****	*****	*****		*****
msa236796.2{282_COH1}	251	AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA	300	TGCTAACTAT
msa236796.2{282_M732}		AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA		TGCTAACTAT
msa236796.2{282_M781}		AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA		TGCTAACTAT
msa236796.2{282_090}		AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA		TGCTAACTAT
msa236796.2{282_CJB110}		AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA		TGCTAACTAT
msa236796.2{282_18RS21}		AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA		TGCTAACTAT
msa236796.2{282_2603}		AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA		TGCTAACTAT
msa236796.2{282_A909}		AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA		TGCTAACTAT
msa236796.2{282_H36B}		AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA		TGCTAACTAT
msa236796.2{282_JM9130013}		AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA		TGCTAACTAT
msa236796.2{282_1169NT}		AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA		TGCTAACTAT
Consensus		*****	*****_*	*****	*****		*****
msa236796.2{282_COH1}	301	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	350	CcATGTTTAA
msa236796.2{282_M732}		ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC		CcATGTTTAA
msa236796.2{282_M781}		ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC		CcATGTTTAA
msa236796.2{282_090}		ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC		CcATGTTTAA
msa236796.2{282_CJB110}		ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC		CcATGTTTAA
msa236796.2{282_18RS21}		ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC		CcATGTTTAA
msa236796.2{282_2603}		ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC		CcATGTTTAA
msa236796.2{282_A909}		ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC		CcATGTTTAA
msa236796.2{282_H36B}		ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC		CcATGTTTAA
msa236796.2{282_JM9130013}		ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC		CcATGTTTAA
msa236796.2{282_1169NT}		ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC		CcATGTTTAA
Consensus		*****	*****	*****	*****		*_*****
msa236796.2{282_COH1}	351	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCCTTCT	400	TTAGTAGCAG
msa236796.2{282_M732}		AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCCTTCT		TTAGTAGCAG
msa236796.2{282_M781}		AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCCTTCT		TTAGTAGCAG
msa236796.2{282_090}		AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCCTTCT		TTAGTAGCAG
msa236796.2{282_CJB110}		AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCCTTCT		TTAGTAGCAG
msa236796.2{282_18RS21}		AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCCTTCT		TTAGTAGCAG



Table 64: Comparative Sequences relating to SAG 0827

msa236796.2{282_2603}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
msa236796.2{282_A909}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
msa236796.2{282_H36B}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
msa236796.2{282_JM9130013}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
msa236796.2{282_1169NT}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
Consensus	*****	*****	*****	*****	*****
401					
msa236796.2{282_COH1}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_M732}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_M781}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_090}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_CJB110}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_18RS21}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_2603}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_A909}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_H36B}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_JM9130013}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_1169NT}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
Consensus	*****	*****	*****	*****	*****
451					
msa236796.2{282_COH1}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_M732}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_M781}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_090}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_CJB110}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_18RS21}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_2603}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_A909}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_H36B}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_JM9130013}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_1169NT}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
Consensus	*****	*****	*****	*****	*****
495					
msa236796.2{282_COH1}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_M732}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_M781}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_090}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_CJB110}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_18RS21}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_2603}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_A909}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_H36B}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_JM9130013}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_1169NT}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
Consensus	*****	*****	*****	*****	*****

## SEQ ID NO. 6412

STRAIN 2603 frame: 1

MNKSCKIENYQLLLQAQALFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELIL  
GPFQGGVSCVHITLKGKVCGESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGK  
LLGVLDLSSSLVADYDEIDQEYLEKFVGIIVHEHTIWNLDMPGVEK

## SEQ ID NO. 6413

STRAIN 090 frame: 3

LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELILGPFQGGVSCVHITLKGKVC  
GESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID  
QEYLEKFVGIIVHEHTIWNLD

## SEQ ID NO. 6414

STRAIN A909 frame: 3

LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELILGPFQGGVSCVHITLKGKVC  
GESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID  
QEYLEKFVGIIVHEHTIWNLDMPGVEK

## SEQ ID NO. 6415

STRAIN H36B frame: 3

LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELILGPFQGGVSCVHITLKGKVC  
GESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID  
QEYLEKFVGIIVHEHTIWNLDMPGVEK

## SEQ ID NO. 6416

STRAIN 18RS21 frame: 3

LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELILGPFQGGVSCVHITLKGKVC  
GESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID  
QEYLEKFVGIIVHEHTIWNLDMPGVEK

## SEQ ID NO. 6417

STRAIN M732 frame: 3

LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELILGPFQGGVSCVHITLKGKVC  
GESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID  
QEYLEKFVGIIVHEHTIWNLDMPGVEK

## SEQ ID NO. 6418

STRAIN COH1 frame: 3

LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELILGPFQGGVSCVHITLKGKVC  
GESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID  
QEYLEKFVGIIVHEHTIWNLDMPGVEK

## SEQ ID NO. 6419

STRAIN M781 frame: 3

LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELILGPFQGGVSCVHITLKGKVC  
GESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID

Table 64: Comparative Sequences relating to SAG 0827

QEYLEKFVGIIVHEHTIWNLD MFGEK

SEQ ID NO. 6420

STRAIN M781 frame: 3

LFSDETNALANLSNASAMLNAMLNPSVFTGFYLFDFGEEILILGPFQGGVSCVHITLGKGV  
 GESAQTAKTLIVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSLVADYDEID  
 QEYLEKFVGIIVHEHTIWNLD MFGEK

SEQ ID NO. 6421

STRAIN CJB110 frame: 3

LFSDETNALANLSNASAMLNAMLNPSVFTGFYLFDFGKEELILGPFQGGVSCVHITLGKGV  
 GESAQTAKTLIVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSLVADYDEID  
 QEYLEKFVGIIVHEHTIWNLD MFGEK

SEQ ID NO. 6422

STRAIN 1169NT frame: 3

LFSDETNALANLSNASAMLNAMLNPSVFTGFYLFDFGEEILILGPFQGGVSCVHITLGKGV  
 GESAQTAKTLIVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSLVADYDEID  
 QEYLEKFVGIIVHEHTIWNLD MFGEK

SEQ ID NO. 6423

STRAIN JM9130013 frame: 3

LFSDETNALANLSNASAMLNAMLNPSVFTGFYLFDFGEEILILGPFQGGVSCVHITLGKGV  
 GESAQTAKTLIVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSLVADYDEID  
 QEYLEKFVGIIVHEHTIWNLD MFGEK

PRETTY of: /biotmp/msa237960.2{\*} February 11, 2003 02:46 ..

	1		50
msa237960.2{282_1169NT}	-----L	FSDETNALAN	LSNASAMLNA
msa237960.2{282_18RS21}	-----L	FSDETNALAN	LSNASAMLNA
msa237960.2{282_2603}	mnkskkieny qlllllqaqaL	FSDETNALAN	LSNASAMLNA
msa237960.2{282_A909}	-----L	FSDETNALAN	LSNASAMLNA
msa237960.2{282_COH1}	-----L	FSDETNALAN	LSNASAMLNA
msa237960.2{282_H36B}	-----L	FSDETNALAN	LSNASAMLNA
msa237960.2{282_JM9130013}	-----L	FSDETNALAN	LSNASAMLNA
msa237960.2{282_M732}	-----L	FSDETNALAN	LSNASAMLNA
msa237960.2{282_M781}	-----L	FSDETNALAN	LSNASAMLNA
msa237960.2{282_090}	-----L	FSDETNALAN	LSNASAMLNA
msa237960.2{282_CJB110}	-----L	FSDETNALAN	LSNASAMLNA
Consensus	*****	*****	*****

	51		100
msa237960.2{282_1169NT}	YLFDFGELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_18RS21}	YLFDFGELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_2603}	YLFDFGELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_A909}	YLFDFGELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_COH1}	YLFDFGELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_H36B}	YLFDFGELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_JM9130013}	YLFDFGELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_M732}	YLFDFGELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_M781}	YLFDFGELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_090}	YLFDFGELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_CJB110}	YLFDFGELIL	GPFQGGVSCV	HITLGKGVCG
Consensus	*****	*****	*****

	101		150
msa237960.2{282_1169NT}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_18RS21}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_2603}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_A909}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_COH1}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_H36B}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_JM9130013}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_M732}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_M781}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_090}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_CJB110}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
Consensus	*****	*****	*****

	151	165
msa237960.2{282_1169NT}	VEHTIWNLDm	fgvek
msa237960.2{282_18RS21}	VEHTIWNLDm	fgvek
msa237960.2{282_2603}	VEHTIWNLDm	fgvek
msa237960.2{282_A909}	VEHTIWNLDm	fgvek
msa237960.2{282_COH1}	VEHTIWNLDm	fgvek
msa237960.2{282_H36B}	VEHTIWNLDm	fgvek
msa237960.2{282_JM9130013}	VEHTIWNLDm	fgvek
msa237960.2{282_M732}	VEHTIWNLDm	fgvek
msa237960.2{282_M781}	VEHTIWNLDm	fgvek
msa237960.2{282_090}	VEHTIWNLDm	fgvek
msa237960.2{282_CJB110}	VEHTIWNLDm	fgvek
Consensus	*****	-----

Table 65: Comparative Sequences relating to SAG0231

## SEQ ID NO. 6501

## STRAIN 2603

ATGAAAAAGAGTACCCAAATAATACTACTAATAGTTGCA  
 TTATTCTACTTGTTTTGTAGCGGAGGATTTTATATGAAAGAACCAACAAAGAAAGAGAA  
 CTAAACCGGAATCGAGAATATGAAGTTAGTCTAGTCAAAGCATTGAAAAATTCCTATGAG  
 AATATAGAAGAAATAAAATCACACATCCTGTTTCAACTGAAATTCCTGGAGATTGGCAT  
 TGTACTGTAAAGATTTCATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAAT  
 TTGGAATCGAAAAAAATTTATAGCGGAAATTTAATGAAAAAAATATGAATTTTTTGAT  
 TCAAGAAATTGGTAAACAAAAAAACTATAAAAAATTATTTTTTCAGATGGTCAGGAGAAG  
 ATACAA

## SEQ ID NO. 6502

## STRAIN 090

GGAGGATTTTATATGAAAGAACA  
 ACAAGAGAAAGAACTAAACCGGAATCGAGAATATGAAGTTAGTCTAG  
 TCAAAGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAATCACACATC  
 CATCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGAT  
 TTCATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGG  
 AATCGAAAAAAATTTATAGCGGAAATTTAATGAAAAAAATATGAATTTT  
 TTTGATTCAAGAAATTGGTAAACAAAAAACTATAAAAAATTATTTTTTC  
 AGATGGTCAGGAGAAGATaCAA

## SEQ ID NO. 6503

## STRAIN A909

GGAGGATTTTATATGAAAGAACAACA  
 AGAAAGAGAACTAAACCGGAATCGAGAATATGAAGTTAGTCTAGTCAA  
 AGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAATCACACATC  
 CTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTCA  
 TTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAATC  
 GAAAAAAATTTATAGCGGAAATTTAATGAAAAAAATATGAATTTTTTG  
 ATTCAAGAAATTGGTAAACAAAAAACTATAAAAAATTATTTTTTCAGAT  
 GGTCAGGAGAAGATaCAA

## SEQ ID NO. 6504

## STRAIN H36B

GGAGGATTTTATATGAAAGAACA  
 ACAAGAGAAAGAACTAAACCGGAATCGAGAATATGAAGTTAGTCTAG  
 TCAAAGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAATCACACATC  
 CATCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGAT  
 TTCATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGG  
 AATCGAAAAAAATTTATAGCGGAAATTTAATGAAAAAAATATGAATTTT  
 TTTGATTCAAGAAATTGGTAAACAAAAAACTATAAAAAATTATTTTTTC  
 AGATGGTCAGGAGAAGATaCAA

## SEQ ID NO. 6505

## STRAIN 18RS21

GGAGGATTTTATATGAAAGAACAAC  
 AAAGAGAAAGAACTAAACCGGAATCGAGAATATGAAGTTAGTCTAGTCT  
 AAAGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAATCACACATC  
 TCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATT  
 CATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAA  
 TCGAAAAAAATTTATAGCGGAAATTTAATGAAAAAAATATGAATTTTT  
 TGATTCAAGAAATTGGTAAACAAAAAACTATAAAAAATTATTTTTTCAG  
 ATGGTCAGGAGAAGATaCAA

## SEQ ID NO. 6506

## STRAIN M781

GGAGGATTTTATATGAAAGAACAACAAGAAAA  
 GAAGAACTAAACCGGAATCGAGAATATGAAGTTAGTCTAGTCAAAGCATT  
 GAAAAATTCCTATGAGAATATAGAAGAAATAAAATCACACATCCTGTTT  
 CAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTTCATTTAAT  
 GATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAATCGAAAAA  
 AAATTATAGCGGAAATTTAATGAAAAAAATATGAATTTTTTTGATTCAAG  
 AATTGGTAAACAAAAAACTATAAAAAATTATTTTTTCAGATGGTCAG  
 GAGAAGATACAA

## SEQ ID NO. 6507

## STRAIN CJB110

GGAGGATTTTATATGAAAGAACAACAAGAAAGAA  
 CTAAACCGGAATCGAGAATATGAAGTTAGTCTAGTCAAAGCATTGAAAAA  
 TTCCTATGAGAATATAGAAGAAATAAAATCACACATCCTGTTTCAACTG  
 AAATTCCTGGAGATTGGCATTGTACTGTAAAGATTTCATTTAATGATAAA  
 AATCTATTGTTTATAATATTACACATAATTTGGAATCGAAAAAAATTA  
 TAGCGGAAATTTAATGAAAAAAATATGAATTTTTTTGATTCAAGAAATTG  
 GTAAACAAAAAACTATAAAAAATTATTTTTTCAGATGGTCAGGAGAAG  
 ATACAA

## SEQ ID NO. 6508

## STRAIN 1169NT

GGAGGATTTTATATGAAAGAACAACAAG  
 AAAAGAGAACTAAACCGGAATCGAGAATATGAAGTTAGTCTAGTCAAAG  
 CATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAATCACACATCCT

Table 65: Comparative Sequences relating to SAG0231

GTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTTTCATT  
 TAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAATCGA  
 AAAAAAATTATAGTGGAAAAATTTAATGAAAAAAATATGAATTTTTTGGAT  
 TCAAGAAATGGTAAACAAAAAACTATAAAAAATTATTTTTTCAGATGG  
 TCAGGAGAAGATACAA

SEQ ID NO. 6509

STRAIN JM9130013

GGAGGATTTTATATGAAAGAACAAC

AAAGAAAAGAACTAAACCGGAATCGAGAATATGAAGTTAGTCTAGTC  
 AAAGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAAATCACACA  
 TCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTT  
 CATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAA  
 TCGAAAAAAATTTATAGCGGAAAAATTTAATGAAAAAAATATGAATTTTTT  
 TGATTCAAGAAATGGTAAACAAAAAACTATAAAAAATTATTTTTTCAG  
 AtGGtCAGGAGAAGATACAA

PRETTY of: /biotmp/msa75400.2{\*} March 10, 2003 09:56 ..

	1				50
msa75400.2{286_090}	-----	-----	-----	-----	-----
msa75400.2{286_CJB110}	-----	-----	-----	-----	-----
msa75400.2{286_18RS21}	-----	-----	-----	-----	-----
msa75400.2{286_2603}	atgaaaaaga	gtacccaaat	aataactacta	atagttgcat	tattcatact
msa75400.2{286_A909}	-----	-----	-----	-----	-----
msa75400.2{286_H36B}	-----	-----	-----	-----	-----
msa75400.2{286_JM9130013}	-----	-----	-----	-----	-----
msa75400.2{286_M781}	-----	-----	-----	-----	-----
msa75400.2{286_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa75400.2{286_090}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_CJB110}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_18RS21}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_2603}	tggtttttagc	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_A909}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_H36B}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_JM9130013}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_M781}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_1169NT}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
Consensus	*****	*****	*****	*****	*****
	101				150
msa75400.2{286_090}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_CJB110}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_18RS21}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_2603}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_A909}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_H36B}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_JM9130013}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_M781}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_1169NT}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
Consensus	*****	*****	*****	*****	*****
	151				200
msa75400.2{286_090}	TCCTATGAGA	ATATAGAAGA	AATAAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_CJB110}	TCCTATGAGA	ATATAGAAGA	AATAAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_18RS21}	TCCTATGAGA	ATATAGAAGA	AATAAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_2603}	TCCTATGAGA	ATATAGAAGA	AATAAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_A909}	TCCTATGAGA	ATATAGAAGA	AATAAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_H36B}	TCCTATGAGA	ATATAGAAGA	AATAAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_JM9130013}	TCCTATGAGA	ATATAGAAGA	AATAAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_M781}	TCCTATGAGA	ATATAGAAGA	AATAAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_1169NT}	TCCTATGAGA	ATATAGAAGA	AATAAAAAATC	ACACATCCTG	TTTCAACTGA
Consensus	*****	*****	*****	*****	*****
	201				250
msa75400.2{286_090}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_CJB110}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_18RS21}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_2603}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_A909}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_H36B}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_JM9130013}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_M781}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_1169NT}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
Consensus	*****	*****	*****	*****	*****
	251				300
msa75400.2{286_090}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT
msa75400.2{286_CJB110}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT
msa75400.2{286_18RS21}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT

Table 65: Comparative Sequences relating to SAG0231

msa75400.2{286_2603}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT
msa75400.2{286_A909}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT
msa75400.2{286_H36B}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT
msa75400.2{286_JM9130013}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT
msa75400.2{286_M781}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT
msa75400.2{286_1169NT}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT
Consensus	*****	*****	*****	*****	*****
msa75400.2{286_090}	AGcGGAAAT	TTAATGAAAA	AAATATGAAT	TTTTTTGATT	CAAGAATTGG
msa75400.2{286_CJB110}	AGcGGAAAT	TTAATGAAAA	AAATATGAAT	TTTTTTGATT	CAAGAATTGG
msa75400.2{286_18RS21}	AGcGGAAAT	TTAATGAAAA	AAATATGAAT	TTTTTTGATT	CAAGAATTGG
msa75400.2{286_2603}	AGcGGAAAT	TTAATGAAAA	AAATATGAAT	TTTTTTGATT	CAAGAATTGG
msa75400.2{286_A909}	AGcGGAAAT	TTAATGAAAA	AAATATGAAT	TTTTTTGATT	CAAGAATTGG
msa75400.2{286_H36B}	AGcGGAAAT	TTAATGAAAA	AAATATGAAT	TTTTTTGATT	CAAGAATTGG
msa75400.2{286_JM9130013}	AGcGGAAAT	TTAATGAAAA	AAATATGAAT	TTTTTTGATT	CAAGAATTGG
msa75400.2{286_M781}	AGcGGAAAT	TTAATGAAAA	AAATATGAAT	TTTTTTGATT	CAAGAATTGG
msa75400.2{286_1169NT}	AGcGGAAAT	TTAATGAAAA	AAATATGAAT	TTTTTTGATT	CAAGAATTGG
Consensus	**-----*	*****	*****	*****	*****
msa75400.2{286_090}	TAAAACAAAA	AAAACATAAA	AAATTATTTT	TTCAGATGGT	CAGGAGAAGA
msa75400.2{286_CJB110}	TAAAACAAAA	AAAACATAAA	AAATTATTTT	TTCAGATGGT	CAGGAGAAGA
msa75400.2{286_18RS21}	TAAAACAAAA	AAAACATAAA	AAATTATTTT	TTCAGATGGT	CAGGAGAAGA
msa75400.2{286_2603}	TAAAACAAAA	AAAACATAAA	AAATTATTTT	TTCAGATGGT	CAGGAGAAGA
msa75400.2{286_A909}	TAAAACAAAA	AAAACATAAA	AAATTATTTT	TTCAGATGGT	CAGGAGAAGA
msa75400.2{286_H36B}	TAAAACAAAA	AAAACATAAA	AAATTATTTT	TTCAGATGGT	CAGGAGAAGA
msa75400.2{286_JM9130013}	TAAAACAAAA	AAAACATAAA	AAATTATTTT	TTCAGATGGT	CAGGAGAAGA
msa75400.2{286_M781}	TAAAACAAAA	AAAACATAAA	AAATTATTTT	TTCAGATGGT	CAGGAGAAGA
msa75400.2{286_1169NT}	TAAAACAAAA	AAAACATAAA	AAATTATTTT	TTCAGATGGT	CAGGAGAAGA
Consensus	*****	*****	*****	*****	*****
msa75400.2{286_090}	TACAA				
msa75400.2{286_CJB110}	TACAA				
msa75400.2{286_18RS21}	TACAA				
msa75400.2{286_2603}	TACAA				
msa75400.2{286_A909}	TACAA				
msa75400.2{286_H36B}	TACAA				
msa75400.2{286_JM9130013}	TACAA				
msa75400.2{286_M781}	TACAA				
msa75400.2{286_1169NT}	TACAA				
Consensus	*****				
SEQ ID NO. 6510					
STRAIN 2603 frame: 1					
MKKSTQIILLIVAFILVFSGGFYMKQQRKEELKRNREYEVSLVKALKNSYENIEEIKI					
THPVSTEIPGDWHCTVKISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGKTK					
KTIKIIIFSDGQEKIQ					
SEQ ID NO. 6511					
STRAIN 090					
GGFYMKQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGD					
WHCTVKISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGKTKTIKIIIFSDGQ					
EKIQ					
SEQ ID NO. 6512					
STRAIN A909					
GGFYMKQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWH					
CTVKISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGKTKTIKIIIFSDGQEK					
IQ					
SEQ ID NO. 6513					
STRAIN H36B					
GGFYMKQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGD					
WHCTVKISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGKTKTIKIIIFSDGQ					
EKIQ					
SEQ ID NO. 6514					
STRAIN 18RS21					
GGFYMKQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDW					
HCTVKISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGKTKTIKIIIFSDGQEK					
KIQ					
SEQ ID NO. 6515					
STRAIN CJB110					
GGFYMKQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWHCTVK					
ISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGKTKTIKIIIFSDGQEKIQ					
SEQ ID NO. 6516					
STRAIN JM9130013					
GGFYMKQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDW					

Table 65: Comparative Sequences relating to SAG0231

HCTVKISFNDKKSIVYNITHNLESKKNYSGKFNEKNMNFDSRIGTKTKTIKIIFSDGQE  
KIQ

SEQ ID NO. 6517

STRAIN 1169NT frame: 1

GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWHCTVKISF  
NDKKSIVYNITHNLESKKNYSGKFNEKNMNFDSRIGTKTKTIKIIFSDGQEKIQ

SEQ ID NO. 6518

STRAIN M781 frame: 1

GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWHCTVKISF  
NDKKSIVYNITHNLESKKNYSGKFNEKNMNFDSRIGTKTKTIKIIFSDGQEKIQ

PRETTY of: /biotmp/msa75376.2{\*} March 10, 2003 10:01 ..

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      1                                     50
msa75376.2{286_090} ----- GGFYMKEQQR KEELKRNREY EVSLVKALKN
msa75376.2{286_1169NT} ----- GGFYMKEQQR KEELKRNREY EVSLVKALKN
msa75376.2{286_18RS21} ----- GGFYMKEQQR KEELKRNREY EVSLVKALKN
msa75376.2{286_2603} mkkstqiill ivalfilvfs GGFYMKEQQR KEELKRNREY EVSLVKALKN
msa75376.2{286_A909} ----- GGFYMKEQQR KEELKRNREY EVSLVKALKN
msa75376.2{286_CJB110} ----- GGFYMKEQQR KEELKRNREY EVSLVKALKN
msa75376.2{286_H36B} ----- GGFYMKEQQR KEELKRNREY EVSLVKALKN
msa75376.2{286_JM9130013} ----- GGFYMKEQQR KEELKRNREY EVSLVKALKN
msa75376.2{286_M781} ----- GGFYMKEQQR KEELKRNREY EVSLVKALKN
Consensus *****

      51                                     100
msa75376.2{286_090} SYENIEEIKI THPVSTEIPG DWHCTVKISF NDKKSIVYNI THNLESKKNY
msa75376.2{286_1169NT} SYENIEEIKI THPVSTEIPG DWHCTVKISF NDKKSIVYNI THNLESKKNY
msa75376.2{286_18RS21} SYENIEEIKI THPVSTEIPG DWHCTVKISF NDKKSIVYNI THNLESKKNY
msa75376.2{286_2603} SYENIEEIKI THPVSTEIPG DWHCTVKISF NDKKSIVYNI THNLESKKNY
msa75376.2{286_A909} SYENIEEIKI THPVSTEIPG DWHCTVKISF NDKKSIVYNI THNLESKKNY
msa75376.2{286_CJB110} SYENIEEIKI THPVSTEIPG DWHCTVKISF NDKKSIVYNI THNLESKKNY
msa75376.2{286_H36B} SYENIEEIKI THPVSTEIPG DWHCTVKISF NDKKSIVYNI THNLESKKNY
msa75376.2{286_JM9130013} SYENIEEIKI THPVSTEIPG DWHCTVKISF NDKKSIVYNI THNLESKKNY
msa75376.2{286_M781} SYENIEEIKI THPVSTEIPG DWHCTVKISF NDKKSIVYNI THNLESKKNY
Consensus *****

      101                                     135
msa75376.2{286_090} SGnFNEKNMN FFDSRIGGTK KTIKIIFSDG QEKIQ
msa75376.2{286_1169NT} SGkFNEKNMN FFDSRIGGTK KTIKIIFSDG QEKIQ
msa75376.2{286_18RS21} SGkFNEKNMN FFDSRIGGTK KTIKIIFSDG QEKIQ
msa75376.2{286_2603} SGkFNEKNMN FFDSRIGGTK KTIKIIFSDG QEKIQ
msa75376.2{286_A909} SGkFNEKNMN FFDSRIGGTK KTIKIIFSDG QEKIQ
msa75376.2{286_CJB110} SGnFNEKNMN FFDSRIGGTK KTIKIIFSDG QEKIQ
msa75376.2{286_H36B} SGkFNEKNMN FFDSRIGGTK KTIKIIFSDG QEKIQ
msa75376.2{286_JM9130013} SGkFNEKNMN FFDSRIGGTK KTIKIIFSDG QEKIQ
msa75376.2{286_M781} SGkFNEKNMN FFDSRIGGTK KTIKIIFSDG QEKIQ
Consensus **-*****

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Table 66: Comparative Sequences relating to SAG 0754

## SEQ ID NO. 6601

## STRAIN 2603

TTGACAAGGCATATAAAAAATTTCTATACTAAATTTACAAAATGAAGGAGAGGGAAGTATG  
GAAATACGTATTGCAGGTGGTAGTGGTTTTTTAGGAAAGCAGATAATAAAGCAGCGCTT  
ACAAAAGGGCATAAAGTGGCTTACTTATCAAGACATGAAGGTAAAGGTGATATATTAAG  
GATCCTAGATTAACTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAA  
GACAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCCAATCAACTAGAT  
GAGCTTAACTTTAAAGCAACCCAAAAGCAGTAGCACTCTGTCAAAAATCAAAATACCA  
AAGTTAGTTTATATTTAGCCCAACAGCGGCTATTAGCTTACATTAAAAGTAAAAGGAAG  
GCAGAGCAGATAATCAAAGCAAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATG  
TATGGTGAAGAGCGACCTCTCTCGATTTCGAAGCCAAGTGTATAAAGTTATTTAGTCAT  
TTGCCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACCTAAGGTTGTAGTAGGGCA  
GAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAATCCTTTCTATTGAAGAA  
TTAAATAATAAA

## SEQ ID NO. 6602

## STRAIN 090

ACAAGGCATATAAAAAATTTCTATACTAAATTTACAAAAT  
GAAGGAGAGGGAACCTATGGAAATACTGATTGCAGGTGGTAGTGGTTTTTT  
AGGAAAGCAGATAATAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTT  
ACTTATCAAGACATGAAGGTAAAGGTGATATATTAAAGGATCCTAGATTAA  
ACCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAAGA  
CAGAACCTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCCAATC  
AAGTAGATGAGCTTAACTTTAAAGCAACCCAAAAGCAGTAGCACTCTGT  
CACAAAATCAAATACCAAGTTAGTTTATATTTAGCCCAACAGCGGCTA  
TTAGCTTACATTAAAAGTAAAGGAAGGCAGAGCAGATAATCAAAGCAA  
GCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGAAGAG  
CGACCTCTCTCGATTTCGAAGCCAAGTGTATAAAGTTATTTAGTCATTT  
GCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACCTAAGGTTGTGA  
TAGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAA  
ATCCTTTCTATTGAAGAATTAATAATAAA

## SEQ ID NO. 6603

## STRAIN A909

ACAAGGCATATAAAAAATTTCTATACTAAATTTACAAAATG  
AAGGAGAGGGAACCTATGGAAATACTGATTGCAGGTGGTAGTGGTTTTTTA  
GGAAAGCAGATAATAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTTAA  
CTTATCAAGACATGAAGGTAAAGGTGATATATTAAAGGATCCTAGATTAA  
CCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAAGAC  
AGAACCTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCCAATCA  
ACTAGATGAGCTTAACTTTAAAGCAACCCAAAAGCAGTAGCACTCTGTCT  
ACAAAATCAAATACCAAGTTAGTTTATATTTAGCCCAACAGCGGCTAT  
TCAGCTTACATTAAAAGTAAAGGAAGGCAGAGCAGATAATCAAAGCAAG  
CGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGAAGAGC  
GACCTCTCTCGATTTCGAAGCCAAGTGTATAAAGTTATTTAGTCATTTG  
CCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACCTAAGGTTGTGAT  
AGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAA  
TCCTTTCTATTGAAGAATTAATAATAAA

## SEQ ID NO. 6604

## STRAIN H36B

TATAAAAATTTCTATACTAAATTTACAAAATGAAGGAGAGGGAAGTATGG  
AAATACGTATTGCAGGTGGTAGTGGTTTTTTAGGAAAGCAGATAATAAAA  
GCAGCGCTTACAAAAGGGCATAAAGTGGCTTACTTATCAAGACATGAAGG  
TAAAGGTGATATATTAAAGGATCCTAGATTAACTTACATTAGGGGAGATA  
TTACAGAAGCTGATAAGATTCAATTTAGAAGACAGAACCTTTTGATATATTA  
ATTGACTGTATTGGAGCGATTAAAGCCCAATCAACTAGATGAGCTTAACGT  
TAAAGCAACCCAAAAGCAGTAGCACTCTGTCAAAAATCAAATACCAA  
AGTTAGTTTATATTTAGCCCAACAGCGGCTATTAGCTTACATTAAAAGT  
AAAAGGAAGGCAGAGCAGATAATCAAAGCAAGCGGTCTGGATTATCTTTT  
TGTAAGACCAGGTTTGATGTATGGTGAAGAGCGACCTCTCTCGATTTC  
AAGCCAAAGTGTATAAAGTTATTTAGTCATTTGCCCTTTCTTAGGTATTGTT  
GTACAAAAGGTCTTTCCAACCTAAGGTTGTAGTAGTGGCAGAAGCAATCGT  
TACTACGCTTAGGAAAAAACCAACCCAAAAATCCTTTCTATTGAAGAAT  
TAAATAATAAA

## SEQ ID NO. 6605

## STRAIN 18RS21

ACAAGGCATATAAAAAATTTCTATACTAAATTTACAAAAT  
GAAGGAGAGGGAACCTATGGAAATACTGATTGCAGGTGGTAGTGGTTTTTT  
AGGAAAGCAGATAATAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTT  
ACTTATCAAGACATGAAGGTAAAGGTGATATATTAAAGGATCCTAGATTAA  
ACCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAAGA  
CAGAACCTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCCAATC  
AAGTAGATGAGCTTAACTTTAAAGCAACCCAAAAGCAGTAGCACTCTGT  
CACAAAATCAAATACCAAGTTAGTTTATATTTAGCCCAACAGCGGCTA  
TTAGCTTACATTAAAAGTAAAGGAAGGCAGAGCAGATAATCAAAGCAA  
GCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGAAGAG  
GACCTCTCTCGATTTCGAAGCCAAGTGTATAAAGTTATTTAGTCATTT  
GCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACCTAAGGTTGTGA  
TAGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAA  
ATCCTTTCTATTGAAGAATTAATAATAAA

Table 66: Comparative Sequences relating to SAG 0754

SEQ ID NO. 6606

STRAIN M732

CAAAATGAAGGAGAGGGAACCTATGgAAATACTGATTGCAGGTGGTAGTGG  
 TTTCTAGGGAAGCAGATAATAAAGCAGCGCTTACAAAAGGGCATAAGG  
 TGGCTTACTTATCAAGGCATGAAGGTAAAGGTGATATATTTAAGGATCCT  
 AGATTAACTTACATTAAAGGAGATATTACAGAAGCTGATAAGATTCAAT  
 AGaACATAGAAATTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGC  
 CCAATCACTAGATGAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCA  
 CTCTGTCACAAAAATCAAATACCAAAGTTAGTTTACATTTAGCCCAATAG  
 CGGCTATTAGCTTACATTAAAGTAAAGGAAGGCAGAGCAGATAATCA  
 AAGCAAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGT  
 GAAGAGCGACCTCTCTCGATTTCAGCAAGGTGTATAAAATTAATTTAG  
 TCATTGCGCTTCTTAGGTATTGTTGTACAAAAGTCTTTCCAACTAAGG  
 TTGTGATAGTGGCAGAAGCAATCGTTACTTCGCTTAGGAAAAACCAACT  
 CAAAAATCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6607

STRAIN COH1

ACAAGGCATATAAAAATTTCTATACTAAATTTAC  
 AAAATGAAGGAGAGGGAACCTATGGAATACTGATTGCAGGTGGTAGTGGT  
 TTTCTAGGGAAGCAGATAATAAAGCAGCGCTTACAAAAGGGCATAAGGT  
 GGCTTACTTATCAAGGCATGAAGGTAAAGGTGATATATTTAAGGATCCTA  
 GATTAACTTACATTAAAGGAGATATTACAGAAGCTGATAAGATTCAATTA  
 GAACATAGAAATTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCC  
 CAATCACTAGATGAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCAC  
 TCTGTCACAAAAATCAAATACCAAAGTTAGTTTACATTTAGCCCAATAGC  
 GGCTATTAGCTTACATTAAAGTAAAGGAAGGCAGAGCAGATAATCAA  
 AGCAAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTG  
 AAGAGCGACCTCTCTCGATTTCAGCAAGGTGTATAAAATTAATTTAGT  
 CATTTGCGCTTCTTAGGTATTGTTGTACAAAAGTCTTTCCAACTAAGGT  
 TGTGATAGTGGCAGAAGCAATCGTTACTTCGCTTAGGAAAAACCAACTC  
 AAAAAATCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6608

STRAIN M781

ACAAGGCATATAAAAATTTCTATACTAAATTTaCA  
 AAATGAAGGAGAGGGAACCTATGGAATACTGATTGCAGGTGGTAGTGGTT  
 TTCTAGGGAAGCAGATAATAAAGCAGCGCTTACAAAAGGGCATAAGGTG  
 GCTTACTTATCAAGGCATGAAGGTAAAGGTGATATATTTAAGGATCCTAG  
 ATTAACCTTACATTAAAGGAGATATTACAGAAGCTGATAAGATTCAATTTAG  
 AACATAGAAATTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCC  
 AATCACTAGATGAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCACT  
 CTGTCACAAAAATCAAATACCAAAGTTAGTTTACATTTAGCCCAATAGCG  
 GCTATTAGCTTACATTAAAGTAAAGGAAGGCAGAGCAGATAATCAA  
 GCAAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGA  
 AGAGCGACCTCTCTCGATTTCAGCAAGGTGTATAAAATTAATTTAGTCT  
 ATTTGCGCTTCTTAGGTATTGTTGTACAAAAGTCTTTCCAACTAAGGTT  
 GTGATAGTGGCAGAAGCAATCGTTACTTCGCTTAGGAAAAACCAACTCA  
 AAAAAATCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6609

STRAIN 1169NT

ACAAGGCATATAAAAATTTCTATACTAAATTTACAAA  
 ATGAAGGAGAGGGAACCTATGGAATACTGATTGCAGGTGGTAGTGGTTT  
 TTAGGAAAGCAGATAATAAAGCAGCGCTTACAAAAGGGCATAAGTTGGC  
 TTACTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGAT  
 TAACCTACATTAAAGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAA  
 GACAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCAA  
 TCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCACTCT  
 GTCACAAAATCAAATACCAAAGTTAGTTTACATTTAGCCCAACAGCGGC  
 TATTAGCTTACATTAGAAGTAAAGGAAGGCAGAGCAGATAATCAAAGC  
 AAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGAAG  
 AGCGACCTCTCTCGATTTCAGCAAGGTGTATAAAATTAATTTAGTCAT  
 TTGCCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACTAAGGTTGT  
 GATAGTGGCAGAAGCAATCGTTACTACGCTTAGGACAAAACCAACTCAA  
 AAATCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6610

STRAIN CJB110

ACAAGGCATATAAAAATTTCTATACTAAATTTACAAA  
 ATGAAGGAGAGGGAACCTATGGAATACTGATTGCAGGTGGTAGTGGTTT  
 TTAGGAAAGCAGATAATAAAGCAGCGCTTACAAAAGGGCATAAGTTGGC  
 TTACTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGAT  
 TAACCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAA  
 GACAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCAA  
 TCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCACTCT  
 GTCACAAAATCAAATACCAAAGTTAGTTTATATTTAGCCCAACAGCGGC  
 TATTAGCTTACATTAAAGTAAAGGAAGGCAGAGCAGATAATCAAAGC  
 AAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGAAG  
 AGCGACCTCTCTCGATTTCAGCAAGGTGTATAAAATTAATTTAGTCAT  
 TTGCCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACTAAGGTTGT  
 GATAGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAACCAACTCAA  
 AAATCCTTTCTATTGAAGAATTAAATAATAAA



Table 66: Comparative Sequences relating to SAG 0754

SEQ ID NO. 6611

STRAIN JM9130013

ACAAGGCATATAAAATTCTTACTAAATTTACAAAATG  
 AAGGAGAGGGAATATGGAAATCTGATTGCAGGTGGTAGTGGTTTTTTA  
 GGAAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTTA  
 CTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGATTAA  
 CcTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAAGAC  
 AGAACITTTTGATATATTAATTGACTGTATTGGAGCGATTAAGCCCAATCA  
 ACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACTCTGTG  
 ACAAAAATCAAATACCAAGTTAGTTTATATTTCAGCCAACACGGGCTAT  
 TCAGCTTACATTAAAGTAAAGGAAGGCAGAGCAGATAATCAAAGCAAG  
 CGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGAAGAGC  
 GACCTCTCTCGATTTTCCAAGCCAAGTGATAAAGTTATTTAGTCAATTG  
 CCTTTCTTAgGTATTGTGTACAAAAGGCTTTCCAACCTAAGGTTGTGAT  
 AGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAAA  
 TCCTTTCTATTGAAGAATTAATAATAAA

PRETTY of: /biotmp/msal37119.2{\*} April 10, 2003 03:30 ..

	1				50
msal37119.2{303_COH1}	---acaaggc	atataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
msal37119.2{303_M732}	-----	-----	-----	-----CAAA	ATGAAGGAGA
msal37119.2{303_m781}	---acaaggc	atataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
msal37119.2{303_090}	---acaaggc	atataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
msal37119.2{303_18RS21}	---acaaggc	atataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
msal37119.2{303_2603}	ttgacaaggc	atataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
msal37119.2{303_A909}	---acaaggc	atataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
msal37119.2{303_CJB110}	---acaaggc	atataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
msal37119.2{303_H36B}	-----	-tataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
msal37119.2{303_JM9130013}	---acaaggc	atataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
msal37119.2{303_1169NT}	---acaaggc	atataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
Consensus	***-----	-----	-----	-----****	*****

	51				100
msal37119.2{303_COH1}	GGGAACCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	cTAGGgAAGC
msal37119.2{303_M732}	GGGAACCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	cTAGGgAAGC
msal37119.2{303_m781}	GGGAACCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	cTAGGgAAGC
msal37119.2{303_090}	GGGAACCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	tTAGGaaAGC
msal37119.2{303_18RS21}	GGGAACCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	tTAGGaaAGC
msal37119.2{303_2603}	GGGAACCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	tTAGGaaAGC
msal37119.2{303_A909}	GGGAACCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	tTAGGaaAGC
msal37119.2{303_CJB110}	GGGAACCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	tTAGGaaAGC
msal37119.2{303_H36B}	GGGAACCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	tTAGGaaAGC
msal37119.2{303_JM9130013}	GGGAACCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	tTAGGaaAGC
msal37119.2{303_1169NT}	GGGAACCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	tTAGGaaAGC
Consensus	*****	*****	*****	*****	*****

	101				150
msal37119.2{303_COH1}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_M732}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_m781}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_090}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_18RS21}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_2603}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_A909}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_CJB110}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_H36B}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_JM9130013}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_1169NT}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
Consensus	*****	*****	*****	*****	*****

	151				200
msal37119.2{303_COH1}	AGgCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_M732}	AGgCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_m781}	AGgCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_090}	AGaCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_18RS21}	AGaCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_2603}	AGaCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_A909}	AGaCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_CJB110}	AGaCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_H36B}	AGaCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_JM9130013}	AGaCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_1169NT}	AGaCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
Consensus	***-----	-----	-----	-----	-----

	201				250
msal37119.2{303_COH1}	TAaGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	cAtAGAAaTT
msal37119.2{303_M732}	TAaGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	cAtAGAAaTT
msal37119.2{303_m781}	TAaGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	cAtAGAAaTT
msal37119.2{303_090}	TAaGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gAcAGAAcTT
msal37119.2{303_18RS21}	TAaGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gAcAGAAcTT
msal37119.2{303_2603}	TAaGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gAcAGAAcTT

Table 66: Comparative Sequences relating to SAG 0754

msa137119.2{303_A909}	TagGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gACAGAAcTT
msa137119.2{303_CJB110}	TagGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gACAGAAcTT
msa137119.2{303_H36B}	TagGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gACAGAAcTT
msa137119.2{303_JM9130013}	TagGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gACAGAAcTT
msa137119.2{303_1169NT}	TaaGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gACAGAAcTT
Consensus	***-*****	*****	*****	*****	-*-*****
251					
msa137119.2{303_COH1}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_M732}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_m781}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_090}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_18RS21}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_2603}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_A909}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_CJB110}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_H36B}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_JM9130013}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_1169NT}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
Consensus	*****	*****	*****	*****	*****
301					
msa137119.2{303_COH1}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_M732}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_m781}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_090}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_18RS21}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_2603}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_A909}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_CJB110}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_H36B}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_JM9130013}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_1169NT}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
Consensus	*****	*****	*****	*****	*****
351					
msa137119.2{303_COH1}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAATAGCGGC	TATTTCAGCTT
msa137119.2{303_M732}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAATAGCGGC	TATTTCAGCTT
msa137119.2{303_m781}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAATAGCGGC	TATTTCAGCTT
msa137119.2{303_090}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAATAGCGGC	TATTTCAGCTT
msa137119.2{303_18RS21}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAATAGCGGC	TATTTCAGCTT
msa137119.2{303_2603}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAATAGCGGC	TATTTCAGCTT
msa137119.2{303_A909}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAATAGCGGC	TATTTCAGCTT
msa137119.2{303_CJB110}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAATAGCGGC	TATTTCAGCTT
msa137119.2{303_H36B}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAATAGCGGC	TATTTCAGCTT
msa137119.2{303_JM9130013}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAATAGCGGC	TATTTCAGCTT
msa137119.2{303_1169NT}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAATAGCGGC	TATTTCAGCTT
Consensus	*****	*****	*-*****	***-*****	*****
401					
msa137119.2{303_COH1}	ACATTAAaAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_M732}	ACATTAAaAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_m781}	ACATTAAaAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_090}	ACATTAAaAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_18RS21}	ACATTAAaAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_2603}	ACATTAAaAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_A909}	ACATTAAaAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_CJB110}	ACATTAAaAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_H36B}	ACATTAAaAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_JM9130013}	ACATTAAaAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_1169NT}	ACATTAgAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
Consensus	*****-***	*****	*****	*****	*****
451					
msa137119.2{303_COH1}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_M732}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_m781}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_090}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_18RS21}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_2603}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_A909}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_CJB110}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_H36B}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_JM9130013}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_1169NT}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
Consensus	*****	*****	*****	*****	*****
501					
msa137119.2{303_COH1}	CTCGATTTC	CAAGCCAAGT	GTATAAAaTT	ATTTAGTCAT	TGCGCTTTCT
msa137119.2{303_M732}	CTCGATTTC	CAAGCCAAGT	GTATAAAaTT	ATTTAGTCAT	TGCGCTTTCT
msa137119.2{303_m781}	CTCGATTTC	CAAGCCAAGT	GTATAAAaTT	ATTTAGTCAT	TGCGCTTTCT
msa137119.2{303_090}	CTCGATTTC	CAAGCCAAGT	GTATAAAaTT	ATTTAGTCAT	TGCGCTTTCT
msa137119.2{303_18RS21}	CTCGATTTC	CAAGCCAAGT	GTATAAAaTT	ATTTAGTCAT	TGCGCTTTCT

Table 66: Comparative Sequences relating to SAG 0754

msa137119.2{303_2603}	CTCGATTTC	CAAGCCAAGT	GTATAAAGTT	ATTTAGTCAT	TGCGCTTTCT
msa137119.2{303_A909}	CTCGATTTC	CAAGCCAAGT	GTATAAAGTT	ATTTAGTCAT	TGCGCTTTCT
msa137119.2{303_CJB110}	CTCGATTTC	CAAGCCAAGT	GTATAAAGTT	ATTTAGTCAT	TGCGCTTTCT
msa137119.2{303_H36B}	CTCGATTTC	CAAGCCAAGT	GTATAAAGTT	ATTTAGTCAT	TGCGCTTTCT
msa137119.2{303_JM9130013}	CTCGATTTC	CAAGCCAAGT	GTATAAAGTT	ATTTAGTCAT	TGCGCTTTCT
msa137119.2{303_1169NT}	CTCGATTTC	CAAGCCAAGT	GTATAAAGTT	ATTTAGTCAT	TGCGCTTTCT
Consensus	*****	*****	*****_*	*****	*****
551					
msa137119.2{303_COH1}	TAGGTATTGT	TGTACAAAAa	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_M732}	TAGGTATTGT	TGTACAAAAa	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_m781}	TAGGTATTGT	TGTACAAAAa	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_090}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_18RS21}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_2603}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_A909}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_CJB110}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_H36B}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_JM9130013}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_1169NT}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
Consensus	*****	*****_*	*****	*****	*****
601					
msa137119.2{303_COH1}	GAAGCAATCG	TTACTtCGCT	TAGGAaAAAA	CCAActCAAA	AAATCCTTTC
msa137119.2{303_M732}	GAAGCAATCG	TTACTtCGCT	TAGGAaAAAA	CCAActCAAA	AAATCCTTTC
msa137119.2{303_m781}	GAAGCAATCG	TTACTtCGCT	TAGGAaAAAA	CCAActCAAA	AAATCCTTTC
msa137119.2{303_090}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAAA	AAATCCTTTC
msa137119.2{303_18RS21}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAAA	AAATCCTTTC
msa137119.2{303_2603}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAAA	AAATCCTTTC
msa137119.2{303_A909}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAAA	AAATCCTTTC
msa137119.2{303_CJB110}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAAA	AAATCCTTTC
msa137119.2{303_H36B}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAAA	AAATCCTTTC
msa137119.2{303_JM9130013}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAAA	AAATCCTTTC
msa137119.2{303_1169NT}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAAA	AAATCCTTTC
Consensus	*****	*****_*	*****_*	*****_*	*****
651					
msa137119.2{303_COH1}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_M732}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_m781}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_090}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_18RS21}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_2603}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_A909}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_CJB110}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_H36B}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_JM9130013}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_1169NT}	TATTGAAGAA	TAAATAATA	AA		
Consensus	*****	*****	**		
672					

## SEQ ID NO. 6612

## STRAIN 2603 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD  
 PRLTYIRGDIETADKIHLEDRFTDILIDCIGAIPKPNQDELNVKATQKAVALKHNQIPK  
 LVYISANSYGSAIYKSKRKAQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSLH  
 PFLGIVQKVFPKVVIVABAIVITLRRKPTQKILSIEELNNK

## SEQ ID NO. 6613

## STRAIN 090 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD  
 PRLTYIRGDIETADKIHLEDRFTDILIDCIGAIPKPNQDELNVKATQKAVALKHNQIPK  
 LVYISANSYGSAIYKSKRKAQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSLH  
 PFLGIVQKVFPKVVIVABAIVITLRRKPTQKILSIEELNNK

## SEQ ID NO. 6614

## STRAIN A909 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD  
 PRLTYIRGDIETADKIHLEDRFTDILIDCIGAIPKPNQDELNVKATQKAVALKHNQIPK  
 LVYISANSYGSAIYKSKRKAQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSLH  
 PFLGIVQKVFPKVVIVABAIVITLRRKPTQKILSIEELNNK

## SEQ ID NO. 6615

## STRAIN H36B frame: 2

IKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKDPRL  
 TYIRGDIETADKIHLEDRFTDILIDCIGAIPKPNQDELNVKATQKAVALKHNQIPKLVY  
 ISANSYGSAIYKSKRKAQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSLH  
 PFLGIVQKVFPKVVIVABAIVITLRRKPTQKILSIEELNNK

## SEQ ID NO. 6616

Table 66: Comparative Sequences relating to SAG 0754

## STRAIN 18RS21 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD  
 PRLTYIRGDI TEADKIHLEDRTFDILIDCIGAIPNQLDELNVKATQKAVALCHKNQIPK  
 LVYISANSYSAYIKSKRKAQEI KASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSL  
 PFLGIVVQKVFPPTKVIVAEIVTTLRKKPTQKILSIEELNNK

## SEQ ID NO. 6617

## STRAIN M732 frame: 1

QNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKDPRLTYIKGDIT  
 EADKIHLEHRNFDILIDCIGAIPNQLDELNVKATQKAVALCHKNQIPKLVYISANSYS  
 AYIKSKRKAQEI KASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSLPFLGIVVQKV  
 PTKVIVAEIVTSLRKKPTQKILSIEELNNK

## SEQ ID NO. 6618

## STRAIN COH1 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD  
 PRLTYIKGDIT EADKIHLEHRNFDILIDCIGAIPNQLDELNVKATQKAVALCHKNQIPK  
 LVYISANSYSAYIKSKRKAQEI KASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSL  
 PFLGIVVQKVFPPTKVIVAEIVTSLRKKPTQKILSIEELNNK

## SEQ ID NO. 6619

## STRAIN M781 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD  
 PRLTYIKGDIT EADKIHLEHRNFDILIDCIGAIPNQLDELNVKATQKAVALCHKNQIPK  
 LVYISANSYSAYIKSKRKAQEI KASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSL  
 PFLGIVVQKVFPPTKVIVAEIVTSLRKKPTQKILSIEELNNK

## SEQ ID NO. 6620

## STRAIN 1169NT frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKLAYLSRHEGKGDIFKD  
 PRLTYIKGDIT EADKIHLEDRTFDILIDCIGAIPNQLDELNVKATQKAVALCHKNQIPK  
 LVYISANSYSAYIKSKRKAQEI KASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSL  
 PFLGIVVQKVFPPTKVIVAEIVTTLRKKPTQKILSIEELNNK

## SEQ ID NO. 6621

## STRAIN CJB110 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD  
 PRLTYIRGDI TEADKIHLEDRTFDILIDCIGAIPNQLDELNVKATQKAVALCHKNQIPK  
 LVYISANSYSAYIKSKRKAQEI KASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSL  
 PFLGIVVQKVFPPTKVIVAEIVTTLRKKPTQKILSIEELNNK

## SEQ ID NO. 6622

## STRAIN JM9130013 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD  
 PRLTYIRGDI TEADKIHLEDRTFDILIDCIGAIPNQLDELNVKATQKAVALCHKNQIPK  
 LVYISANSYSAYIKSKRKAQEI KASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSL  
 PFLGIVVQKVFPPTKVIVAEIVTTLRKKPTQKILSIEELNNK

PRETTY of: /biotmp/msal37299.2{\*} April 10, 2003 03:37 ..

	1				50
msal37299.2{303_COH1}	trhikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msal37299.2{303_M732}	-----	-QNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msal37299.2{303_M781}	trhikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msal37299.2{303_090}	trhikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msal37299.2{303_18RS21}	trhikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msal37299.2{303_2603}	trhikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msal37299.2{303_A909}	trhikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msal37299.2{303_CJB110}	trhikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msal37299.2{303_JM9130013}	trhikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msal37299.2{303_H36B}	---ikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msal37299.2{303_1169NT}	trhikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
Consensus	-----	*****	*****	*****	*****

  

	51				100
msal37299.2{303_COH1}	HEGKGDIFKD	PRLTYIKGDI	TEADKIHLEh	RnFDILIDCI	GAIKPNQLDE
msal37299.2{303_M732}	HEGKGDIFKD	PRLTYIKGDI	TEADKIHLEh	RnFDILIDCI	GAIKPNQLDE
msal37299.2{303_M781}	HEGKGDIFKD	PRLTYIKGDI	TEADKIHLEh	RnFDILIDCI	GAIKPNQLDE
msal37299.2{303_090}	HEGKGDIFKD	PRLTYIKGDI	TEADKIHLEd	RtFDILIDCI	GAIKPNQLDE
msal37299.2{303_18RS21}	HEGKGDIFKD	PRLTYIKGDI	TEADKIHLEd	RtFDILIDCI	GAIKPNQLDE
msal37299.2{303_2603}	HEGKGDIFKD	PRLTYIKGDI	TEADKIHLEd	RtFDILIDCI	GAIKPNQLDE
msal37299.2{303_A909}	HEGKGDIFKD	PRLTYIKGDI	TEADKIHLEd	RtFDILIDCI	GAIKPNQLDE
msal37299.2{303_CJB110}	HEGKGDIFKD	PRLTYIKGDI	TEADKIHLEd	RtFDILIDCI	GAIKPNQLDE
msal37299.2{303_JM9130013}	HEGKGDIFKD	PRLTYIKGDI	TEADKIHLEd	RtFDILIDCI	GAIKPNQLDE
msal37299.2{303_H36B}	HEGKGDIFKD	PRLTYIKGDI	TEADKIHLEd	RtFDILIDCI	GAIKPNQLDE
msal37299.2{303_1169NT}	HEGKGDIFKD	PRLTYIKGDI	TEADKIHLEd	RtFDILIDCI	GAIKPNQLDE
Consensus	*****	*****	*****	*****	*****

Table 66: Comparative Sequences relating to SAG 0754

	101		150
msa137299.2{303_COH1}	LNVKATQKAV	ALCHKNQIPK	LVYISANSKY SAYIKSKRKA EQIIKASGLD
msa137299.2{303_M732}	LNVKATQKAV	ALCHKNQIPK	LVYISANSKY SAYIKSKRKA EQIIKASGLD
msa137299.2{303_M781}	LNVKATQKAV	ALCHKNQIPK	LVYISANSKY SAYIKSKRKA EQIIKASGLD
msa137299.2{303_090}	LNVKATQKAV	ALCHKNQIPK	LVYISANSKY SAYIKSKRKA EQIIKASGLD
msa137299.2{303_18RS21}	LNVKATQKAV	ALCHKNQIPK	LVYISANSKY SAYIKSKRKA EQIIKASGLD
msa137299.2{303_2603}	LNVKATQKAV	ALCHKNQIPK	LVYISANSKY SAYIKSKRKA EQIIKASGLD
msa137299.2{303_A909}	LNVKATQKAV	ALCHKNQIPK	LVYISANSKY SAYIKSKRKA EQIIKASGLD
msa137299.2{303_CJB110}	LNVKATQKAV	ALCHKNQIPK	LVYISANSKY SAYIKSKRKA EQIIKASGLD
msa137299.2{303_JM9130013}	LNVKATQKAV	ALCHKNQIPK	LVYISANSKY SAYIKSKRKA EQIIKASGLD
msa137299.2{303_H36B}	LNVKATQKAV	ALCHKNQIPK	LVYISANSKY SAYIKSKRKA EQIIKASGLD
msa137299.2{303_1169NT}	LNVKATQKAV	ALCHKNQIPK	LVYISANSKY SAYIKSKRKA EQIIKASGLD
Consensus	*****	*****	*****_*****
	151		200
msa137299.2{303_COH1}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL PFLGIVVQKV FPTKVVIVAE
msa137299.2{303_M732}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL PFLGIVVQKV FPTKVVIVAE
msa137299.2{303_M781}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL PFLGIVVQKV FPTKVVIVAE
msa137299.2{303_090}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL PFLGIVVQKV FPTKVVIVAE
msa137299.2{303_18RS21}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL PFLGIVVQKV FPTKVVIVAE
msa137299.2{303_2603}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL PFLGIVVQKV FPTKVVIVAE
msa137299.2{303_A909}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL PFLGIVVQKV FPTKVVIVAE
msa137299.2{303_CJB110}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL PFLGIVVQKV FPTKVVIVAE
msa137299.2{303_JM9130013}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL PFLGIVVQKV FPTKVVIVAE
msa137299.2{303_H36B}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL PFLGIVVQKV FPTKVVIVAE
msa137299.2{303_1169NT}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL PFLGIVVQKV FPTKVVIVAE
Consensus	*****	*****	*****
	201		223
msa137299.2{303_COH1}	AIVTsLRKKP	TQKILSIEEL	NNK
msa137299.2{303_M732}	AIVTsLRKKP	TQKILSIEEL	NNK
msa137299.2{303_M781}	AIVTsLRKKP	TQKILSIEEL	NNK
msa137299.2{303_090}	AIVTtLRKKP	TQKILSIEEL	NNK
msa137299.2{303_18RS21}	AIVTtLRKKP	TQKILSIEEL	NNK
msa137299.2{303_2603}	AIVTtLRKKP	TQKILSIEEL	NNK
msa137299.2{303_A909}	AIVTtLRKKP	TQKILSIEEL	NNK
msa137299.2{303_CJB110}	AIVTtLRKKP	TQKILSIEEL	NNK
msa137299.2{303_JM9130013}	AIVTtLRKKP	TQKILSIEEL	NNK
msa137299.2{303_H36B}	AIVTtLRKKP	TQKILSIEEL	NNK
msa137299.2{303_1169NT}	AIVTtLRtKP	TQKILSIEEL	NNK
Consensus	****-***	*****	***

Table 67: Comparative Sequences relating to SAG0475

SEQ ID NO. 6701

STRAIN 090

CAATAACAACATTTGAAAAATAAAAAAGTTTTAGTCCTTGGTTTAGCACGA  
 TCTGGAGAAGCCGCTGCACGTTTGTAGCTAAGTTAGGAGCAATAGTGAC  
 AGTTAATGATGGCAAACCATTTGATGAAAAATCCACAGCACAGTCTTTGT  
 TGGAAAGAGGGTATTAAAGTGGTTTGTGGTAGTCATCCTTTAGAATTGTTA  
 GATGAGGATTTTTGTTACATGATTAAAAATCCAGGAATACCTTATAACAA  
 TCCTATGGTCAAAAAGCATTAGAAAAACAAATCCCTGTTTTGACTGAAG  
 TGGAAATTAGCATACTTAGTTTCAGAAATCTCAGCTAATAGGTATTACAGGC  
 TCTAACGGGAAAACGACACGACACGATGATGCAGAAAGTCTTAAATGC  
 TGGAGGTCAGAGAGGTTTGTAGCTGGGAATATCGGCTTTCCTGCTAGTG  
 AAGTTGTTTCAAGGCTGCGGATGATAAAGATATTCTAGTTATGGAATTATCA  
 AGTTTTTCAAGCTAATGGGAGTTAAGGAATTTTCCTCATATTGCGAGTAAT  
 TACTAATTTAATGCCAACTCAATTAGATTATCATGGGTCTTTTGAAGATT  
 ATGTTGCTGCAAAATGGAATATCCAAATCAAATGTCTTCATCTGATTTT  
 TTGGTACTTAATTTTAAATCAAGGTATTTCTAAAGAGTTAGCTAAAACCTAC  
 TAAAGCAACAATCGTTCCTTCTCTACTACGGAATAAGTTGATGGTGCTT  
 ACGTACAGACAAGCAACTTTTCTATAAAGGGGAGAAATATTATGTTAGTA  
 GATGACATTGGTGTCCAGGAAGCCATAACGTAGAGAATGCTCTAGCAAC  
 TATTGCGGTTGCTAAACTAGCTGGTATCAGTAATCAAGTTATTAGAGAAA  
 CTTTAAGCAATTTTGGAGGTGTTAAACACCGCTTGCAATCACTCGGTAAAG  
 GTTCATGGTATTAGTTTCTATAACGACAGCAAGTCAACTAATATATTGGC  
 AACTCAAAAAGCATTATCTGGCTTTGATAATACTAAAGTTATCCTAATTG  
 CAGGAGGTCCTTGATCGCGGTAATGAGTTTGATGAATTGATACCAGATATC  
 ACTGGACTTAAACATATGGTTGTTTTAGGGGAATCGGCATCTCGAGTAAA  
 ACGTGCTGCACAAAAGCAGGAGTAACCTTATAGCGATGCTTTAGATGTTA  
 GAGATGCGGTACATAAAGCTTATGAGGTGGCACAACAGGGCGATGTTATC  
 TTGCTAAGTCTGCAATGCATCATGGGACATGTATAAGAATTTTCAAGT  
 CCGTGGTGATGAATTCATTGATACCTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6702

STRAIN A909

CAATAACAACATTTGAAAAATAAAAAAGTTTTAGTCCTTGGTTTAGCACGA  
 TCTGGAGAAGCTGCTGCACGTTTGTAGCTAAGTTAGGAGCAATAGTGAC  
 AGTTAATGATGGCAAACCATTTGATGAAAAATCCACAGCACAGTCTTTGT  
 TGGAAAGAGGGTATTAAAGTGGTTTGTGGTAGTCATCCTTTAGAATTGTTA  
 GATGAGGATTTTTGTTACATGATTAAAAATCCAGGAATACCTTATAACAA  
 TCCTATGGTCAAAAAGCATTAGAAAAACAAATCCCTGTTTTGACTGAAG  
 TGGAAATTAGCATACTTAGTTTCAGAAATCTCAGCTAATAGGTATTACAGGC  
 TCTAACGGGAAAACGACACGACACGATGATGCAGAAAGTCTTAAATGC  
 TGGAGGTCAGAGAGGTTTGTAGCTGGGAATATCGGCTTTCCTGCTAGTG  
 AAGTTGTTTCAAGGCTGCGAATGATAAAGATACTCTAGTTATGGAATTATCA  
 AGTTTTTCAAGCTAATGGGAGTTAAGGAATTTTCCTCATATTGCGAGTAAT  
 TACTAATTTAATGCCAACTCAATTAGATTATCATGGGTCTTTTGAAGATT  
 ATGTTGCTGCAAAATGGAATATCCAAATCAAATGTCTTCATCTGATTTT  
 TTGGTACTTAATTTTAAATCAAGGTATTTCTAAAGAGTTAGCTAAAACCTAC  
 TAAAGCAACAATCGTTCCTTCTCTACTACGGAATAAGTTGATGGTGCTT  
 ACGTACAGACAAGCAACTTTTCTATAAAGGGGAGAAATATTATGTCAGTA  
 GATGACATTGGTGTCCAGGAAGCCATAACGTAAAGAATGCTCTAGCAAC  
 TATTGCGGTTGCTAAACTGCGCTGGTATCAGTAATCAAGTTATTAGAGAAA  
 CTTTAAGCAATTTTGGAGGTGTTAAACACCGCTTGCAATCACTCGGTAAAG  
 GTTCATGGTATTAGTTTCTATAACGACAGCAAGTCAACTAATATATTGGC  
 AACTCAAAAAGCATTATCTGGCTTTGATAATACTAAAGTTATCCTAATTG  
 CAGGAGGTCCTTGATCGCGGTAATGAGTTTGATGAATTGATACCAGATATC  
 ACTGGACTTAAACATATGGTTGTTTTAGGGGAATCGGCATCTCGAGTAAA  
 ACGTGCTGCACAAAAGCAGGAGTAACCTTATAGCGATGCTTTAGATGTTA  
 GAGATGCGGTACATAAAGCTTATGAGGTGGCACAACAGGGCGATGTTATC  
 TTGCTAAGTCTGCAATGCATCATGGGACATGTATAAGAATTTTCAAGT  
 CCGTGGTGATGAATTCATTGATACCTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6703

STRAIN H36B

GGACGAGTAATGAAAACAATAACAACATTTGAAAAT  
 AAAAAAGTTTTAGTCCTTGGTTTAGCACGATCTGGAGAAGCTGCTGCACG  
 TTTGTTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAAACCAT  
 TTGATGAAAATCCACAGCACAGTCTTTGTTGGAAGAGGGTATTAAAGTG  
 GTTTGTGGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTTTGTTACAT  
 GATTAATAATCCAGGAATACCTTATAACCAATCCTATGGTCAAAAAGCAT  
 TAGAAAAACAAAATCCCTGTTTTGACTGAAGTGAAGTTAGCATACTTAGTT  
 TCAGAAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAACGACAA  
 GACAACGATGATTGCAGAAAGTCTTAAATGCTGGAGGTGAGAGAGGTTTGT  
 TAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTCAAGGCTGCGAAT  
 GATAAAGATACTCTAGTTATGGAATTTATCAAGTTTTCAGCTAATGGGAGT  
 TRAGGAATTTCTGCTCATATTGCAAGTAATTAATAATTAAATGCCAACTC  
 ATTTAGATTATCATGGGTCTTTTGAAGATTATGTTGCTGCAAAATGGAAT  
 ATCCAAAATCAAATGTCTTCATCTGATTTTTTGGTACTTAATTTTAAATCA  
 AGGTATTTCTAAAGAGTTAGCTAAAACCTACTAAAGCAACAATCGTTCCTT  
 TCTCTACTACGGAATAAGTTGATGGTGCTTACGTACAAGACAAGCAACTT  
 TTCTATAAAGGGGAGAAATATTATGTCAGTAGATGACATTGGTGTCCAGG  
 AAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTGCTAAACTGG  
 CTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAATTTTGGAGGT  
 GTTAAACACCGCTTCAATCACTCGGTAAGGTTTATGGTATTAGTTTCTA  
 TAACGACAGCAAG

Table 67: Comparative Sequences relating to SAG0475

SEQ ID NO. 6704

STRAIN 18RS21

GGACGAGTAATGAAAAACAATAACAACATTTG  
 AAAATAAAAAAGTTTGTAGTCCTTGGTTTAGCACGATCTGGAGAAGCTGCT  
 GCACGTTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAA  
 ACCATTTGATGAAAAATCCAACAGCACAGTCTTGTGGAAGAGGGTATTA  
 AAGTGGTTTGTGGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTTGT  
 TACATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAA  
 AGCATTAGAAAAACAATCCCTGTTTGTGACTGAAGTGGAATTAGCATACT  
 TAGTTTCAGAAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAAACG  
 ACAACGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTCAGAGAGG  
 TTTGTTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTGAGGCTG  
 CGAATGATAAAGATACTCTAGTTATGGAATTATCAAGTTTTCAGCTAATG  
 GGAGTTAAGGAATTCGTCTCATATTGACAGTAATTACTAATTTAATGCC  
 AACTCATTTAGATTATCATGGGCTCTTTGAAGATTATGTTGCTGCAAAAT  
 GGAATATCCAAAAATCAAATGTCCTCATCTGATTTTGGTACTTAATTTT  
 AATCAAGGTATTTCTAAAGAGTTAGCTAAAACTACTAAAGCAACAATCGT  
 TCCTTTCTCTACTACGGAAAAAGTTGATGGTGCTTACGTACAAGACAAGC  
 AACTTTTCTATAAAGGGGAGAATATTATGTGAGTAGATGACATTGGTGTC  
 CCAGGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTGCTAA  
 ACTGGCTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAATTTTG  
 GAGGTGTTAAACACCGCTTGCAATCACTCGGTAAGGTTTATGTTATTAGT  
 TTCTATAACGACAGCAAGTCACTAATATATTGGCAACTCAAAAAGCATT  
 ATCTGGCTTTGATAATACTAAAGTTATCCTAATTGACAGGAGGCTTGATC  
 GCGGTAATGAGTTTGTGTAATTGATACAGATATCACTGGACTTAAACAT  
 ATGGTTGTTTGGGGGAATCGGCATCTCGAGTAAAACGTGCTGCACAAAA  
 AGCAGGAGTAACCTTAGCGATGCTTTAGATGTTAGAGATGCGGTACATA  
 AAGCTTATGAGGTGGCACAACAGGGCGATGTTATCTTGCTAAGTCTTGCA  
 AATGCATCATGGGACATGTATAAGAATTTGGAAGTCCGTGGTGATGAATT  
 CATTGATACTTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6705

STRAIN M732

GGACGAGTAATGAAAAACAATAACAACATTTGAAA  
 ATAAAAAAGTTTGTAGTCCTTGGTTTAGCACGATCTGGAGAAGCCGCTGCA  
 CGTTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAAACC  
 ATTTGATGAAAAATCCAACAGCACAGTCTTGTGGAAGAGGGTATTAAAG  
 TGGTTTGTGGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTTGTATAC  
 ATGATTAATAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAAAGC  
 ATTAGAAAAACAATCCCTGTTTGTGACTGAAGTGAATTAGCATACTTAG  
 TTTGAGAAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAAACGACA  
 ACCGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTGAGAGAGGTTT  
 GTTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTGAGGCTGCGG  
 aTGATAAAGATATTCTAGTTATGGAATTATCAAGTTTTCAGCTAATGGGA  
 GTTAAGGAATTTGCTCCTCATATTGACAGTAATTACTAATTTAATGCCAAC  
 TCACTTAGATTATCATGGGCTCTTTGAGAGTTATGTTGCTGCAAAATGGA  
 ATATCCAAAAATCAAATGTCCTCATCTGATTTTGGTACTTAATTTAAT  
 CAAGGTATTTCTAAAGAGTTAGCTAAAACTACTAAAGCAACAaTCGTTCC  
 TTTCTCTACTACGGAAAAAGTTGATGGTGCTTACGTACAAGACAAGCAAC  
 TTTTCTATAAAGGGGAGAATATTATGTGAGTAGATGACATTGGTGTCCTCA  
 GGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTGCTAAACT  
 AGCTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAATTTGGAG  
 GTGTTAAACACCGCTTGCAATCACTCGGTAAGGTTTATGTTATTAGTTTC  
 TATAACGACAGCAAGTCACTAATATATTGGCAACTCAAAAAGCATTATC  
 TGGCTTTGATAATACTAAAGTTATCCTAATTGACAGGAGGCTTGTATCGCG  
 GTAATGAGTTTGTGAAATTGATACAGATATCACTGGACTTAAACATATG  
 GTTGTTTTAGGGGAATCGGCATCTCGAGTAAAACGTGCTGCACAAAAAGC  
 AGGAGTAACCTTATAGCGATGCTTTAGATGTTAGAGATGCGGTACATAAAG  
 CTTATGAGGTGGCACAACAGGGCGATGTTATCTTGCTAAGTCTTGCAAA  
 GCATCATGGGACATGTATAAGAATTTGGAAGTCCGTGGTGATGAATTAT  
 TGATACTTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6706

STRAIN COH1

GGACGAGTAATGAAAAACAATAACAACATTTGA  
 AAATAAAAAAGTTTGTAGTCCTTGGTTTAGCACGATCTGGAGAAGCCGCTG  
 CACGTTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAA  
 CCATTTGATGAAAAATCCAACAGCACAGTCTTGTGGAAGAGGGTATTAA  
 AGTGGTTTGTGGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTTGT  
 ACATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAA  
 GCATTAGAAAAACAATCCCTGTTTGTGACTGAAGTGAATTAGCATACT  
 AGTTTCAGAAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAAACGA  
 CAACGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTGAGAGAGT  
 TTGTTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTGAGGCTGC  
 GGAATGATAAAGATATTCTAGTTATGGAATTATCAAGTTTTCAGCTAATGG  
 GAGTTAAGGAATTTGCTCCTCATATTGACAGTAATTACTAATTTAATGCCA  
 ACTCATTTAGATTATCATGGGCTTTTGAAGATTATGTTGCTGCAAAATG  
 GAATATCCAAAAATCAAATGTCCTCATCTGATTTTGGTACTTAATTTTA  
 ATCAAGGTATTTCTAAAGAGTTAGCTAAAACTACTAAAGCAaCAATCGTT  
 CCTTCTCTACTACGGAAAAAGTTGATGGTGCTTACGTACAAGACAAGCA  
 ACTTTTCTATAAAGGGGAGAATATTATGTGAGTAGATGACATTGGTGTC  
 CAGGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTGCTAAA

Table 67: Comparative Sequences relating to SAG0475

CTAGCTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAATTTTGG  
AGGTGTTAAACACCGCTTGCAATCACTCGGTAAAGTTTCATGGTATTAGTT  
TCTATAACGACAGCAAGTCAACTAATATATTGGCAACTCAAAAAGCATTA  
TCTGGCTTTGATAATACTAAAGTTATCCTAATGTCAGGAGGTCCTGATCG  
CGGTAATGAGTTTGATGAATTGATACCAGATATCACTGGACTTAAACATA  
TGGTTCTTTTAGGGGAATCGGCATCTCGAGTAAACGTGCTGCACAAAA  
GCAGGAGTAACTTATAGCGATGCTTTAGATGTTAGAGATGCGGTACATAA  
AGCTTATGAGGTGGCACAAACAGGCGATGTTATCTTGCTAAGTCTTGCAA  
ATGCATCATGGGACATGTATAAGAATTTGAAAGTCCGTGGTGTGAATTC  
ATTGATACCTTCGAAA

SEQ ID NO. 6707

STRAIN M781

GGACGAGTAATGAAAACAATAACAACATT  
TGAAAATAAAAAAGTTTGTAGTCTTGGTTTAGCAGGATCTGGAGAAGCCG  
CTGCACGTTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGC  
AAACCATTTGATGAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGTAT  
TAAAGTGGTTTGTGGTAGTCATCCTTTAGAATTTGTAGATGAGGATTTT  
GTTACATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAA  
AAAGCATTAGAAAAACAATCCTGTTTGGACTGAAGTGAATTAGCATA  
CTTAGTTTCAGAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAA  
CGACACGACAAACGATGATTGAGAAAGTCTTAAATGCTGGAGGTGAGAGA  
GGTTTGTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTTACGGC  
TGCGGATGATAAAGATATTTAGTTATGGAATTTATCAAGTTTTCAGCTAA  
TGGGAGTTAAGGAATTTCTGCTCATATTGTCAGTAATTACTAATTTAATG  
CCAATCATTTAGATTATCATGGGTCTTTTGAAGATTATGTTGCTGCAAA  
ATGGAAATATCCAAATCAAATGTCTTCATCTGATTTTTGGTACTTAAAT  
TTAATCAAGGTATTTCTAAAGAGTTAGCTAAAACCTAAAGCAACAATC  
GTTCTTTTCTACTACGAAAAAGTTGATGGTGTCTACGTACAAGACAA  
GCAACTTTTCTATAAAGGGGAGAATATTTATGTCAGTAGATGACATTGCTG  
TCCCAGGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTTGGGTTGCT  
AAACTAGCTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAATTT  
TGGAGGTGTTAAACACCGCTTGCAATCACTCGGTAAGGTTTATGGTATTA  
GTTTCTATAACGACAGCAAGTCAACTAATATATTGGCAACTCAAAAAGCA  
TTATCTGGCTTTGATAATACTAAAGTTATCTAATTGTCAGGAGGTCTTGA  
TCGCGGTAATGAGTTTGTAGTAATTGATACCAGATATCACTGGACTTAAAC  
ATATGGTTGTTTATAGGGGAATCGGCATCTCGAGTAAACGTGCTGCACAA  
AAAGCAGGAGTAACTTATAGCGATGCTTTAGATGTTAGAGATGCGGTACA  
TAAAGCTTATGAGGTGGCACAAACAGGCGATGTTATCTTGCTAAGTCTG  
CAAAATGCATCATGGACATGTATAAGAATTTGAAAGTCCGTGGTGTGAAT  
TTCATGATACTTTGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6708

STRAIN CJB110

GGACGAGTAATGAAAACAATAACAACATTTGA  
AAATAAAAAAGTTTGTAGTCTTGGTTTAGCAGGATCTGGAGAAGCCGCTG  
CACGTTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAAA  
CCATTGATGAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGTATTAA  
AGTGGTTTGTGGTAGTCATCCTTTAGAATTTGTAGATGAGGATTTTGT  
ACATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAA  
GCATTAGAAAAACAATCCTGTTTGGACTGAAGTGAATTAGCATACTT  
AGTTTCAGAAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAAACGA  
CAACGACAAACGATGATTGACAGAAGTCTTAAATGCTGGAGGTGAGAGAGGT  
TTGTTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTTACGGCTGC  
GGATGATAAAGATATTTAGTTATGGAATTTATCAAGTTTTCAGCTAATGG  
GAGTTAAGGAATTTCTGCTCATATTGTCAGTAATTACTAATTTAATGCCA  
ACTCATTTAGATTATCATGGGTCTTTTGAAGAATATGTTGCTGCAAAATG  
GAATATCCAAAATCAAATGTCTTCATCTGATTTTGGTACTTAAATTTA  
ATCAAGGTATTTCTAAAGAGTTAGCTAAAACCTAAAGCAACAATCGTT  
CCTTTCTCTACTACGAAAAAGTTGATGGTCTTACGTACAAGACAAGCA  
ACTTTTCTATAAAGGGGAGAATATTATGTTAGTAGATGACATTGGTGTCC  
CAGGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTGCTAAA  
CTAGCTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAATTTGG  
AGGTGTTAAACACCGCTTGCAATCACTCGGTAAGGTTTATGGTATTAGTT  
TCTATATGACAGCAAGTCAACTAATATATTGGCAACTCAAAAAGCATTA  
TCTGGCTTTGATAATACTAAAGTTATCCTAATTGTCAGGAGGTCTTGATCG  
CGGTAATGAGTTTGATGAATTGATACCAGATATCACTGGACTTAAACATA  
TGGTTGTTTTAGGGGAATCGGCATCTCGAGTAAACGTGCTGCACAAAA  
GCAGGAGTAACTTATAGCGATGCTTTAGATGTTAGAGATGCGGTACATAA  
AGCTTATGAGGTGGCACAAACAGGCGATGTTATCTTGCTAAGTCTTGCAA  
ATGCATCATGGGACATGTATAAGAATTTGAAAGTCCGTGGTGTGAATTC  
ATTGATACTTTGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6709

STRAIN 1169NT

CAATAACAACATTTGAAAATAAAAAAGTTTGTAGTCTTGGTTTAGCACGA  
TCTGGAGAAGCCGCTGCACGTTTGTAGCTAAGTTAGGAGCAATAGTGAC  
AGTTAATGATGGCAAAACATTTGATGAAAATCCAACAGCACAGTCTTTGT  
TGGAGAGGGTATTAAAGTGGTTTGTGGTAGTCATCCTTTAGAATTTGTTA  
GATGAGGATTTTGTACATGATTAAAAATCCAGGAATACCTTATAACAA  
TCCATATGGTCAAAAAGCATTAGAAAAACAATCCTGTTTGGACTGAAG  
TGAATTAGCATACTTAGTTTCAGAATCTCAGCTAATAGGTATTACAGGC  
TCTAACGGGAAAACGACAAACGACAGATGATTGACAGAAGTCTTGAATGC



Table 67: Comparative Sequences relating to SAG0475

TGGAGGTGAGAGAGGTTTGTAGCTGGGAATATCGGCTTTCTGCTAGTG  
 AAGTTGTTTCAGGCTGCGGATGATAAGATACTAGTTATGGAATATCA  
 AGTTTTCAGCTAATGGGAGTTAAGGAATTCGTCTCATATGTCAGTAAT  
 TACTAATTTAATGCCAACTCATTAGATTATCATGGGTCTTTGAAGACT  
 ATGTGCTGCAAAATGGAATATCCAAATCAAATGCTTCTCATCTGATTTT  
 TTGGTACTTAATTTAATCAAGGTATTTCTAAAGAGTTAGCTAAACTAC  
 TAAAGCACAATCGTTCCTTCTCTACTACGGAAGGTTGATGGTGCTT  
 ACGTACAAGCAAGCAACTTTCTATAAGGGGAGAAATATTATGTCAGTA  
 GACGACATTTGGTGTCCAGGAAGCCATAACGTAGAGAATGCTTAGCAAC  
 TATTGCGGTTGCTAACTAGCTGGTATCAGTAATCAAGTTATTAGAGAAA  
 CTTTAAGCAATTTGGAGGTGTTAAACACCGCTTGCAATCACTCGGTAAG  
 GTTCATGGTATTAGTTTCTATAACGACAGTAAGTCAACTAATATATTGGC  
 AACTCAAAAGCATTATCTGGCTTTGATAATACTAAAGTTATCTTAATTG  
 CAGGAGGTCTTGATCGCGGTAAATGAGTTTGTGAAITGATACCATATC  
 ACTGGACTTAAGCATATGGTTGTTTAGGGGAATCGGCATCTCGAGTAAA  
 ACGTGTGTCACAAAAGCAGGAGTAACCTTATAGCAATGCTTTAGATGTTA  
 GAGATGCGGTACATAAAGCTTATGAGGTGGCAACAGGGCGATGTTATC  
 TTGTTAGTCTCGCAATGCATCATGGGACATGTATAAGAAATTCGAAGT  
 CCGTGGTGATGAATTCATTGATACCTTCG

SEQ ID NO. 6710

STRAIN JM9130013

GGACGAGTAATGAAAACAATAACAACA  
 TTTGAAAATAAAAAAGTTTGTAGCTTGGTTTAGCAGCATCTGGAGAAGC  
 TGCTGCAAGTTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATG  
 GCAAAACCATTTGATGAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGT  
 ATTAAAGTGGTTTGTGGTAGTCATCTTTAGAATTGCTAGATGAGGATTT  
 TTGTTACATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCA  
 AAAAAGCATTAGAAAAACAATCCCTGTTTGTACTGAAGTGAATTAGCA  
 TACTTAGTTTCAAGATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAA  
 AAGCACAACGACAACGATGATTGCAAGTCTTAAATGCTGGAGGTGAGA  
 GAGGTTTGTAGCTGGGAATATCGGCTTTCTGCTAGTGAAGTTGTTGAG  
 GCTGCGAATGATAAAGATACTCTAGTTATGGAATTATCAAGTTTTCAGCT  
 AATGGGAGTTAAGGAATTTCTGCTCATATTGCAAGTAATTACTAATTTAA  
 TGCCCAACTCATTTAGATTATCATGGGTCTTTGAAGATTATGTTGCTGCA  
 AAATGGAATATCCAAATCAAATGCTTCTCATCTGATTTTTGGTACTTAA  
 TTTTAATCAAGGTATTCTAAAGAGTTAGCTAAACTACTAAAGCAACAA  
 TCGTTCTTTCTCTACTACGGAAGGTTGATGGTGTCTACGTACAAGAC  
 AAGCAACTTTCTATAAAGGGGAGAAATATTATGTCAGTAGATGACATTGG  
 TGTCCCAAGCAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTG  
 CTAAACTGGCTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAAT  
 TTTGGAGGTGTTAAACACCGCTTGCAATCACTCGGTAAGGTTTCATGGTAT  
 TAGTTCTATAACGACAGCAAGTCAACTAATATATTGGCAACTCAAAAG  
 CATTATCTGGCTTTGATAATACTAAGGTTATCTTAATGTCAGGAGGTCTT  
 GATCGCAGTAATGAGTTTGTAGTAATGATACCATATCACTGGACTTAA  
 ACATATGGTTGTTTATAGGGGAATCGGCATCTCGAGTAAACGTGCTGCAC  
 AAAAAGCAGGAGTAACCTTATAGCGATGCTTTAGATGTTAGAGATGCGGTA  
 CATAAAGCTTATGAGGTGGCAACAGGGCGATGTTATCTTGTCTAAGTCC  
 TGCAATGTCATCATGGGACATGTATAAGAAATTCGAAGTCCGTGGTGATG  
 AATTCATTGATACCTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6710

STRAIN 2603

ggacgagtaaatgaaaacaataacaacatttgaaaataaaaaagtttagt  
 ccttggttagcacgcatctggagaagctgctgcacgtttagtagtaagt  
 taggagcaatagtgacagttaatgatggcaaacatttgatgaaaatcca  
 acagcacagtcctttagtggaagagggtattaaagtggttttaggttagtca  
 tccttagaattgtagtagaggattttttagtatgattaaaaatccag  
 gaataccttataacaatcctatggtcaaaaaagcattagaaaaacaatc  
 cctgttttgactgaagtgggaattagcatacttagttcagaatctcagct  
 aatagggtattacaggctctaacgggaaaaacgacaacgacacgatgattg  
 cagaagctttaaagctggagggtcagagagggtttagtagctgggaatatc  
 ggcttctctgctagtgaaagttagttcagggtgcaaatgataaagatactct  
 agttatgggaattatcaagttttagctaaatgggagtttaaggaatttcgtc  
 ctcatattgacagtaattactaatttaagccaactcatttagattatcat  
 gggctctttgaagattatgtagctgcaaaatgggaatccaaaatcaa  
 gtctctcatctgattttttagtacttaatttaatacaaggattttctaaag  
 agtttagctaaaactactaaagcaacaatcgttctctctactacggaa  
 aaagttgatgggtgcttacgtacaagacaagcaactttctataaaggga  
 gaattatgtagctagtagatgacattgggtgtcccaggaagccaataacgtag  
 agaattgctctagcaactattgagggtgctaaactgggtggtatcagta  
 caagttattagagaaactttaagcaattttggagggtgtaaacacccgctt  
 gcaatcactcggtaaggttcatgggtatttagtttctataacgacagcaagt  
 caactaatatattggcaactcaaaaagcattatctggctttgataaact  
 aaagttatcctaatttgaggagggtcttgatcgcggttaagtagtttagta  
 attgataccagatatactggacttaaacatattggtttagtttaggggaat  
 cggcatctcaggtaaaacgtgctgcacaaaagcaggagtaacttatagc  
 gatgttttagatgttagagatgcggtacataaagcttatgaggtggcaca  
 acagggcgatggtatcttgctaagtcctgcaaatgcatcatgggacatgt  
 ataagaatttcgaagtcctgggtgatgaattcattgatactttcgaaggt  
 ctttagaggagag

Table 67: Comparative Sequences relating to SAG0475

## MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa30176.2{\*} April 29, 2002 02:09 ..

	1				50
msa30176.2{305_18RS21}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305_2603}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305_A909}	-----	-----CAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305_H36B}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305_JM9130013}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305_COH1}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305_M781}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305e_M732}	-----	-----CAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305_090}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305_CJB110}	-----	-----CAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305_1169NT}	-----	-----CAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
Consensus	-----	-----CAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
	51				100
msa30176.2{305_18RS21}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_2603}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_A909}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_H36B}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_JM9130013}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_COH1}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_M781}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305e_M732}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_090}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_CJB110}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_1169NT}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
Consensus	*****	*****	*****	*****	*****
	101				150
msa30176.2{305_18RS21}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_2603}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_A909}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_H36B}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_JM9130013}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_COH1}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_M781}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305e_M732}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_090}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_CJB110}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_1169NT}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
Consensus	*****	*****	*****	*****	*****
	151				200
msa30176.2{305_18RS21}	ACAGCACAGT	CTTTGTTTGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_2603}	ACAGCACAGT	CTTTGTTTGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_A909}	ACAGCACAGT	CTTTGTTTGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_H36B}	ACAGCACAGT	CTTTGTTTGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_JM9130013}	ACAGCACAGT	CTTTGTTTGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_COH1}	ACAGCACAGT	CTTTGTTTGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_M781}	ACAGCACAGT	CTTTGTTTGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305e_M732}	ACAGCACAGT	CTTTGTTTGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_090}	ACAGCACAGT	CTTTGTTTGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_CJB110}	ACAGCACAGT	CTTTGTTTGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_1169NT}	ACAGCACAGT	CTTTGTTTGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
Consensus	*****	*****	*****	*****	*****
	201				250
msa30176.2{305_18RS21}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_2603}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_A909}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_H36B}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_JM9130013}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_COH1}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_M781}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305e_M732}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_090}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_CJB110}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_1169NT}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
Consensus	*****	*****	*****	*****	*****
	251				300
msa30176.2{305_18RS21}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_2603}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_A909}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_H36B}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_JM9130013}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_COH1}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_M781}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305e_M732}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_090}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC

Table 67: Comparative Sequences relating to SAG0475

msa30176.2{305_CJB110}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCAITAGA	AAAACAAATC
msa30176.2{305_1169NT}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCAITAGA	AAAACAAATC
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	301				350
msa30176.2{305_2603}	CCTGTTTGA	CTGAAGTGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_A909}	CCTGTTTGA	CTGAAGTGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_H36B}	CCTGTTTGA	CTGAAGTGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_JM9130013}	CCTGTTTGA	CTGAAGTGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_COH1}	CCTGTTTGA	CTGAAGTGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_M781}	CCTGTTTGA	CTGAAGTGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305e_M732}	CCTGTTTGA	CTGAAGTGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_090}	CCTGTTTGA	CTGAAGTGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_CJB110}	CCTGTTTGA	CTGAAGTGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_1169NT}	CCTGTTTGA	CTGAAGTGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	351				400
msa30176.2{305_2603}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_A909}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_H36B}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_JM9130013}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_COH1}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_M781}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305e_M732}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_090}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_CJB110}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_1169NT}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	401				450
msa30176.2{305_2603}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
msa30176.2{305_A909}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
msa30176.2{305_H36B}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
msa30176.2{305_JM9130013}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
msa30176.2{305_COH1}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
msa30176.2{305_M781}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
msa30176.2{305e_M732}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
msa30176.2{305_090}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
msa30176.2{305_CJB110}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
msa30176.2{305_1169NT}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	451				500
msa30176.2{305_2603}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_A909}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_H36B}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_JM9130013}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_COH1}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_M781}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305e_M732}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_090}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_CJB110}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_1169NT}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	501				550
msa30176.2{305_2603}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_A909}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_H36B}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_JM9130013}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_COH1}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_M781}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305e_M732}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_090}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_CJB110}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_1169NT}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	551				600
msa30176.2{305_2603}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCAITT	AGATTATCAT
msa30176.2{305_A909}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCAITT	AGATTATCAT
msa30176.2{305_H36B}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCAITT	AGATTATCAT
msa30176.2{305_JM9130013}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCAITT	AGATTATCAT
msa30176.2{305_COH1}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCAITT	AGATTATCAT
msa30176.2{305_M781}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCAITT	AGATTATCAT
msa30176.2{305e_M732}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCAITT	AGATTATCAT

Table 67: Comparative Sequences relating to SAG0475

msa30176.2{305_090}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATTT	AGATTATCAT
msa30176.2{305_CJB110}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATTT	AGATTATCAT
msa30176.2{305_1169NT}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATTT	AGATTATCAT
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_2603}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_A909}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_H36B}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_JM9130013}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_COH1}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_M781}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305e_M732}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_090}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_CJB110}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_1169NT}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_2603}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_A909}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_H36B}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_JM9130013}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_COH1}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_M781}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305e_M732}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_090}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_CJB110}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_1169NT}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCTTTTCTC	TACTACGGAA
msa30176.2{305_2603}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCTTTTCTC	TACTACGGAA
msa30176.2{305_A909}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCTTTTCTC	TACTACGGAA
msa30176.2{305_H36B}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCTTTTCTC	TACTACGGAA
msa30176.2{305_JM9130013}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCTTTTCTC	TACTACGGAA
msa30176.2{305_COH1}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCTTTTCTC	TACTACGGAA
msa30176.2{305_M781}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCTTTTCTC	TACTACGGAA
msa30176.2{305e_M732}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCTTTTCTC	TACTACGGAA
msa30176.2{305_090}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCTTTTCTC	TACTACGGAA
msa30176.2{305_CJB110}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCTTTTCTC	TACTACGGAA
msa30176.2{305_1169NT}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCTTTTCTC	TACTACGGAA
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_2603}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_A909}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_H36B}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_JM9130013}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_COH1}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_M781}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305e_M732}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_090}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_CJB110}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_1169NT}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_2603}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_A909}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_H36B}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_JM9130013}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_COH1}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_M781}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305e_M732}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_090}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_CJB110}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_1169NT}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
Consensus	*****	*-*****	*****	*****	*****
msa30176.2{305_18RS21}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT
msa30176.2{305_2603}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT
msa30176.2{305_A909}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT
msa30176.2{305_H36B}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT
msa30176.2{305_JM9130013}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT
msa30176.2{305_COH1}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT
msa30176.2{305_M781}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT

Table 67: Comparative Sequences relating to SAG0475

msa30176.2{305e_M732}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTaGCTGG	TATCAGTAAT
msa30176.2{305_090}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTaGCTGG	TATCAGTAAT
msa30176.2{305_CJB110}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTaGCTGG	TATCAGTAAT
msa30176.2{305_1169NT}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTaGCTGG	TATCAGTAAT
Consensus	*****	*****	*****	****_****	*****
msa30176.2{305_18RS21}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_2603}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_A909}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_H36B}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_JM9130013}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_COH1}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_M781}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305e_M732}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_090}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_CJB110}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_1169NT}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_2603}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_A909}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_H36B}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_JM9130013}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_COH1}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_M781}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305e_M732}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_090}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_CJB110}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_1169NT}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305_2603}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305_A909}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305_H36B}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305_JM9130013}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305_COH1}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305_M781}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305e_M732}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305_090}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305_CJB110}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305_1169NT}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
Consensus	-----	-----	-----	-----	-----
msa30176.2{305_18RS21}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaaatg	agtttgatga
msa30176.2{305_2603}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaaatg	agtttgatga
msa30176.2{305_A909}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaaatg	agtttgatga
msa30176.2{305_H36B}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaaatg	agtttgatga
msa30176.2{305_JM9130013}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaaatg	agtttgatga
msa30176.2{305_COH1}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaaatg	agtttgatga
msa30176.2{305_M781}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaaatg	agtttgatga
msa30176.2{305e_M732}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaaatg	agtttgatga
msa30176.2{305_090}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaaatg	agtttgatga
msa30176.2{305_CJB110}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaaatg	agtttgatga
msa30176.2{305_1169NT}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaaatg	agtttgatga
Consensus	-----	-----	-----	-----	-----
msa30176.2{305_18RS21}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305_2603}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305_A909}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305_H36B}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305_JM9130013}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305_COH1}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305_M781}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305e_M732}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305_090}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305_CJB110}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305_1169NT}	attgatacca	gatatactg	gacttaagca	tatggttggtt	ttaggggaat
Consensus	-----	-----	-----	-----	-----
msa30176.2{305_18RS21}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_2603}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_A909}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_H36B}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_JM9130013}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_COH1}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc

Table 67: Comparative Sequences relating to SAG0475

msa30176.2{305_M781}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305e_M732}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_090}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_CJB110}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_1169NT}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
Consensus	-----	-----	-----	-----	-----
msa30176.2{305_18RS21}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_2603}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_A909}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_H36B}	-----	-----	-----	-----	-----
msa30176.2{305_JM9130013}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_COH1}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_M781}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305e_M732}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_090}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_CJB110}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_1169NT}	aatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
Consensus	-----	-----	-----	-----	-----
msa30176.2{305_18RS21}	acagggcgat	gttatcttgc	taagtcctgc	aaatgcatca	tgggacatgt
msa30176.2{305_2603}	acagggcgat	gttatcttgc	taagtcctgc	aaatgcatca	tgggacatgt
msa30176.2{305_A909}	acagggcgat	gttatcttgc	taagtcctgc	aaatgcatca	tgggacatgt
msa30176.2{305_H36B}	-----	-----	-----	-----	-----
msa30176.2{305_JM9130013}	acagggcgat	gttatcttgc	taagtcctgc	aaatgcatca	tgggacatgt
msa30176.2{305_COH1}	acagggcgat	gttatcttgc	taagtcctgc	aaatgcatca	tgggacatgt
msa30176.2{305_M781}	acagggcgat	gttatcttgc	taagtcctgc	aaatgcatca	tgggacatgt
msa30176.2{305e_M732}	acagggcgat	gttatcttgc	taagtcctgc	aaatgcatca	tgggacatgt
msa30176.2{305_090}	acagggcgat	gttatcttgc	taagtcctgc	aaatgcatca	tgggacatgt
msa30176.2{305_CJB110}	acagggcgat	gttatcttgc	taagtcctgc	aaatgcatca	tgggacatgt
msa30176.2{305_1169NT}	acagggcgat	gttatcttgc	taagtcctgc	aaatgcatca	tgggacatgt
Consensus	-----	-----	-----	-----	-----
msa30176.2{305_18RS21}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt
msa30176.2{305_2603}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt
msa30176.2{305_A909}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt
msa30176.2{305_H36B}	-----	-----	-----	-----	-----
msa30176.2{305_JM9130013}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt
msa30176.2{305_COH1}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaa--
msa30176.2{305_M781}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt
msa30176.2{305e_M732}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt
msa30176.2{305_090}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt
msa30176.2{305_CJB110}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt
msa30176.2{305_1169NT}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt
Consensus	-----	-----	-----	-----	-----
msa30176.2{305_18RS21}	cttagaggag	ag			
msa30176.2{305_2603}	cttagaggag	ag			
msa30176.2{305_A909}	cttagaggag	ag			
msa30176.2{305_H36B}	-----	---			
msa30176.2{305_JM9130013}	cttagaggag	ag			
msa30176.2{305_COH1}	-----	---			
msa30176.2{305_M781}	cttagaggag	ag			
msa30176.2{305e_M732}	cttagaggag	ag			
msa30176.2{305_090}	cttagaggag	ag			
msa30176.2{305_CJB110}	cttagaggag	ag			
msa30176.2{305_1169NT}	-----	---			
Consensus	-----	---			

SEQ ID NO. 6711

STRAIN 090 frame: 3

ITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLEEGI KVVCGS  
HPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQIIGITGSNGK  
TTTTTMAIEVLNAGGQRLLAGNIGFPASEVVQAADKDI LVMELSSFQLMGVKEFRPHI  
AVITNLMPTHLDDYHGSFEDYVAAKWNINQMSSSDFLVLFNQGISKEKAKTTKATIVPF  
STTEKVDGAYVQDKQLFYKGENIMLVDDIGVPGSHNVENALATIAVAKLAGISNQVIRET  
LSNFGGVKHLRQSLGKVHGISFYNDKSTNIIATQKALSGFDNTKVIL IAGGLDRGNEFD  
ELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGDVILLSP  
ANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6712

STRAIN A909 frame: 3

ITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLEEGI KVVCGS  
HPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQIIGITGSNGK  
TTTTTMAIEVLNAGGQRLLAGNIGFPASEVVQAANDKDTLVMELSSFQLMGVKEFRPHI  
AVITNLMPTHLDDYHGSFEDYVAAKWNINQMSSSDFLVLFNQGISKEKAKTTKATIVPF  
STTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVXNALATIAVAKLAGISNQVIRET  
LSNFGGVKHLRQSLGKVHGISFYNDKSTNIIATQKALSGFDNTKVIL IAGGLDRGNEFD

Table 67: Comparative Sequences relating to SAG0475

ELIPDITGLKHMVVLGESASRVKRAAQKAGVTYS DALDVRDAVHKAYEVAQQGDVILLSP  
ANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6713

STRAIN H36B frame: 1

GRVMKTIITTFENKKVLVLGLARSGEAAARLLAKLGAI VTNVNDGKPF DENPTAQSLLEEGI  
KVVC GSHPLELLDEDFCYMIKNPGI PYNPNMVKKALEKQI PVLTEVELAYLVSESQ LIGI  
TGSNGKTTTTTMTIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELSS FQLMGVK  
EFRPHIAVITNLMPTHLDDYHGSFEDYVAAKWNIONQMSSSDFLVLFNFNQGISKE LAKTTK  
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATI AVAKLAGISN  
QVIRETLSNFGGVKHLRQLSLGKVHGISFYND SKSTNIIATQKALSGFDNTKVIL IAGGLD  
RGNEFDELI PDITGLKHMVVLGESASRVKRAAQKAGVTYS DALDVRDAVHKAYEVAQQGD

SEQ ID NO. 6714

STRAIN 18RS21 frame: 1

GRVMKTIITTFENKKVLVLGLARSGEAAARLLAKLGAI VTNVNDGKPF DENPTAQSLLEEGI  
KVVC GSHPLELLDEDFCYMIKNPGI PYNPNMVKKALEKQI PVLTEVELAYLVSESQ LIGI  
TGSNGKTTTTTMTIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELSS FQLMGVK  
EFRPHIAVITNLMPTHLDDYHGSFEDYVAAKWNIONQMSSSDFLVLFNFNQGISKE LAKTTK  
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATI AVAKLAGISN  
QVIRETLSNFGGVKHLRQLSLGKVHGISFYND SKSTNIIATQKALSGFDNTKVIL IAGGLD  
RGNEFDELI PDITGLKHMVVLGESASRVKRAAQKAGVTYS DALDVRDAVHKAYEVAQQGD  
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6715

STRAIN M732 frame: 1

GRVMKTIITTFENKKVLVLGLARSGEAAARLLAKLGAI VTNVNDGKPF DENPTAQSLLEEGI  
KVVC GSHPLELLDEDFCYMIKNPGI PYNPNMVKKALEKQI PVLTEVELAYLVSESQ LIGI  
TGSNGKTTTTTMTIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELSS FQLMGVK  
EFRPHIAVITNLMPTHLDDYHGSFEDYVAAKWNIONQMSSSDFLVLFNFNQGISKE LAKTTK  
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATI AVAKLAGISN  
QVIRETLSNFGGVKHLRQLSLGKVHGISFYND SKSTNIIATQKALSGFDNTKVIL IAGGLD  
RGNEFDELI PDITGLKHMVVLGESASRVKRAAQKAGVTYS DALDVRDAVHKAYEVAQQGD  
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6716

STRAIN COH1 frame: 1

GRVMKTIITTFENKKVLVLGLARSGEAAARLLAKLGAI VTNVNDGKPF DENPTAQSLLEEGI  
KVVC GSHPLELLDEDFCYMIKNPGI PYNPNMVKKALEKQI PVLTEVELAYLVSESQ LIGI  
TGSNGKTTTTTMTIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELSS FQLMGVK  
EFRPHIAVITNLMPTHLDDYHGSFEDYVAAKWNIONQMSSSDFLVLFNFNQGISKE LAKTTK  
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATI AVAKLAGISN  
QVIRETLSNFGGVKHLRQLSLGKVHGISFYND SKSTNIIATQKALSGFDNTKVIL IAGGLD  
RGNEFDELI PDITGLKHMVVLGESASRVKRAAQKAGVTYS DALDVRDAVHKAYEVAQQGD  
VILLSPANASWDMYKNFEVRGDEFIDTFE

SEQ ID NO. 6717

STRAIN M781 frame: 1

GRVMKTIITTFENKKVLVLGLARSGEAAARLLAKLGAI VTNVNDGKPF DENPTAQSLLEEGI  
KVVC GSHPLELLDEDFCYMIKNPGI PYNPNMVKKALEKQI PVLTEVELAYLVSESQ LIGI  
TGSNGKTTTTTMTIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELSS FQLMGVK  
EFRPHIAVITNLMPTHLDDYHGSFEDYVAAKWNIONQMSSSDFLVLFNFNQGISKE LAKTTK  
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATI AVAKLAGISN  
QVIRETLSNFGGVKHLRQLSLGKVHGISFYND SKSTNIIATQKALSGFDNTKVIL IAGGLD  
RGNEFDELI PDITGLKHMVVLGESASRVKRAAQKAGVTYS DALDVRDAVHKAYEVAQQGD  
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6718

STRAIN CJB110 frame: 1

GRVMKTIITTFENKKVLVLGLARSGEAAARLLAKLGAI VTNVNDGKPF DENPTAQSLLEEGI  
KVVC GSHPLELLDEDFCYMIKNPGI PYNPNMVKKALEKQI PVLTEVELAYLVSESQ LIGI  
TGSNGKTTTTTMTIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELSS FQLMGVK  
EFRPHIAVITNLMPTHLDDYHGSFEYVAAKWNIONQMSSSDFLVLFNFNQGISKE LAKTTK  
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATI AVAKLAGISN  
QVIRETLSNFGGVKHLRQLSLGKVHGISFYND SKSTNIIATQKALSGFDNTKVIL IAGGLD  
RGNEFDELI PDITGLKHMVVLGESASRVKRAAQKAGVTYS DALDVRDAVHKAYEVAQQGD  
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6719

STRAIN 1169NT frame: 3

ITTFENKKVLVLGLARSGEAAARLLAKLGAI VTNVNDGKPF DENPTAQSLLEEGI KVVC GS  
HPLELLDEDFCYMIKNPGI PYNPNMVKKALEKQI PVLTEVELAYLVSESQ LIGITGSNGK  
TTTTTMTIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELSS FQLMGVKEFRPHI  
AVITNLMPTHLDDYHGSFEDYVAAKWNIONQMSSSDFLVLFNFNQGISKE LAKTTKATIVPF  
STTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATI AVAKLAGISNQVIRET  
LSNFGGVKHLRQLSLGKVHGISFYND SKSTNIIATQKALSGFDNTKVIL IAGGLDRGNEF  
ELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSN ALDVRDAVHKAYEVAQQGDVILXSP  
ANASWDMYKNFEVRGDEFIDTF

Table 67: Comparative Sequences relating to SAG0475

SEQ ID NO. 6720

STRAIN JM9130013 frame: 1

GRVMKTIITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEEGI  
 KVVCGSHPLELLEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQILIGI  
 TGSNGKTTTTTMAIEVLNAGGQRLLAGNIGFPASEVVQAANDKDTLVMELSSFQLMGVK  
 EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNINQMSSSDFLVLNFNQGISKELAKTTK  
 ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN  
 QVIRETLSNFGGVKHLQSLGKVHGISFYNDKSTNIIATQKALSGFDNTKVILAGGLD  
 RSNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGD  
 VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6721

STRAIN 2603 frame: 1

GRVMKTIITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEEGI  
 KVVCGSHPLELLEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQILIGI  
 TGSNGKTTTTTMAIEVLNAGGQRLLAGNIGFPASEVVQAANDKDTLVMELSSFQLMGVK  
 EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNINQMSSSDFLVLNFNQGISKELAKTTK  
 ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN  
 QVIRETLSNFGGVKHLQSLGKVHGISFYNDKSTNIIATQKALSGFDNTKVILAGGLD  
 RGNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGD  
 VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

## MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa25243.2{\*} April 29, 2002 02:20 ..

	1		50
msa25243.2{305_18RS21}	grvmktITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIVTV NDGKPFDENP
msa25243.2{305_2603}	grvmktITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIVTV NDGKPFDENP
msa25243.2{305_JM9130013}	grvmktITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIVTV NDGKPFDENP
msa25243.2{305_COH1}	grvmktITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIVTV NDGKPFDENP
msa25243.2{305_M732}	grvmktITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIVTV NDGKPFDENP
msa25243.2{305_M781}	grvmktITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIVTV NDGKPFDENP
msa25243.2{305_1169NT}	-----ITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIVTV NDGKPFDENP
msa25243.2{305_A909}	-----ITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIVTV NDGKPFDENP
msa25243.2{305_CJB110}	grvmktITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIVTV NDGKPFDENP
msa25243.2{305_090}	-----ITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIVTV NDGKPFDENP
msa25243.2{305_H36B}	grvmktITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIVTV NDGKPFDENP
Consensus	-----****	*****	*****
	51		100
msa25243.2{305_18RS21}	TAQSLLEEGI	KVVCGSHPLE	LLDEDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_2603}	TAQSLLEEGI	KVVCGSHPLE	LLDEDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_JM9130013}	TAQSLLEEGI	KVVCGSHPLE	LLDEDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_COH1}	TAQSLLEEGI	KVVCGSHPLE	LLDEDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_M732}	TAQSLLEEGI	KVVCGSHPLE	LLDEDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_M781}	TAQSLLEEGI	KVVCGSHPLE	LLDEDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_1169NT}	TAQSLLEEGI	KVVCGSHPLE	LLDEDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_A909}	TAQSLLEEGI	KVVCGSHPLE	LLDEDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_CJB110}	TAQSLLEEGI	KVVCGSHPLE	LLDEDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_090}	TAQSLLEEGI	KVVCGSHPLE	LLDEDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_H36B}	TAQSLLEEGI	KVVCGSHPLE	LLDEDFCYMI KNPGIPYNNP MVKKALEKQI
Consensus	*****	*****	*****
	101		150
msa25243.2{305_18RS21}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_2603}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_JM9130013}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_COH1}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_M732}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_M781}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_1169NT}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_A909}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_CJB110}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_090}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_H36B}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
Consensus	*****	*****	*****
	151		200
msa25243.2{305_18RS21}	GFPASEVVQA	AnDKDtLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_2603}	GFPASEVVQA	AnDKDtLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_JM9130013}	GFPASEVVQA	AnDKDtLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_COH1}	GFPASEVVQA	AdDKDiLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_M732}	GFPASEVVQA	AdDKDiLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_M781}	GFPASEVVQA	AdDKDiLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_1169NT}	GFPASEVVQA	AdDKDtLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_A909}	GFPASEVVQA	AnDKDtLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_CJB110}	GFPASEVVQA	AdDKDiLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_090}	GFPASEVVQA	AdDKDiLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_H36B}	GFPASEVVQA	AnDKDtLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
Consensus	*****	*-***-*****	*****



Table 67: Comparative Sequences relating to SAG0475

	201		250
msa25243.2{305_18RS21}	GSFEdYVAAK WNIQNMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE		
msa25243.2{305_2603}	GSFEdYVAAK WNIQNMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE		
msa25243.2{305_JM9130013}	GSFEdYVAAK WNIQNMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE		
msa25243.2{305_COH1}	GSFEdYVAAK WNIQNMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE		
msa25243.2{305_M732}	GSFEdYVAAK WNIQNMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE		
msa25243.2{305_M781}	GSFEdYVAAK WNIQNMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE		
msa25243.2{305_1169NT}	GSFEdYVAAK WNIQNMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE		
msa25243.2{305_A909}	GSFEdYVAAK WNIQNMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE		
msa25243.2{305_CJB110}	GSFEdYVAAK WNIQNMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE		
msa25243.2{305_090}	GSFEdYVAAK WNIQNMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE		
msa25243.2{305_H36B}	GSFEdYVAAK WNIQNMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE		
Consensus	****-*****	*****	*****
	251		300
msa25243.2{305_18RS21}	KVDGAYVQDK QLIFYKGENIM sVDDIGVPGS HNveNALATI AVAKLAGISN		
msa25243.2{305_2603}	KVDGAYVQDK QLIFYKGENIM sVDDIGVPGS HNveNALATI AVAKLAGISN		
msa25243.2{305_JM9130013}	KVDGAYVQDK QLIFYKGENIM sVDDIGVPGS HNveNALATI AVAKLAGISN		
msa25243.2{305_COH1}	KVDGAYVQDK QLIFYKGENIM sVDDIGVPGS HNveNALATI AVAKLAGISN		
msa25243.2{305_M732}	KVDGAYVQDK QLIFYKGENIM sVDDIGVPGS HNveNALATI AVAKLAGISN		
msa25243.2{305_M781}	KVDGAYVQDK QLIFYKGENIM sVDDIGVPGS HNveNALATI AVAKLAGISN		
msa25243.2{305_1169NT}	KVDGAYVQDK QLIFYKGENIM sVDDIGVPGS HNveNALATI AVAKLAGISN		
msa25243.2{305_A909}	KVDGAYVQDK QLIFYKGENIM sVDDIGVPGS HNveNALATI AVAKLAGISN		
msa25243.2{305_CJB110}	KVDGAYVQDK QLIFYKGENIM sVDDIGVPGS HNveNALATI AVAKLAGISN		
msa25243.2{305_090}	KVDGAYVQDK QLIFYKGENIM sVDDIGVPGS HNveNALATI AVAKLAGISN		
msa25243.2{305_H36B}	KVDGAYVQDK QLIFYKGENIM sVDDIGVPGS HNveNALATI AVAKLAGISN		
Consensus	*****	*****	*****
	301		350
msa25243.2{305_18RS21}	QVIRETLSNF GGVKHLRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt		
msa25243.2{305_2603}	QVIRETLSNF GGVKHLRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt		
msa25243.2{305_JM9130013}	QVIRETLSNF GGVKHLRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt		
msa25243.2{305_COH1}	QVIRETLSNF GGVKHLRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt		
msa25243.2{305_M732}	QVIRETLSNF GGVKHLRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt		
msa25243.2{305_M781}	QVIRETLSNF GGVKHLRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt		
msa25243.2{305_1169NT}	QVIRETLSNF GGVKHLRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt		
msa25243.2{305_A909}	QVIRETLSNF GGVKHLRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt		
msa25243.2{305_CJB110}	QVIRETLSNF GGVKHLRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt		
msa25243.2{305_090}	QVIRETLSNF GGVKHLRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt		
msa25243.2{305_H36B}	QVIRETLSNF GGVKHLRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt		
Consensus	*****	*****	*****
	351		400
msa25243.2{305_18RS21}	kviliaggld rgnefdelip ditglkhmvv lgesasrvkr aakgagvtys		
msa25243.2{305_2603}	kviliaggld rgnefdelip ditglkhmvv lgesasrvkr aakgagvtys		
msa25243.2{305_JM9130013}	kviliaggld rgnefdelip ditglkhmvv lgesasrvkr aakgagvtys		
msa25243.2{305_COH1}	kviliaggld rgnefdelip ditglkhmvv lgesasrvkr aakgagvtys		
msa25243.2{305_M732}	kviliaggld rgnefdelip ditglkhmvv lgesasrvkr aakgagvtys		
msa25243.2{305_M781}	kviliaggld rgnefdelip ditglkhmvv lgesasrvkr aakgagvtys		
msa25243.2{305_1169NT}	kviliaggld rgnefdelip ditglkhmvv lgesasrvkr aakgagvtys		
msa25243.2{305_A909}	kviliaggld rgnefdelip ditglkhmvv lgesasrvkr aakgagvtys		
msa25243.2{305_CJB110}	kviliaggld rgnefdelip ditglkhmvv lgesasrvkr aakgagvtys		
msa25243.2{305_090}	kviliaggld rgnefdelip ditglkhmvv lgesasrvkr aakgagvtys		
msa25243.2{305_H36B}	kviliaggld rgnefdelip ditglkhmvv lgesasrvkr aakgagvtys		
Consensus	-----	-----	-----
	401		450
msa25243.2{305_18RS21}	daldvrdavh kayevagggd villspanas wdmyknfevr gdefidtfes		
msa25243.2{305_2603}	daldvrdavh kayevagggd villspanas wdmyknfevr gdefidtfes		
msa25243.2{305_JM9130013}	daldvrdavh kayevagggd villspanas wdmyknfevr gdefidtfes		
msa25243.2{305_COH1}	daldvrdavh kayevagggd villspanas wdmyknfevr gdefidtfes		
msa25243.2{305_M732}	daldvrdavh kayevagggd villspanas wdmyknfevr gdefidtfes		
msa25243.2{305_M781}	daldvrdavh kayevagggd villspanas wdmyknfevr gdefidtfes		
msa25243.2{305_1169NT}	daldvrdavh kayevagggd villspanas wdmyknfevr gdefidtfes		
msa25243.2{305_A909}	daldvrdavh kayevagggd villspanas wdmyknfevr gdefidtfes		
msa25243.2{305_CJB110}	daldvrdavh kayevagggd villspanas wdmyknfevr gdefidtfes		
msa25243.2{305_090}	daldvrdavh kayevagggd villspanas wdmyknfevr gdefidtfes		
msa25243.2{305_H36B}	daldvrdavh kayevagggd villspanas wdmyknfevr gdefidtfes		
Consensus	-----	-----	-----
	451		
msa25243.2{305_18RS21}	lrge		
msa25243.2{305_2603}	lrge		
msa25243.2{305_JM9130013}	lrge		
msa25243.2{305_COH1}	-----		
msa25243.2{305_M732}	lrge		
msa25243.2{305_M781}	lrge		
msa25243.2{305_1169NT}	-----		
msa25243.2{305_A909}	lrge		
msa25243.2{305_CJB110}	lrge		
msa25243.2{305_090}	lrge		
msa25243.2{305_H36B}	-----		
Consensus	----		

Table 68: Comparative Sequences relating to SAG 0499

## SEQ ID NO. 6801

## STRAIN 2603

ATGGCTAAAGAGAGGGTAGATGTTCTTGCCTATAAACAGGGACTTTTGTATACACGAGAG  
CAAGCGAAACGTTGGTGTATGGCAGGAATGGTGTATTAACGTTATCAATGGAGAACGTTAT  
GATAAACCGAGGTGAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAACTA  
AAATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTGAAATTTCA  
GTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGTGGTTTTACTGATGTTATG  
CTACAATCAGGAGCGCGTTTAGTTTACGCAGTAGATGTAGGAACAAATCAATTAGTTTGG  
AAGTTACGTGAGGATCATCGTGTTCGTTCTATGGAACAATATAATTTTAGGTATGCCCAA  
AAAGAAGATTTCAAGGAGGACTGCCTGAATTTGCATCGATAGATGTCTCATTATCTCT  
CTTAATTTGATTTTACCAGCTCTAAAAGAAATTTAGTGGATGGTGGACAAGTAGTGGCA  
TTAATTAACCAATTTGAAAGCAGGTGCTGAGCAAATTTGGTAAAATGTTATGTCAAA  
GACAAGTTGGTTTCATGAAAAGGTTTGGACAACAGTGACCAATTTACGAAAGATTATGGA  
TATACGGTTAAACATCTTGATTTTTCGCCCATTCAGGTGGACATGGAAATATTGAGTTT  
TTAATGCATTTGCAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAATACAGAT  
GTTATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

## SEQ ID NO. 6802

## STRAIN 090

GCTAAAGAGAGGGTAGATGTTCTTGCCT  
ATAAACAGGGACTTTTGTATACACGAGAGCAAGCGAAACGTTGGTGTATG  
GCAGGAATGGTGATTAACTTATCAATGGAGAACGTTATGATAAACAGG  
TGAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAACTAA  
AATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTT  
GAAATTTGAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGG  
TGGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAG  
TAGATGTAGGAACAAATCAATTAGTTTGGAGTTACGTCAGGATCATCGT  
GTTGCTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAGAGATT  
CAAGGAGGAGCTGCCTGAATTTGTCATCGATAGATGTCTCATTATCTCTC  
TTAATTTGATTTTACCAGCTCTAAAAGAAATTTAGTGGATGGTGGACAA  
GTAGTGGCATTAAATTAACCAATTTGAAGCAGGTGCTGAGCAAATTTGG  
TAAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTTGACAA  
CAGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGAT  
TTTTCGCCCATTCAGGTGGACATGGAATATTGAGTTTTTAATGCATTT  
GCAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAATACAGATG  
TTATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

## SEQ ID NO. 6803

## STRAIN A909

GCTAAAGAGAGGGTAGATGTTCTTGCCTA  
TAAACAGGGACTTTTGTATACACGAGAGCAAGCGAAACGTTGGTGTATGG  
CAGGAATGGTGATTAACTTATCAATGGAGAACGTTATGATAAACAGGT  
GAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAACTAAA  
ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTG  
AAATTTCAAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGG  
GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT  
AGATGTAGGAACAAATCAATTAGTTTGGAGTTACGTCAGGATCATCGTG  
TTGCTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAGAGATTTC  
AAGGAGGAGCTGCCTGAATTTGTCATCGATAGATGTCTCATTATCTCTCT  
TAATTTGATTTTACCAGCTCTAAAAGAAATTTAGTGGATGGTGGACAAG  
TAGTGGCATTAAATTAACCAATTTGAAGCAGGTGCTGAGCAAATTTGGT  
AAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTTGACAA  
AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGAT  
TTTTCGCCCATTCAGGTGGACATGGAATATTGAGTTTTTAATGCATTTG  
CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAATACAGATGT  
TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

## SEQ ID NO. 6804

## STRAIN H36B

GCTAAAGAGAGGGTAGATGTTCTTGCCTATAAACAGG  
GACTTTTGTATACACGAGAGCAAGCGAAACGTTGGTGTATGGCAGGAATG  
GTGATTAACTTATCAATGGAGAACGTTATGATAAACAGGTGAAAAGGT  
TGCAAGACGATACTGAATTAAAACTAAAAGGTGAAAACTAAAATATGTTA  
GTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTGAAATTTCA  
GTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGTGGTTTTAC  
TGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGTAGATGTAG  
GAACAAATCAATTAGTTTGGAGTTACGTCAGGATCATCGTGTTCGTTCT  
ATGGAACAATATAATTTTAGGTATGCCCAAAAGAGATTTCAGGAGGG  
ACTGCCTGAATTTGCATCGATAGATGTCTCATTATCTCTCTTAATTTGA  
TTTACCAGCTCTAAAAGAAATTTAGTGGATGGTGGACAAGTAGTGGCA  
TTAATTAACCAATTTGAAGCAGGTGCTGAGCAAATTTGGTAAAAATGG  
TATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTTGACAACAGTGACCA  
ATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATTTTTCGCCC  
ATTCAGGTGGACATGGAATATTGAGTTTTTAATGCATTTGCAAAAGTG  
TCAGATCCACAAAATCTTGTGCTTGACCAATACAGATGTTATAGAAA  
AAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

## SEQ ID NO. 6805

## STRAIN 18RS21

GCTAAAGAGAGGGTAGATGTTCTTGCCTA  
TAAACAGGGACTTTTGTATACACGAGAGCAAGCGAAACGTTGGTGTATGG  
CAGGAATGGTGATTAACTTATCAATGGAGAACGTTATGATAAACAGGT

Table 68: Comparative Sequences relating to SAG 0499

GAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAACTAAA  
 ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTGTG  
 AAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT  
 GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT  
 AGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGT CAGGATCATCGTG  
 TTCGTTCTATGGAACAAATATAATTTAGGTATGCCCAAAAGAAGATTTC  
 AAGGAGGACTGCCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTCT  
 TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG  
 TAGTGGCATTAAATTAACCACAATTTGAAGCAGGTCGTGAGCAAATGGT  
 AAAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTGGACAAC  
 AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATT  
 TTTCCGCCATTCAAGGTGGACATGGAAATATTGAGTTTAAATGCATTTG  
 CAAAAGTGTCAAGATCCACAAATCTTGTGCTTGACCAAAATACAAGATGT  
 TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

## SEQ ID NO. 6806

## STRAIN M732

GCTAAAGAGAGGGTAGATGTTCTTGCCTA

TAAACAGGGACTTTTGTATACAGAGAGCAAGCGAAACGTGGTGTATGG  
 CAGGACTGGTGATTAACTGTTATCAATGGAGAACGTTATGATAAACAGGC  
 GAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAACTAAA  
 ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTGTG  
 AAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT  
 GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT  
 AGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGT CAGGATCATCGTG  
 TTCGTTCTATGGAACAAATATAATTTAGGTATGCCCAAAAGAAGATTTC  
 AAGGAGGACTGCCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTCT  
 TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG  
 TAGTGGCATTAAATTAACCAACAATTTGAAGCAGGTCGTGAGCAAATGGT  
 AAAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTGGACAAC  
 AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATT  
 TTTCCGCCGTTCAAGGTGGACATGGAAATATTGAGTTTAAATGCATTTG  
 CAAAAGTGTCAAGATCCACAAATCTTGTGCTTGACCAAAATACAAGATGT  
 TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

## SEQ ID NO. 6807

## STRAIN COH1

GCTAAAGAGAGGGTAGATGTTCTTGCCT

ATAAACAGGGACTTTTGTATACAGAGAGCAAGCGAAACGTGGTGTATG  
 GCAGGACTGGTGATTAACTGTTATCAATGGAGAACGTTATGATAAACAGG  
 CGAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAACTAA  
 AATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTGT  
 GAAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGG  
 TGGTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAG  
 TAGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGT CAGGATCATCGT  
 GTTCGTTCTATGGAACAAATATAATTTAGGTATGCCCAAAAGAAGATTTC  
 CAAGGAGGACTGCCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTC  
 TTAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAA  
 GTAGTGGCATTAAATTAACCAACAATTTGAAGCAGGTCGTGAGCAAATGG  
 TAAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTGGACAA  
 CAGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGAT  
 TTTTCGCCCGTTCAAGGTGGACATGGAAATATTGAGTTTAAATGCATTT  
 GCAAAAGTGTCAAGATCCACAAATCTTGTGCTTGACCAAAATACAAGATG  
 TTATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

## SEQ ID NO. 6808

## STRAIN M781

GCTAAAGAGAGGGTAGATGTTCTTGCCT

ATAAACAGGGACTTTTGTATACAGAGAGCAAGCGAAACGTGGTGTATG  
 GCAGGACTGGTGATTAACTGTTATCAATGGAGAACGTTATGATAAACAGG  
 CGAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAACTAA  
 AATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTGT  
 GAAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGG  
 TGGTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAG  
 TAGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGT CAGGATCATCGT  
 GTTCGTTCTATGGAACAAATATAATTTAGGTATGCCCAAAAGAAGATTTC  
 CAAGGAGGACTGCCCTGAATTTGCATCGATAGATGTCTCATTTATCTCTC  
 TTAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAA  
 GTAGTGGCATTAAATTAACCAACAATTTGAAGCAGGTCGTGAGCAAATGG  
 TAAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTGGACAA  
 CAGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGAT  
 TTTTCGCCCGTTCAAGGTGGACATGGAAATATTGAGTTTAAATGCATTT  
 GCAAAAGTGTCAAGATCCACAAATCTTGTGCTTGACCAAAATACAAGATG  
 TTATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

## SEQ ID NO. 6809

## STRAIN CJB110

GCTAAAGAGAGGGTAGATGTTCTTGCCTA

TAAACAGGGACTTTTGTATACAGAGAGCAAGCGAAACGTGGTGTATGG  
 CAGGAATGGTGATTAACTGTTATCAATGGAGAACGTTATGATAAACAGGT  
 GAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAACTAAA  
 ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTGTG  
 AAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT

Table 68: Comparative Sequences relating to SAG 0499

GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTAGTTTACGCAGT  
 AGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGTCAGGATCATCGTG  
 TTCGTTCTATGGAACAATATAATTTTAGGTATGCCAAAAAGAGATTTC  
 AAGGAGGGAGCTGCCTGAATTTGCATCGATAGATGTCATTATCTCTCT  
 TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG  
 TAGTGGCATTAAATTAACCACAATTTGAAGCAGGTCGTGAGCAAATTTGGT  
 AAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTTGACAAC  
 AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATT  
 TTTCCGCCATTCAAGGTGGACATGGAAATATTGAGTTTTAATGCATTTG  
 CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT  
 TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6810

STRAIN 1169NT

GCTAAAGAGAGGGTAGATGTTCTTGCCTA

TAAACAGGGACTTTTGTATACAGAGAGCAAGCAACGTTGGTGTATGG  
 CAGGACTGGTGATTACGTTATCAATGGAGAACGTTATGATAAACAGGC  
 GAAAAGGTTGCAGACGATCTGAATTAACCTAAAAGGTGAAAACTAAA  
 ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTG  
 AAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCTCTACGGGT  
 GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTAGTTTACGCAGT  
 AGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGTCAGGATCATCGTG  
 TTCGTTCTATGGAACAATATAATTTTAGGTATGCCAAAAAGAGATTTC  
 AAGGAGGGAGCTGCCTGAATTTGCATCGATAGATGTCATTATCTCTCT  
 TAATTTGATTTTCCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG  
 TAGTGGCATTAAATTAACCACAATTTGAAGCAGGTCGTGAGCAAATTTGGT  
 AAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTTGACAAC  
 AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATT  
 TTTCCGCCATTCAAGGTGGACATGGAAATATTGAGTTTTAATGCATTTG  
 CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT  
 TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6811

STRAIN JM9130013

GCTAAAGAGAGGGTAGATGTTCTTGCCTA

TAAACAGGGACTTTTGTATACAGAGAGCAAGCAACGTTGGTGTATGG  
 CAGGAATGGTGATTAAACGTTATCAATGGAGAACGTTATGATAAACAGGT  
 GAAAAGGTTGCAGACGATCTGAATTAACCTAAAAGGTGAAAACTAAA  
 ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTG  
 AAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCTCTACGGGT  
 GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTAGTTTACGCAGT  
 AGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGTCAGGATCATCGTG  
 TTCGTTCTATGGAACAATATAATTTTAGGTATGCCAAAAAGAGATTTC  
 AAGGAGGGAGCTGCCTGAATTTGCATCGATAGATGTCATTATCTCTCT  
 TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG  
 TAGTGGCATTAAATTAACCACAATTTGAAGCAGGTCGTGAGCAAATTTGGT  
 AAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTTGACAAC  
 AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATT  
 TTTCCGCCATTCAAGGTGGACATGGAAATATTGAGTTTTAATGCATTTG  
 CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT  
 TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

PRETTY of: /biotmp/msa236683.2{\*} May 14, 2003 02:57 ..

	1		50
msa236683.2{310_090}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_18R521}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_2603}	atgGCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_A909}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_CJB110}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_H36B}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_JM9130013}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_COH1}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_M732}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_M781}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_1169NT}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
Consensus	*****	*****	*****
	51		100
msa236683.2{310_090}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_18R521}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_2603}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_A909}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_CJB110}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_H36B}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_JM9130013}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_COH1}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_M732}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_M781}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_1169NT}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
Consensus	*****	*****	*****

Table 68: Comparative Sequences relating to SAG 0499

		101			150
msa236683.2{310_090}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GtGAAAAGGT	TGCAGACGAT
msa236683.2{310_18RS21}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GtGAAAAGGT	TGCAGACGAT
msa236683.2{310_2603}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GtGAAAAGGT	TGCAGACGAT
msa236683.2{310_A909}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GtGAAAAGGT	TGCAGACGAT
msa236683.2{310_CJB110}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GtGAAAAGGT	TGCAGACGAT
msa236683.2{310_H36B}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GtGAAAAGGT	TGCAGACGAT
msa236683.2{310_JM9130013}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GtGAAAAGGT	TGCAGACGAT
msa236683.2{310_COH1}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GcGAAAAGGT	TGCAGACGAT
msa236683.2{310_M732}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GcGAAAAGGT	TGCAGACGAT
msa236683.2{310_M781}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GcGAAAAGGT	TGCAGACGAT
msa236683.2{310_1169NT}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GcGAAAAGGT	TGCAGACGAT
Consensus		*****	*****	*****	*****
		151			200
msa236683.2{310_090}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTGA	GTAGAGGTGG
msa236683.2{310_18RS21}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTGA	GTAGAGGTGG
msa236683.2{310_2603}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTGA	GTAGAGGTGG
msa236683.2{310_A909}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTGA	GTAGAGGTGG
msa236683.2{310_CJB110}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTGA	GTAGAGGTGG
msa236683.2{310_H36B}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTGA	GTAGAGGTGG
msa236683.2{310_JM9130013}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTGA	GTAGAGGTGG
msa236683.2{310_COH1}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTGA	GTAGAGGTGG
msa236683.2{310_M732}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTGA	GTAGAGGTGG
msa236683.2{310_M781}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTGA	GTAGAGGTGG
msa236683.2{310_1169NT}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTGA	GTAGAGGTGG
Consensus		*****	*****	*****	*****
		201			250
msa236683.2{310_090}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_18RS21}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_2603}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_A909}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_CJB110}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_H36B}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_JM9130013}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_COH1}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_M732}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_M781}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_1169NT}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
Consensus		*****	*****	*****	*****
		251			300
msa236683.2{310_090}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_18RS21}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_2603}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_A909}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_CJB110}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_H36B}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_JM9130013}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_COH1}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_M732}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_M781}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_1169NT}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
Consensus		*****	*****	*****	*****
		301			350
msa236683.2{310_090}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_18RS21}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_2603}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_A909}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_CJB110}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_H36B}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_JM9130013}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_COH1}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_M732}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_M781}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_1169NT}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
Consensus		*****	*****	*****	*****
		351			400
msa236683.2{310_090}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_18RS21}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_2603}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_A909}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_CJB110}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_H36B}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_JM9130013}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_COH1}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_M732}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_M781}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_1169NT}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
Consensus		*****	*****	*****	*****

Table 68: Comparative Sequences relating to SAG 0499

		401			450
msa236683.2{310_090}	ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_18RS21}	ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_2603}	ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_A909}	ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_CJB110}	ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_H36B}	ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_JM9130013}	ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_COH1}	ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_M732}	ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_M781}	ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_1169NT}	ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
Consensus	*****	*****	*****	*****	*****
		451			500
msa236683.2{310_090}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_18RS21}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_2603}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_A909}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_CJB110}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_H36B}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_JM9130013}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_COH1}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_M732}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_M781}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_1169NT}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
Consensus	*****	*****	*****	*****	*****
		501			550
msa236683.2{310_090}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_18RS21}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_2603}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_A909}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_CJB110}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_H36B}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_JM9130013}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_COH1}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_M732}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_M781}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_1169NT}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
Consensus	*****	*****	*****	*****	*****
		551			600
msa236683.2{310_090}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATG	TATTGTCAAA
msa236683.2{310_18RS21}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATG	TATTGTCAAA
msa236683.2{310_2603}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATG	TATTGTCAAA
msa236683.2{310_A909}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATG	TATTGTCAAA
msa236683.2{310_CJB110}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATG	TATTGTCAAA
msa236683.2{310_H36B}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATG	TATTGTCAAA
msa236683.2{310_JM9130013}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATG	TATTGTCAAA
msa236683.2{310_COH1}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATG	TATTGTCAAA
msa236683.2{310_M732}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATG	TATTGTCAAA
msa236683.2{310_M781}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATG	TATTGTCAAA
msa236683.2{310_1169NT}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATG	TATTGTCAAA
Consensus	*****	*****	*****	*****	*****
		601			650
msa236683.2{310_090}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTCAACGAA
msa236683.2{310_18RS21}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTCAACGAA
msa236683.2{310_2603}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTCAACGAA
msa236683.2{310_A909}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTCAACGAA
msa236683.2{310_CJB110}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTCAACGAA
msa236683.2{310_H36B}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTCAACGAA
msa236683.2{310_JM9130013}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTCAACGAA
msa236683.2{310_COH1}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTCAACGAA
msa236683.2{310_M732}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTCAACGAA
msa236683.2{310_M781}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTCAACGAA
msa236683.2{310_1169NT}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTCAACGAA
Consensus	*****	*****	*****	*****	*****
		651			700
msa236683.2{310_090}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_18RS21}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_2603}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_A909}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_CJB110}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_H36B}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_JM9130013}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_COH1}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_M732}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_M781}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_1169NT}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG

Table 68: Comparative Sequences relating to SAG 0499

Consensus	*****	*****	*****	*****	*****	*****
	701					750
msa236683.2{310_090}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_18RS21}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_2603}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_A909}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_CJB110}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_H36B}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_JM9130013}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_COH1}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_M732}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_M781}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_1169NT}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
Consensus	*****	*****	*****	*****	*****	*****
	751					800
msa236683.2{310_090}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_18RS21}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_2603}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_A909}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_CJB110}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_H36B}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_JM9130013}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_COH1}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_M732}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_M781}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_1169NT}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
Consensus	*****	*****	*****	*****	*****	*****
	801					825
msa236683.2{310_090}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_18RS21}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_2603}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_A909}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_CJB110}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_H36B}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_JM9130013}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_COH1}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_M732}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_M781}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_1169NT}	GGAATTTAAG	AAAAATGAAG	AAGAG			
Consensus	*****	*****	*****			
<b>SEQ ID NO. 6812</b>						
<b>STRAIN 2603 frame: 1</b>						
MAKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTTELKLKGEKLLK						
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK						
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL						
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL						
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEB						
<b>SEQ ID NO. 6813</b>						
<b>STRAIN 090 frame: 1</b>						
AKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTTELKLKGEKLLK						
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK						
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL						
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL						
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEB						
<b>SEQ ID NO. 6814</b>						
<b>STRAIN A909 frame: 1</b>						
AKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTTELKLKGEKLLK						
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK						
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL						
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL						
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEB						
<b>SEQ ID NO. 6815</b>						
<b>STRAIN 18RS21 frame: 1</b>						
AKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTTELKLKGEKLLK						
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK						
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL						
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL						
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEB						
<b>SEQ ID NO. 6816</b>						
<b>STRAIN M732 frame: 1</b>						
AKERVDVLAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTTELKLKGEKLLK						
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK						
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL						

Table 68: Comparative Sequences relating to SAG 0499

IKPQFEAGREIQKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL  
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6817

STRAIN COH1 frame: 1

AKERVDVLAAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLG  
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTVNQLVWK  
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL  
IKPQFEAGREIQKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL  
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6818

STRAIN M781 frame: 1

AKERVDVLAAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLG  
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTVNQLVWK  
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL  
IKPQFEAGREIQKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL  
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6819

STRAIN CJB110 frame: 1

AKERVDVLAAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLG  
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTVNQLVWK  
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL  
IKPQFEAGREIQKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL  
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6820

STRAIN 1169NT frame: 1

AKERVDVLAAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLG  
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTVNQLVWK  
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL  
IKPQFEAGREIQKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL  
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6821

STRAIN JM9130013 frame: 1

AKERVDVLAAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLG  
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTVNQLVWK  
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL  
IKPQFEAGREIQKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL  
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6822

STRAIN H36B frame: 1

AKERVDVLAAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLG  
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTVNQLVWK  
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL  
IKPQFEAGREIQKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL  
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

PRETTY of: /biotmp/msa236800.2{\*} May 14, 2003 02:58 ..

	1		50
msa236800.2{310_090}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGm VINVINGERY DKPGEKVADD
msa236800.2{310_18R21}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGm VINVINGERY DKPGEKVADD
msa236800.2{310_2603}	mAKERVDVLA	YKQGLFDTRE	QAKRGVMAGm VINVINGERY DKPGEKVADD
msa236800.2{310_A909}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGm VINVINGERY DKPGEKVADD
msa236800.2{310_CJB110}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGm VINVINGERY DKPGEKVADD
msa236800.2{310_H36B}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGm VINVINGERY DKPGEKVADD
msa236800.2{310_JM9130013}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGm VINVINGERY DKPGEKVADD
msa236800.2{310_COH1}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGl VINVINGERY DKPGEKVADD
msa236800.2{310_M732}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGl VINVINGERY DKPGEKVADD
msa236800.2{310_M781}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGl VINVINGERY DKPGEKVADD
msa236800.2{310_1169NT}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGl VINVINGERY DKPGEKVADD
Consensus	*****	*****	*****

  

	51		100
msa236800.2{310_090}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_18R21}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_2603}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_A909}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_CJB110}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_H36B}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_JM9130013}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_COH1}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_M732}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_M781}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_1169NT}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
Consensus	*****	*****	*****

101

150



Table 68: Comparative Sequences relating to SAG 0499

msa236800.2{310_090}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_18RS21}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_2603}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_A909}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_CJB110}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_H36B}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_JM9130013}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_COH1}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_M732}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_M781}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_1169NT}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
Consensus	*****	*****	*****	*****	*****
151					
msa236800.2{310_090}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_18RS21}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_2603}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_A909}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_CJB110}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_H36B}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_JM9130013}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_COH1}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_M732}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_M781}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_1169NT}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
Consensus	*****	*****	*****	*****	*****
201					
msa236800.2{310_090}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_18RS21}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_2603}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_A909}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_CJB110}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_H36B}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_JM9130013}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_COH1}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	vQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_M732}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	vQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_M781}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	vQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_1169NT}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
Consensus	*****	*****	*****	*****	*****
251					
msa236800.2{310_090}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_18RS21}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_2603}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_A909}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_CJB110}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_H36B}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_JM9130013}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_COH1}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_M732}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_M781}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_1169NT}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
Consensus	*****	*****	*****		
275					

Table 69: Comparative Sequences relating to SAG0032

SEQ ID NO. 6901

STRAIN 2603

ATGAATAAAAAGGTACTATTGACATCGACAATGGCAGCTTCGCTATTATCAGTCGCAAGT  
 GTTCAAGCACAAAGAACAGATACGACGTGGACAGCAGTACTGTTTCAGAGGTAAGGCT  
 GATTGGTAAAGCAAGACAAATAAATCATCATATACTGTGAAATATGGTGATACACTAAGC  
 GTTATTTTCAGAAGCAATGTCAATTGATATGAATGTCTTAGCAAAAATAAATAACATTGCA  
 GATATCAATCTTATTATCTCTGAGACAACACTGACAGTAACCTACGATCAGAAGAGTCAT  
 ACTGCCACTTCAATGAAAATAGAAACACCAGCAACAAATGCTGCTGGTCAAACACAGCT  
 ACTGTGGATTTGAAAACCAATCAAGTTTCTGTTCAGACCAAAAAGTTTCTCTCAATACA  
 ATTTTCGAAGGTATGACACCAGAAGCAGCAACACGATTGTTTCGCCAATGAAGACATAT  
 TCTTCTGCGCCAGCTTTGAAATCAAAGAAGTATTAGCACAAGAGCAAGCTGTTAGTCAA  
 GCAGCAGCTAATGAACAGGTATCACAGCTCCTGTGAAGTCGATTACTTCAGAAAGTTCCA  
 GCAGCTAAGAGGAGGTTAAACCAACTCAGACGTCAGTCAGTCAGTCAACACAGTATCA  
 CCAGCTTCTGTTGCCGTGAAACACCAGCTCCAGTAGCTAAAGTAGCACCAGGTAAAGAACT  
 GTAGCAGCCCCTAGAGTGGCAAGTGTAAAGTAGTCACTCCTAAAGTAGAAACTGGTGCA  
 TCACCAGAGCATGTATCAGCTCCAGCAGTTCTGTGACTACGACTTCACCAGCTACAGAC  
 AGTAAGTTACAAGCGACTGAAGTTAAGAGCGTTCCGGTAGCACAAAAGCTCCAAACAGCA  
 ACACCGGTAGCACAACAGCTTCAACAACAAATGCAGTAGCTGCACATCTGAAAATGCA  
 GGGCTCCAACCTCATGTTGCGAGCTTATAAAGAAAAGTAGCGTCAACTTTATGGAGTTAAT  
 GAATTCAGTACATACCTGCGGGAGATCCAGGTGATCATGGTAAAGGTTTAGCAGTTGAC  
 TTTATTTAGGTACTAATCAAGCACTTGGTAATAAAGTTGCACAGTACTTACACAAAAT  
 ATGCGAGCAAAATACATTTTCAATATGTTATCTGGCAACAAAAGTTTACTCAAATACAAAC  
 AGTATTTATGGAGCTGCTAATACCTTGGAAATGCAATGCCAGATCGTGGTGGCGTTACTGCC  
 AACCCTATGACCAGTTACGATATCATTTAACAATAATATAAAAAAGGAAGCTATTG  
 GCTTCTTTTATATGCTTGAATAGACTTCAAGGTTCTTATATAATTTTATTA

SEQ ID NO. 6902

STRAIN 090

TGAGACAACACTGACAGTAACCTACGATCAGAAGAGTCATACTGCCACTT  
 CAATGAAAATAGAAAACACCAGCAACAAATGCTGCTGGTCAAACACCAGCT  
 ACTGTGGATTTGAAAACCAATCAAGTTTCTGTTCAGACCAAAAAGTTTC  
 TCTCAATACAATTTCCGAAGGTATGACACCAGAAGCAGCAACACAGATTG  
 TTTCCCAATGAAGACATATTCTTCTGCGCCAGCTTTGAAATCAAAGAAG  
 GTATTAGCACAAGAGCAAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGT  
 ATCAACAGCTCCTGTGAAGTCGATTACTTCAGAAGTTCCAGCAGCTAAAG  
 AGGAAGTTAAACCACTCAGACGTCAGTCAGTCAGTCAACACAGTATCA  
 CCAGCTTCTGTTGCCGTGAAACACCAGCTCCAGTAGCTAAAGTAGCACC  
 GGTAAGAAGCTGTAGCAGCCCCTAGAGTGGCAAGTGTAAAGTAGTCACTC  
 CTAAAGTAGAAACTGGTGATCACCAGAGCATGTATCAGCTCCAGCAGTT  
 CCTGTGACTACGACTTCAACAGCTACAGACAGTAAGTTACAAGCGACTGA  
 AGTTAAGAGCGTTCCGGTAGCACAAAAGCTCCAAACAGCAACACCGGTAG  
 CACAACAGCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCA  
 GGGCTCCAACCTCATGTTGCGAGCTTATAAAGAAAAGTAGCGTCAACTTA  
 TGGAGTTAATGAATTCACTACATACCGTGCAGGTGATCCAGGTGATCATG  
 GTAAGGTTTAGCAGTCGACTTTATTGTAGGTAACCAAGCACTTGGT  
 AATGAAGTTGCACAGTACTCTACACAAAATATGGCAGCAAAATACATTTT  
 ATATGTTATCTGGCAACAAAAGTTTACTCAAATACAAATAGTATTATG  
 GACCTGCTAATACTTGAATGCAATGCCAGATCGTGGTGGCGTTACTGCC  
 AACCATTATGACCAGTTTACGATATCATTTAACAATAATATAAAAAAGG  
 AAGCTATTGGCTTCTTTTATATGCTTGAATAGACTTCAAGGTTCT  
 TATATAATTTTATTA

SEQ ID NO. 6903

STRAIN A909

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAA  
 ATATGGTGATACACTAAGCGTTATTTTCAGAAGCAATGTCAATTGATATGA  
 ATGTCTTAGCAAAAATTAATAACATTGCAGATATCAATCTTATTTATCCT  
 GAGACAACACTGACAGTAACCTACGATCAGAAGAGTCATACTGCTACTTC  
 AATGAAAATAGAAAACACCAGCAACAAATGCTGCTGGTCAAACAAAGCTA  
 CTGTGATTTGAAAACCAATCAAGTTTCTGTTCAGACCAAAAAGTTTCT  
 CTCATACAAATTTCCGAAGGTATGACACCAGAAGCAGCAACACGATTTGT  
 TTCGCCAATGAAGACATATTCTTCTGCGCCAGCTTTGAAATCAAAGAAG  
 TATTAGCACAAGGCAAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGTA  
 TCACAGCTCTGTGAAGTCGATTACTTCAGAAGTTCCAGCAGCTAAAGA  
 GGAAGTTAAACCACTCAGACGTCAGTCAGTCAGTCAACACAGTATCAC  
 CAGCTTCTGTTGCCGTGAAACACCAGCTCCAGTAGCTAAAGTAGCACC  
 GTAAGAAGCTGTAGCAGCCCCTAGAGTGGCAAGTGTAAAGTAGTCACTCC  
 TAAAGTAGAACTGGTGATCACCAGAGCATGTATCAGCTCCAGCAGTTT  
 CTGTGACTACGACTTCAACAGCTACAGACAGTAAGTTACAAGCGACTGAA  
 GTTAAGAGCGTTCCGGTAGCACAAAAGCTCCAAACAGCAACACCGGTAGC  
 ACAACAGCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCA  
 GGGCTCCAACCTCATGTTGCGAGCTTATAAAGAAAAGTAGCGTCAACTTA  
 GGAGTTAATGAATTCACTACATACCGTGCAGGTGATCCAGGTGATCATG  
 TAAAGGTTTAGCAGTTGACTTTATTGTAGGTAACCAAGCACTTGGTA  
 ATGAAGTTGCACAGTACTCTACACAAAATATGGCAGCAAAATACATTTT  
 TATGTTATCTGGCAACAAAAGTTTACTCAAATACAAATAGTATTATG  
 ACCTGCTAATACTTGAATGCAATGCCAGATCGTGGTGGCGTTACTGCC  
 ACCAATATGACCAGTTTACGATATCATTTAACAATAATATAAAAAAGG  
 AGCTATTGGCTTCTTTTATATGCTTGAATAGACTTCAAGGTTCTT  
 ATATAATTTTATTA

SEQ ID NO. 6904

STRAIN H36B

Table 69: Comparative Sequences relating to SAG0032

CTGATTGGTAAAGCAAGACAATAAATCATCATATAcTGTGAAATA  
 TGGTGATACAcTAAGCGTTATTTGAGAAGCAATGTCaATTGATATGAATG  
 TCTTAGCAAAAATTAAATACATTGCAGATATCAATCTTATTTATCCTGAG  
 ACAACaCTGaCAGTAaCTTACGATCAGAAGAGTCATACTGCTACTTCAAT  
 GAAAAATAGAAACACCAGCAACAATGCTGCTGGTCAAAACACAGCTACTG  
 TCGATTGGAAAACCAATCAAGTTTCGTTGCGAGACCAAAAAGTTCTCTC  
 AATACAATTTTCGGAAGGTATGACACCAGAAGCAGCAACAACGATTGTTTC  
 GCCAATGAAGACATATTCTTCTGCGCCAGCTTTGAAATCAAAAGAAGTAT  
 TAGCACAAGGGCAAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGTATCA  
 CCAGCTCCTGTGAAGTCGATTACTTCAAGGTTCCAGCAGCTAAAGAGGA  
 AGTTAAACCAACTCAGACCTCAGTCAGTCAGTCAGTCAACAACAGTATCACCAG  
 CTTCTGTGCGCTGAAAACACCAGCTCCAGTAGcTAAAGTAGCACCAGTA  
 AGAATCTGTAGCAGCCCTAGAGTGGCAAGTGTAAAGTAGTCACTCCTAA  
 AGTAGAAACTGGTGATCACCAGAGCATGTATCAGCTCCAGCAGTTCCTG  
 TGACTACGACTTCAACAGCTACAGACAGTAAGTTACAAGCGACTGAAGTT  
 AAGAGCGTTCCGGTAGCACAAGAGCTCCAACAGCAACACCGGTAGCACA  
 ACCAGCTTCAACAACAATGCGAGTAGCTGCACATCCTGAAAAATGCAAGGC  
 TCCAACCTCATGTTGCGAGCTTATAAGAAAAAGTAGCGTCAACTTATGGA  
 GTTAATGAATTCACTACATACCGTGGGAGATCCAGGTGATCATGGTAA  
 AGGTTTAGCAGTTGACTTTATTGTAGGTAAAAACCAAGCACTTGGTAAATG  
 AAGTTGCACAGTACTCTACACAAAATaTGGCAGCAAAATACATTTTATAT  
 GTTATCTGGCAaCAAAAAGTTTACTCAAAATACAAATAGTATTTATGGACC  
 TGCTAATACTTGAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCC  
 ACTATGACCAGCTTCACTATCATTTAACAATAATATAAAAAAGGAAGC  
 TATTGGCTTCTTTTATATGCCTTGCATAGAcTTCAAGGTTCTTATA  
 TAATTTTATTA

SEQ ID NO. 6905

STRAIN 18RS21

CTGATTGGTAAAGCAAGACAAT  
 AAATCATCATATACCTGTGAAATATGGTGATACAcTAAGCGTTATTTGAGA  
 AGCAATGTCAATTGATATGAATGCTCTTAGCAAAAaTAAATAACATTGCAG  
 ATATCAATCTTATTTATCCTGAGACAAcCTGaCAGTAACCTTACGATCAG  
 AAGAGTCATACTGCCaCTTCAATGAAAATAGAAACACCAGCAaCAAAATGC  
 TGCTGGTCaaACAaCAGCTACTGTGGATTGAAAACCAATCAAGTTTCTG  
 TTGCGAGACCAAAAAGTTTCTCTCAATACAATTTTCGGAAGGTATGACACCA  
 GAAGCAGCAACAACGATTGTTTTCGCCAATGAAGAcTATTCTTCTGCGCC  
 AGCTTTGAAaTCAAAAGAAGTATTAGCACAAGAGCAAGCTGTTAGTCAAG  
 CAGCAGCTAATGAACAGGTATCACCAGCTCCTGTGAAGTCGATTACTTCA  
 GAAGTTCCAGCAGCTAAAGAGGAAGTTAAACCAACTCAGACGTCAGTCAG  
 TCAGTCAACAACAGTATCACCAGCTTCTGTTGCGCTGAAAACACCAGCTC  
 CAGTAGCTAAAGTAGCACCGGTAAAGAACTGTAGCAGCCCTAGAGTGGCA  
 AGTGTAAAGTAGTCACTCCTAAAGTAGAAACTGGTGATCACCAGAGCA  
 TGTATCAGCTCCAGCAGTTCCTGTGACTACGACTTCAACAGCTACAGACA  
 GTAAGTTACAAGCGACTGAAGTTAAGAGCGTTCCGGTAGCACA AAAAGCT  
 CCAACAGCAACACCGGTAGCACAACACAGCTTCAACAACAATGCAAGTAGC  
 TGCACATCCTGAAAATGCAAGGCTCCAACCTCATGTTGCGAGCTTATAAAG  
 AAAAAGTAGCGTCAACTTATGGAGTTAATGAATTCACTACATACCGTGCG  
 GGAGATCCAGGTGATCATGGTAAAGGTTTAGCAGTTGACTTTATTGTAGG  
 TACTAATCAAGCACTTGGTAATAAAGTTGCACAGTACTcTACACAAAATA  
 TGGCAGCAAAATAACATTTATATGTTATCTGGCAACAAAAGTTTACTCA  
 AATACAAACAGTATTTATGGACCTGCTAATCTTGAATGCAATGCCAGA  
 TCGTGGTGGCGTTACTGCCAACCACTATGACCAGGTTACGTATCATTTA  
 ACAATAATATAAAAAAGGAAGCTATTGGCTTCTTTTTATATGCCTTG  
 AATAGACTTTCAAGGTTCTTATATAATTTTATTA

SEQ ID NO. 6906

STRAIN COH1

CTGATT  
 GGTAAAGCAAGACAATAAATCATCATATACCTGTGAAATATGGTGATACAC  
 TAAGCGTTATTTGAGAAGCAATGTCAATTGATATGAATGTCTTAGCAAAA  
 ATTAATAACATTGCAGATATCAATCTTATTTATCCTGAGACAACACTGAC  
 AGTAACCTTACGATCAGAAGAGTCATACTGCCACTTCAATGAAAATAGAAA  
 CACCAGCAACAATGCTGCTGGTCAAAACAACAGcTACTGTGATTGAAA  
 ACCAATCAAGTTTTGTTGCGAGACCAAAAAGTTTCTCTCAATACAATTC  
 GGAAGGTATGACACCAGaaGCAGCAACAACGATTGTTTTCGCCAATGAAGA  
 CaTATTCTTCTGCGCCAGCTTTGAAATCAAAAGAAGTATTAGCACAAGAG  
 CAAGCTGTTAGTCAAGTAGCAGCTAATGAACAGGTATCACCAGCTCCTGT  
 GAAGTCGATTACTTCAAGGTTCCAGCAGCTAAAGAGGAAGTTAAACCAA  
 CTCAGACGTCAGTCAGTCAGTTAACAACAGTATCACCAGCTTCTGTTGCC  
 GCTGAAAACACCAGCTCCAGTAGCTAAGTAGCACCGGTAAAGAACTGTAGC  
 AGCCCCTAGAGTGGCAAGTGcTAAAGTAGTCACTCCTAAAGTAGAACTG  
 GTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCCTGTGACTACGACT  
 TCACCAGCTACAGACAGTAAGTTACAAGCGACTGAAGTTAAGAGCGTTCC  
 GGTAGCACA AAAAGCTCCAACAGCAACACCGGTAGCACAACAGCTTCAA  
 CAACAATGCAAGTAGCTGCATCCTGAAAATGCAAGGCTCCAACCTCAT  
 GTTGACGCTTATAAAGAAAAAGTAGCGTCAACTTATGGAGTTAATGAATT  
 CAGTACATACCGTGCGGAGATCCAGGTGATCATGGTAAAGGTTTAGCAG  
 TTGACTTTATTGTAGGTAAAAACCAAGCACTTGGTAATGAAGTTGCACAG  
 TaCTCTACACAAAATATGGCAGCAAAATAACATTTATATGTTATCTGGCA  
 ACAAAAGTTTTATTCAAATACAAATAGTATTTATGGACCTGCTAATACTT  
 GGAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCACTATGACCAC  
 GTTCAGTATCATTTAACAATAATATAAAAAAGGAAGCTATTGGCTTCT

Table 69: Comparative Sequences relating to SAG0032

TTTTTTATATGCCTTGAATAGACTTTCAAGGTTCTTATATAATTTTTATT  
A

SEQ ID NO. 6907

STRAIN M732

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGT  
GATACAnTAAGCGTTATTTTCAGAAGCAATGTCAATTGATATGAATGTCTT  
AGCAAAAATTAATAACATTGCAGATATCAATCTTATTTATCCTGAGACAA  
CACTGACAGTAACCTTACGATCAGAAGAGTCATCTGCCACTTCAATGAAA  
ATAGAAAACACCAGCAACAAATGCTGCTGGTCAAACAACAGCTACTGTcGA  
TTTGAAAACCAATCAAGTTTGTGTTGCAGACCAAAAAGTTTCTCTCAATA  
CAATTTCCGAAGGTATGACACCAGAAGCAGCAACAACGATTGTTTCGCCA  
ATGAAGACATATTTCTTCTGCCCGAGCTTTGAAATCAAAGAAGTATTAGC  
ACAAGAGCAAGCTGTTAGTCAAGTAGCAGCTAATGAACAGGTATCACCAG  
CTCCTGTGAAGTCGATTACTTCAGAAGTTCCAGCAGCTAAAGAGGAAGTT  
AAACCACTCAGACGTCAGTCAGTCAGTTAAACAACAGTATCACCAGCTTC  
TGTTGCCGCTGAAACACCAGCTCCAGTAGCTAAAGTAGCACCGGTAAGAA  
CTGTAGCAGCCCCCTAGAGTGGCAAGTGCTAAAGTAGTCACTCCTAAAGTA  
GAAACTGGTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCTGTGAC  
TACGACTTCACCAGCTACAGACAGTAAGTTACAAGCGACTGAAGTTAAGA  
GCGTTCCGGTAGCACAAAAGCTCCAACAGCAACACCGGTAGCACAAACCA  
GCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCAGGGCTCCA  
ACCTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTATGGAGTTA  
ATGAATTCAAGTACATACCGTGGCGGAGATCCAGGTGATCATGGTAAAGGT  
TTAGCAGTTGACTTTAttgtaggtaaaaaaccAAGCACTTGGTAATGAAGT  
TGCACAGTACTcTACACAAAATATGGCAGCAAAATAACATTTATATGTTA  
TCTGGCAACAAAAGTTTATTCAAATACAAATAGTATTATGGACCTGCT  
AATACCTTGAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCACTA  
TGACCACGTTACGATATCATTTAAACAAATAATATAAAAAAGGAAGCTATT  
TGGCTTCTTTTTTATATGCCTTGAATAGACTTTCAAGGTTCTTATATAAT  
TTTTATTA

SEQ ID NO. 6908

STRAIN M781

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGT  
GATACACTAAGCGTTATTTTCAGAAGCAATGTCAATTGATATGAATGTCTT  
AGCAAAAATTAATAACATTGCAGATATCAATCTTATTTATCCTGAGACAA  
CACTGACAGTAACCTTACGATCAGAAGAGTCATACTGCCACTTCAATGAAA  
ATAGAAAACACCAGCAACAAATGCTGCTGGTCAAACAACAGCTACTGTcGA  
TTTGAAAACCAATCAAGTTTGTGTTGCAGACCAAAAAGTTTCTCTCAATA  
CAATTTCCGAAGGTATGACACCAGAAGCAGCAACAACGATTGTTTCGCCA  
ATGAAGACATATTTCTTCTGCCCGAGCTTTGAAATCAAAGAAGTATTAGC  
ACAAGAGCAAGCTGTTAGTCAAGTAGCAGCTAATGAACAGGTATCACCAG  
CTCCTGTGAAGTCGATTACTTCAGAAGTTCCAGCAGCTAAAGAGGAAGTT  
AAACCACTCAGACGTCAGTCAGTCAGTTAAACAACAGTATCACCAGCTTC  
TGTTGCCGCTGAAACACCAGCTCCAGTAGCTAAAGTAGCACCGGTAAGAA  
CTGTAGCAGCCCCCTAGAGTGGCAAGTGCTAAAGTAGTCACTCCTAAAGTA  
GAAACTGGTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCTGTGAC  
TACGACTTCACCAGCTACAGACAGTaaGTTACAAGCGACTGAAGTTAAGA  
GCGTTCCGGTAGCACAAAAGCTCCAACAGCAACACCGGTAGCACAAACCA  
GCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCAGGGCTCCA  
ACCTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTATGGAGTTA  
ATGAATTCAAGTACATACCGTGGCGGAGATCCAGGTGATCATGGTAAAGGT  
TTAGCAGTTGACTTTATTGTAGGTAAAAACCAAGCACTTGGTAATGAAGT  
TGCACAGTACTCTACACAAAATATGGCAGCAAAATAACATTTATATGTTA  
TCTGGCAACAAAAGTTTATTCAAATACAAATAGTATTATGGACCTGCT  
AATACCTTGAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCACTA  
TGACCACGTTACGATATCATTTAAACAAATAATATAAAAAAGGAAGCTATT  
TGGCTTCTTTTTTATATGCCTTGAATAGACTTTCAAGGTTCTTATATAAT  
TTTTATTA

SEQ ID NO. 6909

STRAIN CJB110

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAAA  
TATGGTGATACACTAAGCGTTATTTTCAGAAGCAATGTCAATTGATATGAA  
TGCTTTAGCAAAAATTAATAACATTGCAGATATCAATCTTATTTATCCTG  
AGACAACACTGCAGTAACCTTACGATCAGAAGAGTCATACTGCCACTTCA  
ATGAAAATAGAAAACACCAGCAACAAATGCTGCTGGTCAAACAACAGCTAC  
TGTGGATTTGAAAACCAATCAAGTTTcTGTGTCAGACCAAAAAGTTTCTC  
TCAATACAATTTCCGAAGGTATGACACCAGAAGCAGCAACAACGATTGTT  
TCGCCAATGAAGACATATTTCTTCTGCCCGAGCTTTGAAATCAAAGAAGT  
ATTAGCACAAGAGCAAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGTAT  
CAACAGCTCCTGTGAAGTCGATTACTTCAGAAGTTCCAGCAGCTAAAGAG  
GAAGTTAAACCAACTCAGACGTCAGTCAGTCAGTCAACAACAGTATCACC  
AGCTTCTGTGTCGCTGAAACACCAGCTCCAGTAGCTAAAGTAGCACCGG  
TAAGAACTGTAGCAGCCCCCTAGAGTGGCAAGTGTTAAAGTAGTCACTCCT  
AAAGTAGAAAACCTGGTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCC  
TGTGACTACGACTTCAACAGcTACAGACAGTaaGTTaCAAGCGACTGAAG  
TTAAGAGCGTTCCGGTAGCACAAAAGCTCCAACAGCAACACCGGTAGCA  
CAACAGCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCAGG  
GCTCCAACCTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTATG  
GAGTTAATGAATTCAGTACATaCCGTGCAAGTGATCCAgGTGATCATGGT  
AAAGGTTTAGCAGTcGACTTTATTGTAGTAAAAACCAAGCACTTGGTAA

Table 69: Comparative Sequences relating to SAG0032

TGAAGTTGCACAGTACTCTACACAAAATATGGCAGCAAATAACATTTTCAT  
ATGTTTATCTGGCAACAAAAGTTTTACTCAAATACAAATAGTATTTATGGA  
CCTGCTAATACTTGGAAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAA  
CCATTATGACCATGTTACGATATCATTTAAACAAATAATATAAAAAAGGAA  
GCTATTTGGCTTCTTTTATATGCCTTGAATAGACTTCAAGGTTCTTA  
TATAATTTTTATTA

SEQ ID NO. 6910

STRAIN 1169NT

CTGATTTG

GTAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGTGATACACT  
AAGCGTTATTTTTCAGAACCAATGTCAATTGATATGAATGTCTTAGCAAAAA  
TTAATAACATTGTCAGATATCAATCTTATTTATCCTGAGACCAACTGACA  
GTAACCTTACGATCAGAGAGTCATCTGCCACTTCAATGAAAATAGAAAC  
ACCAAGCAACAAATGCTGCTGGTCAAACACAGCTACTGTGGATTTGAAAA  
CCAATCAAGTTTCTGTGTCAGACCAAAAAGTTTCTCTCAATCAATTTTCG  
GAAGGTATGACACCAAGAGCAGCAACAACGATTGTTTCGCCAATGAAGAC  
ATATTTCTTCTGCGCCAGCTTTGAAATCAAAGAGTATTAGCACAAAGAGC  
AAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGTATCACCAGCTCCTGTG  
AAGTCGATTACTTCAAGAGTTCCAGCAGCTAAAGAGGAAGTTAGACCAaC  
TcAGACGTCAGTCAGTCAGTCAACAACAGTATCACCAGCTTCTGTGCGCG  
CTGAAACACCCAGCTCCAGTAGCTAAAGTAGCACCGGTAAGAAGCTTAGCA  
GCCCCAGCCCCCTAGAGTGGCAAGTGCTAAAGTAGTCACTCTTAAAGTAGA  
AaCTGGTGATCACCAGAGCATGTACCAGCTCCAGCAGTTCTGTGACTA  
cGACTTCAACAGCTACaGACaTaAGTTACAAGCGACTGAAGTTAAAGAGC  
GTCTCGGTTGGCAAAAAGCTTCAACAGCAACACCGGTAGCAACACCCAGC  
TTcAACAAACAAATGTCAGTAGcTGACATCTGAAATGCAGGACTCCAAC  
CTCATGTTGTCAGCTTATAAAGAAAAAGTAGCGTCAACTTATGGAGTTAAT  
GAATTCAGTACATaCCGTGCGGAGATCCAGGTGATCATGGTAAAGGTTT  
AGCAGTTGACTTTATTTGTAGTAAAGCAAGCACTTGGTAATGAAGTTG  
CACAGTACTCTACACAAAATATGGCAGCAAATAACATTTTCATATGTTATC  
TGGCAACAAAAGTTTACTCAAATACAAATAGTATTTATGGACCTGCTAA  
TACTTGGAAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCACTATG  
ACCAGGTTACGATCATTTAAACAAATAATATAAAAAAGGAAGCTATTTG  
GCTTCTTTTATATGCCTTGAATAGACTTCAAGGCTCTTATATAATTT  
TTATTA

SEQ ID NO. 6911

STRAIN JM9130013

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACT

GTGAAATATGGTGATACACTAAGCGTTATTTTCAGAAAGCAATGTCAATTGA  
TATGAATGTCTTAGCAAAAAATAAATCAATTCAGATATCAATCTTATTT  
ATCCTGAGACAACACTGACAGTAACCTACGATCAGAAGAGTCATACCTGCC  
ACTTCAATGAAAATAGAAACACCAGCAACAAATGCTGCTGGTCAAACAA  
AGCTACTGTGGATTTGAAAACCAATCAAGTTTCTGTTGTCAGACCAAAAAG  
TTTCTCTCAATACAATTCGGAAGGTATGACACCAGAAGCAGCAACCAAG  
ATTGTTTCCGCAATGAAGACATATTTCTTGCAGCAGCTTTGAAATCAA  
AGAAGTATTAGCACAAAGAGCAAGCTGTTAGTCAAGCAGCAGTAAAGAAC  
AGGTATCACCAGCTCCTGTGAAGTCGATTACTTCAAGAGTTCCAGCAGCT  
AAAGAGGAAGTTAAACCAACTCAGACGTCAGTCAGTCAGTCAACAACAGT  
ATCACCAgCTTCTGTTGCGGCTGAAACACCAGCTCCAGTAGCTAAAGTAG  
CACCGGTAAGAAGCTGTCAGCCCCCTAGAGTGGCAAGTGTAAAGTAGTC  
ACTCTTAAAGTAGAACTGGTGCATCACCAGAGCATGTATCAGCTCCAGC  
AGTTCTGTGACTACGACTTCAACAGCTACAGaCAGTAAGTTACAAGCGA  
cTGAAGTTAAGAGCGTTCCGCTAGCACAAAAGCTTCAACAGCAACACCG  
GTAGCaCAACCAAGCTTCAACAAATGCAGTAGCTGCACATCTGAAAA  
TGCAGGGCTCCAACCTCATGTTGTCAGCTTATAAAGAAAAAGTAGCGTCAA  
CTTATGGAGTTAATGAATTCAGTACATACCGTGGGAGATCCAGGTGAT  
CATGGTAAAGGTTTAGCAGTTGACTTTATTTGAGGTACTAATCAAGCACT  
TGGTAATAAAGTTGTCAGTACTCTACACAAAATATGGCAGCAAATAACA  
TTTCTATATGTTATCTGGCAACAAAAGTTTACTCAAATACAAACAGTATT  
TATGGACCTGCTAATACTTGGAAATGCAATGCCAGATCGTGGTGGCGTTAC  
TGCCAACCACTATGACCAGCTTCAAGTATCATTTAAACAAATAATATAAAA  
AAGGAAGCTATTTGGCTTCTTTTATATGCCTTGAATAGACTTCAAGG  
TTCTTATATAATTTTTATTA

PRETTY of: /biotmp/msa167919.2{\*} March 11, 2003 08:55 ..

	1				50
msa167919.2{322_COH1}	-----	-----	-----	-----	-----
msa167919.2{322_M781}	-----	-----	-----	-----	-----
msa167919.2{322_M732}	-----	-----	-----	-----	-----
msa167919.2{322_18RS21}	-----	-----	-----	-----	-----
msa167919.2{322_2603}	atgaataaaa	aggtactatt	gacatcgaca	atggcagctt	cgctattatc
msa167919.2{322_JM9130013}	-----	-----	-----	-----	-----
msa167919.2{322_090}	-----	-----	-----	-----	-----
msa167919.2{322_CJB110}	-----	-----	-----	-----	-----
msa167919.2{322_A909}	-----	-----	-----	-----	-----
msa167919.2{322_H36B}	-----	-----	-----	-----	-----
msa167919.2{322_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****

51

100

Table 69: Comparative Sequences relating to SAG0032

msa167919.2{322_COH1}	-----	-----	-----	-----	-----
msa167919.2{322_M781}	-----	-----	-----	-----	-----
msa167919.2{322_M732}	-----	-----	-----	-----	-----
msa167919.2{322_18RS21}	-----	-----	-----	-----	-----
msa167919.2{322_2603}	agtcgcaagt	gttcaagcac	aagaaacaga	tacgacgtgg	acagcacgta
msa167919.2{322_JM9130013}	-----	-----	-----	-----	-----
msa167919.2{322_090}	-----	-----	-----	-----	-----
msa167919.2{322_CJB110}	-----	-----	-----	-----	-----
msa167919.2{322_A909}	-----	-----	-----	-----	-----
msa167919.2{322_H36B}	-----	-----	-----	-----	-----
msa167919.2{322_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
msa167919.2{322_COH1}	-----	-----	-----	-----	-----
msa167919.2{322_M781}	-----	-----	-----	-----	-----
msa167919.2{322_M732}	-----	-----	-----	-----	-----
msa167919.2{322_18RS21}	-----	-----	-----	-----	-----
msa167919.2{322_2603}	ctgtttcaga	ggtaaaggct	gatttggtta	agcaagacaa	taaatcatca
msa167919.2{322_JM9130013}	-----	-----	-----	-----	-----
msa167919.2{322_090}	-----	-----	-----	-----	-----
msa167919.2{322_CJB110}	-----	-----	-----	-----	-----
msa167919.2{322_A909}	-----	-----	-----	-----	-----
msa167919.2{322_H36B}	-----	-----	-----	-----	-----
msa167919.2{322_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	-----	-----	-----
msa167919.2{322_COH1}	-----	-----	-----	-----	-----
msa167919.2{322_M781}	-----	-----	-----	-----	-----
msa167919.2{322_M732}	-----	-----	-----	-----	-----
msa167919.2{322_18RS21}	-----	-----	-----	-----	-----
msa167919.2{322_2603}	tatactgtga	aatatggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_JM9130013}	-----	-----	-----	-----	-----
msa167919.2{322_090}	-----	-----	-----	-----	-----
msa167919.2{322_CJB110}	-----	-----	-----	-----	-----
msa167919.2{322_A909}	-----	-----	-----	-----	-----
msa167919.2{322_H36B}	-----	-----	-----	-----	-----
msa167919.2{322_1169NT}	-----	-----	-----	-----	-----
Consensus	-----	-----	-----	-----	-----
msa167919.2{322_COH1}	-----	-----	-----	-----	-----
msa167919.2{322_M781}	-----	-----	-----	-----	-----
msa167919.2{322_M732}	-----	-----	-----	-----	-----
msa167919.2{322_18RS21}	-----	-----	-----	-----	-----
msa167919.2{322_2603}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_JM9130013}	-----	-----	-----	-----	-----
msa167919.2{322_090}	-----	-----	-----	-----	-----
msa167919.2{322_CJB110}	-----	-----	-----	-----	-----
msa167919.2{322_A909}	-----	-----	-----	-----	-----
msa167919.2{322_H36B}	-----	-----	-----	-----	-----
msa167919.2{322_1169NT}	-----	-----	-----	-----	-----
Consensus	-----	-----	-----	-----	-----
msa167919.2{322_COH1}	-----	-----	-----	-----	-----
msa167919.2{322_M781}	-----	-----	-----	-----	-----
msa167919.2{322_M732}	-----	-----	-----	-----	-----
msa167919.2{322_18RS21}	-----	-----	-----	-----	-----
msa167919.2{322_2603}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_JM9130013}	-----	-----	-----	-----	-----
msa167919.2{322_090}	-----	-----	-----	-----	-----
msa167919.2{322_CJB110}	-----	-----	-----	-----	-----
msa167919.2{322_A909}	-----	-----	-----	-----	-----
msa167919.2{322_H36B}	-----	-----	-----	-----	-----
msa167919.2{322_1169NT}	-----	-----	-----	-----	-----
Consensus	-----	*****	*****	*****	*****
msa167919.2{322_COH1}	-----	-----	-----	-----	-----
msa167919.2{322_M781}	-----	-----	-----	-----	-----
msa167919.2{322_M732}	-----	-----	-----	-----	-----
msa167919.2{322_18RS21}	-----	-----	-----	-----	-----
msa167919.2{322_2603}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_JM9130013}	-----	-----	-----	-----	-----
msa167919.2{322_090}	-----	-----	-----	-----	-----
msa167919.2{322_CJB110}	-----	-----	-----	-----	-----
msa167919.2{322_A909}	-----	-----	-----	-----	-----
msa167919.2{322_H36B}	-----	-----	-----	-----	-----
msa167919.2{322_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****

Table 69: Comparative Sequences relating to SAG0032

	351		400
msa167919.2{322_COH1}	AACaACAGCT	ACTGTcGATT	TGAAAACCAA TCAAGTTTtT GTTGCAGACC
msa167919.2{322_M781}	AACaACAGCT	ACTGTcGATT	TGAAAACCAA TCAAGTTTtT GTTGCAGACC
msa167919.2{322_M732}	AACaACAGCT	ACTGTcGATT	TGAAAACCAA TCAAGTTTtT GTTGCAGACC
msa167919.2{322_18RS21}	AACaACAGCT	ACTGTgGATT	TGAAAACCAA TCAAGTTTcT GTTGCAGACC
msa167919.2{322_2603}	AACaACAGCT	ACTGTgGATT	TGAAAACCAA TCAAGTTTcT GTTGCAGACC
msa167919.2{322_JM9130013}	AACaACAGCT	ACTGTgGATT	TGAAAACCAA TCAAGTTTcT GTTGCAGACC
msa167919.2{322_090}	AACaACAGCT	ACTGTgGATT	TGAAAACCAA TCAAGTTTcT GTTGCAGACC
msa167919.2{322_CJB110}	AACaACAGCT	ACTGTgGATT	TGAAAACCAA TCAAGTTTcT GTTGCAGACC
msa167919.2{322_A909}	AACaACAGCT	ACTGTcGATT	TGAAAACCAA TCAAGTTTcT GTTGCAGACC
msa167919.2{322_H36B}	AACaACAGCT	ACTGTcGATT	TGAAAACCAA TCAAGTTTcT GTTGCAGACC
msa167919.2{322_1169NT}	AACaACAGCT	ACTGTgGATT	TGAAAACCAA TCAAGTTTcT GTTGCAGACC
Consensus	*****	*****	*****
	401		450
msa167919.2{322_COH1}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_M781}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_M732}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_18RS21}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_2603}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_JM9130013}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_090}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_CJB110}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_A909}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_H36B}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_1169NT}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
Consensus	*****	*****	*****
	451		500
msa167919.2{322_COH1}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_M781}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_M732}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_18RS21}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_2603}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_JM9130013}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_090}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_CJB110}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_A909}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_H36B}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_1169NT}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
Consensus	*****	*****	*****
	501		550
msa167919.2{322_COH1}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC TGTAGTCAA GtAGCAGCTA
msa167919.2{322_M781}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC TGTAGTCAA GtAGCAGCTA
msa167919.2{322_M732}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC TGTAGTCAA GtAGCAGCTA
msa167919.2{322_18RS21}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC TGTAGTCAA GcAGCAGCTA
msa167919.2{322_2603}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC TGTAGTCAA GcAGCAGCTA
msa167919.2{322_JM9130013}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC TGTAGTCAA GcAGCAGCTA
msa167919.2{322_090}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC TGTAGTCAA GcAGCAGCTA
msa167919.2{322_CJB110}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC TGTAGTCAA GcAGCAGCTA
msa167919.2{322_A909}	ATCAAAAGAA	GTATTAGCAC	AAGgGCAAGC TGTAGTCAA GcAGCAGCTA
msa167919.2{322_H36B}	ATCAAAAGAA	GTATTAGCAC	AAGgGCAAGC TGTAGTCAA GcAGCAGCTA
msa167919.2{322_1169NT}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC TGTAGTCAA GcAGCAGCTA
Consensus	*****	*****	*****
	551		600
msa167919.2{322_COH1}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_M781}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_M732}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_18RS21}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_2603}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_JM9130013}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_090}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_CJB110}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_A909}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_H36B}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_1169NT}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
Consensus	*****	*****	*****
	601		650
msa167919.2{322_COH1}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
msa167919.2{322_M781}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
msa167919.2{322_M732}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
msa167919.2{322_18RS21}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
msa167919.2{322_2603}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
msa167919.2{322_JM9130013}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
msa167919.2{322_090}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
msa167919.2{322_CJB110}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
msa167919.2{322_A909}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
msa167919.2{322_H36B}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
msa167919.2{322_1169NT}	GCAGCTAAAG	AGGAAGTTAg	ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
Consensus	*****	*****	*****

Table 69: Comparative Sequences relating to SAG0032

		651			700
msa167919.2{322_COH1}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_M781}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_M732}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_18RS21}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_2603}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_JM9130013}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_090}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_CJB110}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_A909}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_H36B}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_1169NT}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
Consensus		*****	*****	*****	*****
		701			750
msa167919.2{322_COH1}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_M781}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_M732}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_18RS21}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_2603}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_JM9130013}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_090}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_CJB110}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_A909}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_H36B}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_1169NT}	AAGTAGCACC	GGTAAGAACT	GTAGcagccc	CAGCCCCTAG	AGTGGCAAGT
Consensus		*****	*****	*****	*****
		751			800
msa167919.2{322_COH1}	GcTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_M781}	GcTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_M732}	GcTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_18RS21}	GtTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_2603}	GtTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_JM9130013}	GtTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_090}	GtTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_CJB110}	GtTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_A909}	GtTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_H36B}	GtTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_1169NT}	GcTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
Consensus		*..*****	*****	*****	*****
		801			850
msa167919.2{322_COH1}	AtcCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_M781}	AtcCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_M732}	AtcCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_18RS21}	AtcCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_2603}	AtcCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_JM9130013}	AtcCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_090}	AtcCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_CJB110}	AtcCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_A909}	AtcCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_H36B}	AtcCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_1169NT}	AccCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACaTA
Consensus		*..*****	*****	*****	*****
		851			900
msa167919.2{322_COH1}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_M781}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_M732}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_18RS21}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_2603}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_JM9130013}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_090}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_CJB110}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_A909}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_H36B}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_1169NT}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTgGCACA	AAAAGCTCCA
Consensus		*****	*****	*****	*****
		901			950
msa167919.2{322_COH1}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_M781}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_M732}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_18RS21}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_2603}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_JM9130013}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_090}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_CJB110}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_A909}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_H36B}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_1169NT}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC



Table 69: Comparative Sequences relating to SAG0032

Consensus	*****	*****	*****	*****	*****
	951				1000
msa167919.2{322_COH1}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_M781}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_M732}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_18RS21}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_2603}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_JM9130013}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_090}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_CJB110}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_A909}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_H36B}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_1169NT}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
Consensus	*****	*****-*-*	*****	*****	*****
	1001				1050
msa167919.2{322_COH1}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGGA
msa167919.2{322_M781}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGGA
msa167919.2{322_M732}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGGA
msa167919.2{322_18RS21}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGGA
msa167919.2{322_2603}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGGA
msa167919.2{322_JM9130013}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGGA
msa167919.2{322_090}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGGA
msa167919.2{322_CJB110}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGGA
msa167919.2{322_A909}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGGA
msa167919.2{322_H36B}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGGA
msa167919.2{322_1169NT}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGGA
Consensus	*****	*****	*****	*****	*****-*-*
	1051				1100
msa167919.2{322_COH1}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_M781}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_M732}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_18RS21}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_2603}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_JM9130013}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_090}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_CJB110}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_A909}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_H36B}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_1169NT}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
Consensus	*****	*****	*****	*****	*****-*-*
	1101				1150
msa167919.2{322_COH1}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_M781}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_M732}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_18RS21}	tAAtCAAGCA	CTTGGTAATa	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_2603}	tAAtCAAGCA	CTTGGTAATa	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_JM9130013}	tAAtCAAGCA	CTTGGTAATa	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_090}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_CJB110}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_A909}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_H36B}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_1169NT}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
Consensus	-*-*****	*****	*****	*****	*****
	1151				1200
msa167919.2{322_COH1}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_M781}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_M732}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_18RS21}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_2603}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_JM9130013}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_090}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_CJB110}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_A909}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_H36B}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_1169NT}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
Consensus	*****	*****	*****	*****	*****
	1201				1250
msa167919.2{322_COH1}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_M781}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_M732}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_18RS21}	ACAAAcAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_2603}	ACAAAcAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_JM9130013}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_090}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_CJB110}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_A909}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_H36B}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG

Table 69: Comparative Sequences relating to SAG0032

msal67919.2{322_1169NT}	ACAAATAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
Consensus	*****	*****	*****	*****	*****
	1251				1300
msal67919.2{322_COH1}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msal67919.2{322_M781}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msal67919.2{322_M732}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msal67919.2{322_18RS21}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msal67919.2{322_2603}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msal67919.2{322_JM9130013}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msal67919.2{322_090}	TGGTGGCGTT	ACTGCCAACC	AtTATGACCA	tGTTcACGTA	TCATTTAACA
msal67919.2{322_CJB110}	TGGTGGCGTT	ACTGCCAACC	AtTATGACCA	tGTTcACGTA	TCATTTAACA
msal67919.2{322_A909}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msal67919.2{322_H36B}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msal67919.2{322_1169NT}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
Consensus	*****	*****	*-*****	-*****	*****
	1301				1350
msal67919.2{322_COH1}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTtTATA	TGCCTTGaAT
msal67919.2{322_M781}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTtTATA	TGCCTTGaAT
msal67919.2{322_M732}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTtTATA	TGCCTTGaAT
msal67919.2{322_18RS21}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTtTATA	TGCCTTGaAT
msal67919.2{322_2603}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTtTATA	TGCCTTGaAT
msal67919.2{322_JM9130013}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTtTATA	TGCCTTGaAT
msal67919.2{322_090}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTtTATA	TGCCTTGaAT
msal67919.2{322_CJB110}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTtTATA	TGCCTTGaAT
msal67919.2{322_A909}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTtTATA	TGCCTTGcAT
msal67919.2{322_H36B}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTtTATA	TGCCTTGcAT
msal67919.2{322_1169NT}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTtTATA	TGCCTTGaAT
Consensus	*****	*****	*****	*****	*****_**
	1351				1382
msal67919.2{322_COH1}	AGACTTTCAA	GGTTCtTATA	TAATTTtTAT	TA	
msal67919.2{322_M781}	AGACTTTCAA	GGTTCtTATA	TAATTTtTAT	TA	
msal67919.2{322_M732}	AGACTTTCAA	GGTTCtTATA	TAATTTtTAT	TA	
msal67919.2{322_18RS21}	AGACTTTCAA	GGTTCtTATA	TAATTTtTAT	TA	
msal67919.2{322_2603}	AGACTTTCAA	GGTTCtTATA	TAATTTtTAT	TA	
msal67919.2{322_JM9130013}	AGACTTTCAA	GGTTCtTATA	TAATTTtTAT	TA	
msal67919.2{322_090}	AGACTTTCAA	GGTTCtTATA	TAATTTtTAT	TA	
msal67919.2{322_CJB110}	AGACTTTCAA	GGTTCtTATA	TAATTTtTAT	TA	
msal67919.2{322_A909}	AGACTTTCAA	GGTTCtTATA	TAATTTtTAT	TA	
msal67919.2{322_H36B}	AGACTTTCAA	GGTTCtTATA	TAATTTtTAT	TA	
msal67919.2{322_1169NT}	AGACTTTCAA	GGTTCtTATA	TAATTTtTAT	TA	
Consensus	*****	*****	*****	**	
<b>SEQ ID NO. 6912</b>					
STRAIN 2603 frame: 1					
MNKKVLLTSTMAASLLSVASVQAQETDITWTARTVSEVKADLVKQDNKSSYTVKYGDTLS					
VISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSHATSMKIEPATNAAGQTTA					
TVDLKTNQVSVADQKVSINLI SEGMPPEAATTIVSPMKTYSSAPALKSKEVLQAQVQAVS					
AAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVSPASVAEETPAPVAKVAPVRT					
VAAPRVASVKVVT PKVETGASPEHVSAPAVPVTTTSPATDSKLQATEVKSVPVQAQKAPT					
TPVAQPASTTNAVAHHPENAGLQPHVAAYKEKVASTYGVNEFSTYRAGDPGDHGKGLAVD					
FIVGTNQALGNKVAQYSTQNMAANNISYVIWQQKFYSNTNSIYGPANTWNAMPDRGGVTA					
NHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY					
<b>SEQ ID NO. 6913</b>					
STRAIN 090 frame: 2					
ETTLTVTYDQKSHATSMKIEPATNAAGQTPATVTLKTNQVSVADQKVSINLI SEGMP					
EAATTIVSPMKTYSSAPALKSKEVLQAQVQAVSQAANEQVSTAPVKSITSEVPAAKEEVK					
PTQTSVSQSTTVSPASVAEETPAPVAKVAPVRTVAAPRVASVKVVT PKVETGASPEHVS					
PAVPVTTTSTATDSKLQATEVKSVPVQAQKAPTATPVAQPASTTNAVAHHPENAGLQPHVA					
AYKEKVASTYGVNEFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNIS					
YVIWQQKFYSNTNSIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYAL					
NRLSRFLYNFY					
<b>SEQ ID NO. 6914</b>					
STRAIN A909 frame: 3					
DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH					
TATSMKIEPATNAAGQTTATVTLKTNQVSVADQKVSINLI SEGMPPEAATTIVSPMKTY					
SSAPALKSKEVLQAQVQAVSQAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS					
PASVAEETPAPVAKVAPVRTVAAPRVASVKVVT PKVETGASPEHVSAPAVPVTTTSTATD					
SKLQATEVKSVPVQAQKAPTATPVAQPASTTNAVAHHPENARLQPHVAAYKEKVASTYGVN					
EFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQQKFYSNTN					
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALHRLSRFLYNFY					
<b>SEQ ID NO. 6915</b>					
STRAIN H36B frame: 3					
DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH					
TATSMKIEPATNAAGQTTATVTLKTNQVSVADQKVSINLI SEGMPPEAATTIVSPMKTY					
SSAPALKSKEVLQAQVQAVSQAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS					
PASVAEETPAPVAKVAPVRTVAAPRVASVKVVT PKVETGASPEHVSAPAVPVTTTSTATD					
SKLQATEVKSVPVQAQKAPTATPVAQPASTTNAVAHHPENARLQPHVAAYKEKVASTYGVN					

Table 69: Comparative Sequences relating to SAG0032

EFSTYRAGDPGDHKGGLAVDFIVGKNQALGNEVAQYSTQNMANNISYVIWQKQFYSNTN  
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

## SEQ ID NO. 6916

STRAIN 18RS21 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH  
TATSMKIETPATNAAGQTTATVDLKTINQVSVADQKVSINLTISEGMTPEAATTIVSPMKTY  
SSAPALKSKEVLAEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS  
PASVAAETPAPVAKVAPVRTVAAPRVASVKVVT PKVETGASPEHVSAPAVPVTTTSPATD  
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAAHPENAGLQPHVAAYKEKVASTYGVN  
EFSTYRAGDPGDHKGGLAVDFIVGKNQALGNEVAQYSTQNMANNISYVIWQKQFYSNTN  
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

## SEQ ID NO. 6917

STRAIN M732 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH  
TATSMKIETPATNAAGQTTATVDLKTINQVSVADQKVSINLTISEGMTPEAATTIVSPMKTY  
SSAPALKSKEVLAEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS  
PASVAAETPAPVAKVAPVRTVAAPRVASAKVVT PKVETGASPEHVSAPAVPVTTTSPATD  
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAAHPENAGLQPHVAAYKEKVASTYGVN  
EFSTYRAGDPGDHKGGLAVDFIVGKNQALGNEVAQYSTQNMANNISYVIWQKQFYSNTN  
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

## SEQ ID NO. 6918

STRAIN COH1 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH  
TATSMKIETPATNAAGQTTATVDLKTINQVSVADQKVSINLTISEGMTPEAATTIVSPMKTY  
SSAPALKSKEVLAEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS  
PASVAAETPAPVAKVAPVRTVAAPRVASAKVVT PKVETGASPEHVSAPAVPVTTTSPATD  
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAAHPENAGLQPHVAAYKEKVASTYGVN  
EFSTYRAGDPGDHKGGLAVDFIVGKNQALGNEVAQYSTQNMANNISYVIWQKQFYSNTN  
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

## SEQ ID NO. 6919

STRAIN M781 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH  
TATSMKIETPATNAAGQTTATVDLKTINQVSVADQKVSINLTISEGMTPEAATTIVSPMKTY  
SSAPALKSKEVLAEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS  
PASVAAETPAPVAKVAPVRTVAAPRVASAKVVT PKVETGASPEHVSAPAVPVTTTSPATD  
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAAHPENAGLQPHVAAYKEKVASTYGVN  
EFSTYRAGDPGDHKGGLAVDFIVGKNQALGNEVAQYSTQNMANNISYVIWQKQFYSNTN  
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

## SEQ ID NO. 6920

STRAIN CJB110 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH  
TATSMKIETPATNAAGQTTATVDLKTINQVSVADQKVSINLTISEGMTPEAATTIVSPMKTY  
SSAPALKSKEVLAEQAVSQAAANEQVSTAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS  
PASVAAETPAPVAKVAPVRTVAAPRVASVKVVT PKVETGASPEHVSAPAVPVTTTSTATD  
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAAHPENAGLQPHVAAYKEKVASTYGVN  
EFSTYRAGDPGDHKGGLAVDFIVGKNQALGNEVAQYSTQNMANNISYVIWQKQFYSNTN  
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

## SEQ ID NO. 6921

STRAIN 1169NT frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH  
TATSMKIETPATNAAGQTTATVDLKTINQVSVADQKVSINLTISEGMTPEAATTIVSPMKTY  
SSAPALKSKEVLAEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS  
PASVAAETPAPVAKVAPVRTVAAPRVASAKVVT PKVETGASPEHVPAPAVPVTTTSTA  
TDNKLQATEVKSVPVAQKAPTATPVAQPASTTNAAHPENAGLQPHVAAYKEKVASTYGVN  
VNEFSTYRAGDPGDHKGGLAVDFIVGKNQALGNEVAQYSTQNMANNISYVIWQKQFYSN  
TNSIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

## SEQ ID NO. 6922

STRAIN JM9130013 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH  
TATSMKIETPATNAAGQTTATVDLKTINQVSVADQKVSINLTISEGMTPEAATTIVSPMKTY  
SSAPALKSKEVLAEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS  
PASVAAETPAPVAKVAPVRTVAAPRVASVKVVT PKVETGASPEHVSAPAVPVTTTSPATD  
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAAHPENAGLQPHVAAYKEKVASTYGVN  
EFSTYRAGDPGDHKGGLAVDFIVGKNQALGNEVAQYSTQNMANNISYVIWQKQFYSNTN  
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

PRETTY of: /biotmp/msa237049.2{\*} May 14, 2003 03:04 ..

	1	50
msa237049.2{322_COH1}	-----	dlvkqdnkss
msa237049.2{322_M781}	-----	dlvkqdnkss
msa237049.2{322_M732}	-----	dlvkqdnkss
msa237049.2{322_A909}	-----	dlvkqdnkss
msa237049.2{322_H36B}	-----	dlvkqdnkss
msa237049.2{322_090}	-----	-----

Table 69: Comparative Sequences relating to SAG0032

msa237049.2{322_CJB110}	-----	-----	-----	-----	dlvkqdnkss
msa237049.2{322_18RS21}	-----	-----	-----	-----	dlvkqdnkss
msa237049.2{322_2603}	mnkvvlltst	maasllsvas	vqagetdtw	tartvsevka	dlvkqdnkss
msa237049.2{322_JM9130013}	-----	-----	-----	-----	dlvkqdnkss
msa237049.2{322_1169NT}	-----	-----	-----	-----	dlvkqdnkss
Consensus	*****	*****	*****	*****	-----
msa237049.2{322_COH1}	51				100
msa237049.2{322_M781}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_M732}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_A909}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_H36B}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_090}	-----	-----	-----	-----	ETT LTVTYDQKSH
msa237049.2{322_CJB110}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_18RS21}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_2603}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_JM9130013}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_1169NT}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
Consensus	-----	-----	-----	-----	*****
msa237049.2{322_COH1}	101				150
msa237049.2{322_M781}	TATSMKIETP	ATNAAGQTtA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
msa237049.2{322_M732}	TATSMKIETP	ATNAAGQTtA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
msa237049.2{322_A909}	TATSMKIETP	ATNAAGQTtA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
msa237049.2{322_H36B}	TATSMKIETP	ATNAAGQTtA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
msa237049.2{322_090}	TATSMKIETP	ATNAAGQTpA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
msa237049.2{322_CJB110}	TATSMKIETP	ATNAAGQTpA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
msa237049.2{322_18RS21}	TATSMKIETP	ATNAAGQTtA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
msa237049.2{322_2603}	TATSMKIETP	ATNAAGQTtA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
msa237049.2{322_JM9130013}	TATSMKIETP	ATNAAGQTtA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
msa237049.2{322_1169NT}	TATSMKIETP	ATNAAGQTtA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
Consensus	*****	*****	*****	*****	*****
msa237049.2{322_COH1}	151				200
msa237049.2{322_M781}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	VAANEQVSpA	PVKSIITSEVP
msa237049.2{322_M732}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	VAANEQVSpA	PVKSIITSEVP
msa237049.2{322_A909}	TTIVSPMKTY	SSAPALKSKE	VLAQgQAVSQ	AAANEQVSpA	PVKSIITSEVP
msa237049.2{322_H36B}	TTIVSPMKTY	SSAPALKSKE	VLAQgQAVSQ	AAANEQVSpA	PVKSIITSEVP
msa237049.2{322_090}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	AAANEQVStA	PVKSIITSEVP
msa237049.2{322_CJB110}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	AAANEQVStA	PVKSIITSEVP
msa237049.2{322_18RS21}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	AAANEQVSpA	PVKSIITSEVP
msa237049.2{322_2603}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	AAANEQVSpA	PVKSIITSEVP
msa237049.2{322_JM9130013}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	AAANEQVSpA	PVKSIITSEVP
msa237049.2{322_1169NT}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	AAANEQVSpA	PVKSIITSEVP
Consensus	*****	*****	*****	*****	*****
msa237049.2{322_COH1}	201				250
msa237049.2{322_M781}	AAKEEVkPTQ	TSVSQlTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_M732}	AAKEEVkPTQ	TSVSQlTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_A909}	AAKEEVkPTQ	TSVSQlTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_H36B}	AAKEEVkPTQ	TSVSQlTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_090}	AAKEEVkPTQ	TSVSQlTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_CJB110}	AAKEEVkPTQ	TSVSQlTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_18RS21}	AAKEEVkPTQ	TSVSQlTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_2603}	AAKEEVkPTQ	TSVSQlTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_JM9130013}	AAKEEVkPTQ	TSVSQlTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_1169NT}	AAKEEVrPTQ	TSVSQlTTVS	PASVAAETPA	PVAKVAPVRT	VaapAPRVAS
Consensus	*****	*****	*****	*****	*****
msa237049.2{322_COH1}	251				300
msa237049.2{322_M781}	aKVVTpKVET	GASPEHVsAP	AVPVTTTSpA	TdSKLQATEV	KSVpVAQKAP
msa237049.2{322_M732}	aKVVTpKVET	GASPEHVsAP	AVPVTTTSpA	TdSKLQATEV	KSVpVAQKAP
msa237049.2{322_A909}	aKVVTpKVET	GASPEHVsAP	AVPVTTTStA	TdSKLQATEV	KSVpVAQKAP
msa237049.2{322_H36B}	aKVVTpKVET	GASPEHVsAP	AVPVTTTStA	TdSKLQATEV	KSVpVAQKAP
msa237049.2{322_090}	aKVVTpKVET	GASPEHVsAP	AVPVTTTStA	TdSKLQATEV	KSVpVAQKAP
msa237049.2{322_CJB110}	aKVVTpKVET	GASPEHVsAP	AVPVTTTStA	TdSKLQATEV	KSVpVAQKAP
msa237049.2{322_18RS21}	aKVVTpKVET	GASPEHVsAP	AVPVTTTSpA	TdSKLQATEV	KSVpVAQKAP
msa237049.2{322_2603}	aKVVTpKVET	GASPEHVsAP	AVPVTTTSpA	TdSKLQATEV	KSVpVAQKAP
msa237049.2{322_JM9130013}	aKVVTpKVET	GASPEHVsAP	AVPVTTTSpA	TdSKLQATEV	KSVpVAQKAP
msa237049.2{322_1169NT}	aKVVTpKVET	GASPEHVsAP	AVPVTTTStA	TdSKLQATEV	KSVpVAQKAP
Consensus	*****	*****	*****	*****	*****
msa237049.2{322_COH1}	301				350
msa237049.2{322_M781}	TATpVAQPAS	TTNAVAHPE	NagLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_M732}	TATpVAQPAS	TTNAVAHPE	NagLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_A909}	TATpVAQPAS	TTNAVAHPE	NarLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_H36B}	TATpVAQPAS	TTNAVAHPE	NarLQPHVAA	YKEKVASTYG	VNEFSTYRAG

Table 69: Comparative Sequences relating to SAG0032

msa237049.2{322_090}	TatPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_CJB110}	TatPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_18RS21}	TatPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_2603}	TatPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_JM9130013}	TatPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_1169NT}	TatPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
Consensus	***-*****	*****-***	***-*****	*****-***	*****-***
351 400					
msa237049.2{322_COH1}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_M781}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_M732}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_A909}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_H36B}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_090}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_CJB110}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_18RS21}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_2603}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_JM9130013}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_1169NT}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
Consensus	*****	*****-***	***-*****	*****-***	*****-***
401 450					
msa237049.2{322_COH1}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFYALn
msa237049.2{322_M781}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFYALn
msa237049.2{322_M732}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFYALn
msa237049.2{322_A909}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFYALh
msa237049.2{322_H36B}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFYALh
msa237049.2{322_090}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFYALn
msa237049.2{322_CJB110}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFYALn
msa237049.2{322_18RS21}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFYALn
msa237049.2{322_2603}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFYALn
msa237049.2{322_JM9130013}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFYALn
msa237049.2{322_1169NT}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFYALn
Consensus	*****	*****	*****	*****	*****-***
451 460					
msa237049.2{322_COH1}	RLSRFLYNFY				
msa237049.2{322_M781}	RLSRFLYNFY				
msa237049.2{322_M732}	RLSRFLYNFY				
msa237049.2{322_A909}	RLSRFLYNFY				
msa237049.2{322_H36B}	RLSRFLYNFY				
msa237049.2{322_090}	RLSRFLYNFY				
msa237049.2{322_CJB110}	RLSRFLYNFY				
msa237049.2{322_18RS21}	RLSRFLYNFY				
msa237049.2{322_2603}	RLSRFLYNFY				
msa237049.2{322_JM9130013}	RLSRFLYNFY				
msa237049.2{322_1169NT}	RLSRFLYNFY				
Consensus	*****				

Table 70: Comparative Sequences relating to SAG 1280

SEQ ID. NO. 7001

STRAIN 2603

ATGGGAGGGAAAATGAATCAAGAAGTCTTACTACAAATGATGAGAGCCACTATTCTC  
 GTGATAGAGCCTTGCTTGAGGCATTTTATATATACCAAGCAGAGCATTTTGATGAGGAGT  
 GGGATAGTCTTATTATCATGATTATGACCAATAGGCAAGAAATAAATAAGTCTGTTCAAG  
 TACTTCACTTTGAGACAGATGTTTCAGCTTTTGTCCAGGCTAGTCTTATGATAGTCTC  
 ATGATCTATTGACCTATACACAAGTTTTCGGCCAAAGTGGTCTTCAAAACTAGATAAAC  
 TATCGCCGTCTGAAAAAACTTGGTGTAGAAAGTGGCCTTGTTCAATCTGGCCACTCGTT  
 TTCAATTATTGGATTCCCAATGGACACTACCAAAACCATATCGCCGGATTCACTCTTACAAA  
 AGAGTAGGGGAGCTAATTTGGTCAATGTGTATCGTGTGGCTAATAATTAGCGGATCGTA  
 TTAGTCGAGATATTGAACAGTTTCTCTTAACCTACGAGCCTGAGCTTGAACTAGAGCTG  
 ATGAAACTGTTCTAGAAAAATGAAGAACTGTTGATGAGCACAAAACAGTGTTCATCAAG  
 CAATATCTTTTCGAGAAGAGGGCTCTCTGGTTATTGTCTAGTTTGGATGTAGATTGTCTC  
 AACTAGATGTTCAAAATAGGAAAAACAGTCACTCTGCCAGCTTATGAAGAGTTATCCTTAC  
 GACGTAATTTGAGATTCTAACATATTTTGACCAATTCGAAATGAACGTTCCAAAGTCC  
 CAAGTTTGTAGCAGAGGTGATTTTGACACAGAGATGGAAATGACACCACTCTTGTAGTGGC  
 AGGAAATTACTTACTTATCTCGAAGCTGATGGCAGTCCCTATGAGCTGAAACGAACCTGA  
 CTACAGTCGAAGAAAGGAATTAGAAAAAATTGGACAAGCCATTAGGATAGAAAAATCAAG  
 AAAAATTGACTCAGCTAGGAGATTGATTTATCTCAGTTTGACCCAGACCGAGTCTGTTATT  
 TATTGGATGACAGAGGTGTTTTCGTTTAAAAAATGCAGACCTTGCTTTACTAGGTGGTT  
 ATCCCAAAGCCTCGTAACCTCAACTAGCCCTTGCGACAGAACTACTCCAAATGGGACTAA  
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